

genes which GAM2179 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[30387] Nucleotide sequences of the GAM2179 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2179 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2179 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2179 are further described hereinbelow with reference to Table 1.

[30388] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2179 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[30389] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2180 (GAM2180) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[30390] GAM2180 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2180 was detected is described hereinabove with reference to Figs. 2-8.

[30391] GAM2180 gene, herein designated GAM GENE, and GAM2180 target gene, herein designated GAM TARGET GENE, are human genes contained in the



human genome.

[30392] GAM2180 gene, herein designated GAM GENE, encodes a GAM2180 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2180 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2180 precursor RNA is designated SEQ ID:2157, and is provided hereinbelow with reference to the sequence listing part.

[30393] GAM2180 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2180 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30394] An enzyme complex designated DICER COMPLEX, dices the GAM2180 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2180 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 91%) nucleotide sequence of GAM2180 RNA is designated SEQ ID:4771, and is provided

hereinbelow with reference to the sequence listing part.

[30395] GAM2180 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2180 target RNA, herein designated GAM TARGET RNA. GAM2180 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30396] GAM2180 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2180 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2180 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2180 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2180 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30397] The complementary binding of GAM2180 RNA, herein designated GAM RNA, to target binding sites on GAM2180 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2180 target RNA, herein designated GAM TARGET RNA, into GAM2180 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[30398] It is appreciated that GAM2180 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2180 target genes. The mRNA of each one of this plurality of GAM2180 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2180 RNA, herein designated GAM RNA, and which when bound by GAM2180 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2180 target proteins.

[30399] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2180 gene, herein designated GAM GENE, on one or more GAM2180 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30400] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2180 correlate with, and may be deduced from, the identity of the target genes which GAM2180 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[30401] Nucleotide sequences of the GAM2180 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2180 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2180 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2180 are further described hereinbelow with reference to Table 1.

[30402] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2180 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[30403] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2181 (GAM2181) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[30404] GAM2181 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2181 was detected is described hereinabove with reference to Figs. 2-8.

[30405] GAM2181 gene, herein designated GAM GENE, and GAM2181 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[30406] GAM2181 gene, herein designated GAM GENE, encodes a GAM2181 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2181 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2181 precursor RNA is designated SEQ ID:2158, and is provided hereinbelow with reference to the sequence listing part.

[30407] GAM2181 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2181 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30408] An enzyme complex designated DICER COMPLEX, dices the GAM2181 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2181 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 92%) nucleotide sequence of GAM2181 RNA is designated SEQ ID:4772, and is provided hereinbelow with reference to the sequence listing part.

[30409] GAM2181 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2181 target RNA, herein designated GAM TARGET RNA. GAM2181 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30410] GAM2181 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2181 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2181 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2181 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2181 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30411] The complementary binding of GAM2181 RNA, herein designated GAM RNA, to target binding sites on GAM2181 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2181 target RNA, herein designated GAM TARGET RNA, into GAM2181 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[30412] It is appreciated that GAM2181 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2181 target genes. The mRNA of each one of this plurality of GAM2181 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2181 RNA, herein designated GAM RNA, and which when bound by GAM2181 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2181 target proteins.

[30413] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2181 gene, herein designated GAM GENE, on one or more GAM2181 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30414] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2181 correlate with, and may be deduced from, the identity of the target genes which GAM2181 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[30415] Nucleotide sequences of the GAM2181 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2181 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2181 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2181 are further described hereinbelow with reference to Table 1.

[30416] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2181 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[30417] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2182 (GAM2182) gene, which modulates



expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[30418] GAM2182 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2182 was detected is described hereinabove with reference to Figs. 2-8.

[30419] GAM2182 gene, herein designated GAM GENE, and GAM2182 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[30420] GAM2182 gene, herein designated GAM GENE, encodes a GAM2182 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2182 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2182 precursor RNA is designated SEQ ID:2159, and is provided hereinbelow with reference to the sequence listing part.

[30421] GAM2182 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2182 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

- [30422] An enzyme complex designated DICER COMPLEX, dices the GAM2182 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2182 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 83%) nucleotide sequence of GAM2182 RNA is designated SEQ ID:4773, and is provided hereinbelow with reference to the sequence listing part.
- [30423] GAM2182 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2182 target RNA, herein designated GAM TARGET RNA. GAM2182 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [30424] GAM2182 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2182 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2182 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2182 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2182 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30425] The complementary binding of GAM2182 RNA, herein designated GAM RNA, to target binding sites on GAM2182 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2182 target RNA, herein designated GAM TARGET RNA, into GAM2182 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[30426] It is appreciated that GAM2182 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2182 target genes. The mRNA of each one of this plurality of GAM2182 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2182 RNA, herein designated GAM RNA, and which when bound by GAM2182 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2182 target proteins.

[30427] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2182 gene, herein designated GAM GENE, on one or more GAM2182 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30428] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2182 correlate with, and may be deduced from, the identity of the target genes which GAM2182 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[30429] Nucleotide sequences of the GAM2182 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2182 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2182 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2182 are further described hereinbelow with reference to Table 1.

[30430] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2182 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

[30431] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2183 (GAM2183) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[30432] GAM2183 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2183 was detected is described hereinabove with reference to Figs. 2-8.

[30433] GAM2183 gene, herein designated GAM GENE, and GAM2183 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[30434] GAM2183 gene, herein designated GAM GENE, encodes a GAM2183 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2183 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2183 precursor RNA is designated SEQ ID:2160, and is provided hereinbelow with reference to the sequence listing part.

[30435] GAM2183 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2183 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30436] An enzyme complex designated DICER COMPLEX, dices the GAM2183 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2183 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 85%) nucleotide sequence of GAM2183 RNA is designated SEQ ID:4774, and is provided hereinbelow with reference to the sequence listing part.

[30437] GAM2183 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2183 target RNA, herein designated GAM TARGET RNA. GAM2183 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30438] GAM2183 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2183 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2183 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2183 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2183 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30439] The complementary binding of GAM2183 RNA, herein designated GAM RNA, to target binding sites on GAM2183 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2183 target RNA, herein designated GAM TARGET RNA, into GAM2183 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[30440] It is appreciated that GAM2183 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2183 target genes. The mRNA of each one of this plurality of GAM2183 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2183 RNA, herein designated GAM RNA, and which when bound by GAM2183 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2183 target proteins.

[30441] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2183 gene, herein designated GAM GENE, on one or more GAM2183 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30442] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2183 correlate with, and may be deduced from, the identity of the target genes which GAM2183 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[30443] Nucleotide sequences of the GAM2183 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2183 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2183 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2183 are further described hereinbelow with reference to Table 1.



- [30444] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2183 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.
- [30445] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2184 (GAM2184) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.
- [30446] GAM2184 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2184 was detected is described hereinabove with reference to Figs. 2-8.
- [30447] GAM2184 gene, herein designated GAM GENE, and GAM2184 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.
- [30448] GAM2184 gene, herein designated GAM GENE, encodes a GAM2184 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2184 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2184 precursor RNA is designated SEQ ID:2161, and is provided hereinbelow with reference to the sequence listing part.

[30449] GAM2184 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2184 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30450] An enzyme complex designated DICER COMPLEX, dices the GAM2184 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2184 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2184 RNA is designated SEQ ID:4775, and is provided hereinbelow with reference to the sequence listing part.

[30451] GAM2184 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2184 target RNA, herein designated GAM TARGET RNA. GAM2184 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30452] GAM2184 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2184 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2184 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2184 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2184 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30453] The complementary binding of GAM2184 RNA, herein designated GAM RNA, to target binding sites on GAM2184 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2184 target RNA, herein designated GAM TARGET RNA, into GAM2184 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[30454] It is appreciated that GAM2184 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2184 target genes. The

mRNA of each one of this plurality of GAM2184 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2184 RNA, herein designated GAM RNA, and which when bound by GAM2184 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2184 target proteins.

[30455] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2184 gene, herein designated GAM GENE, on one or more GAM2184 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30456] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2184 correlate with, and may be deduced from, the identity of the target genes which GAM2184 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[30457] Nucleotide sequences of the GAM2184 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2184 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2184 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2184 are further described hereinbelow with reference to Table 1.

[30458] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2184 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[30459] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2185 (GAM2185) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[30460] GAM2185 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2185 was detected is described hereinabove with reference to Figs. 2-8.

[30461] GAM2185 gene, herein designated GAM GENE, and GAM2185 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[30462] GAM2185 gene, herein designated GAM GENE, encodes a GAM2185 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2185 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2185 precursor RNA is designated SEQ ID:2162, and is provided hereinbelow with reference to the sequence listing part.

[30463] GAM2185 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2185 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30464] An enzyme complex designated DICER COMPLEX, dices the GAM2185 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2185 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2185 RNA is designated SEQ ID:4776, and is provided hereinbelow with reference to the sequence listing part.

[30465] GAM2185 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2185 target RNA, herein designated GAM TARGET RNA. GAM2185 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30466] GAM2185 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2185 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2185 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2185 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2185 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30467] The complementary binding of GAM2185 RNA, herein designated GAM RNA, to target binding sites on GAM2185 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2185 target RNA, herein designated GAM TARGET RNA, into GAM2185 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[30468] It is appreciated that GAM2185 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2185 target genes. The mRNA of each one of this plurality of GAM2185 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2185 RNA, herein designated GAM RNA, and which when bound by GAM2185 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2185 target proteins.

[30469] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2185 gene, herein designated GAM GENE, on one or more GAM2185 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30470] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2185 correlate with, and may be deduced from, the identity of the target



genes which GAM2185 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[30471] Nucleotide sequences of the GAM2185 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2185 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2185 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2185 are further described hereinbelow with reference to Table 1.

[30472] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2185 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[30473] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2186 (GAM2186) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[30474] GAM2186 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2186 was detected is described hereinabove with reference to Figs. 2-8.

[30475] GAM2186 gene, herein designated GAM GENE, and GAM2186 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

[30476] GAM2186 gene, herein designated GAM GENE, encodes a GAM2186 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2186 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2186 precursor RNA is designated SEQ ID:2163, and is provided hereinbelow with reference to the sequence listing part.

[30477] GAM2186 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2186 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30478] An enzyme complex designated DICER COMPLEX, dices the GAM2186 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2186 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 92%) nucleotide sequence of GAM2186 RNA is designated SEQ ID:4777, and is provided

hereinbelow with reference to the sequence listing part.

[30479] GAM2186 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2186 target RNA, herein designated GAM TARGET RNA. GAM2186 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30480] GAM2186 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2186 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2186 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2186 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2186 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30481] The complementary binding of GAM2186 RNA, herein designated GAM RNA, to target binding sites on GAM2186 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2186 target RNA, herein designated GAM TARGET RNA, into GAM2186 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[30482] It is appreciated that GAM2186 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2186 target genes. The mRNA of each one of this plurality of GAM2186 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2186 RNA, herein designated GAM RNA, and which when bound by GAM2186 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2186 target proteins.

[30483] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2186 gene, herein designated GAM GENE, on one or more GAM2186 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30484] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2186 correlate with, and may be deduced from, the identity of the target genes which GAM2186 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[30485] Nucleotide sequences of the GAM2186 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2186 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2186 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2186 are further described hereinbelow with reference to Table 1.

[30486] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2186 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[30487] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2187 (GAM2187) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[30488] GAM2187 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2187 was detected is described hereinabove with reference to Figs. 2-8.

[30489] GAM2187 gene, herein designated GAM GENE, and GAM2187 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[30490] GAM2187 gene, herein designated GAM GENE, encodes a GAM2187 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2187 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2187 precursor RNA is designated SEQ ID:2164, and is provided hereinbelow with reference to the sequence listing part.

[30491] GAM2187 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2187 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30492] An enzyme complex designated DICER COMPLEX, dices the GAM2187 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2187 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of GAM2187 RNA is designated SEQ ID:4778, and is provided hereinbelow with reference to the sequence listing part.

[30493] GAM2187 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2187 target RNA, herein designated GAM TARGET RNA. GAM2187 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30494] GAM2187 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2187 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2187 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2187 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2187 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30495] The complementary binding of GAM2187 RNA, herein designated GAM RNA, to target binding sites on GAM2187 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2187 target RNA, herein designated GAM TARGET RNA, into GAM2187 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[30496] It is appreciated that GAM2187 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2187 target genes. The mRNA of each one of this plurality of GAM2187 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2187 RNA, herein designated GAM RNA, and which when bound by GAM2187 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2187 target proteins.

[30497] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2187 gene, herein designated GAM GENE, on one or more GAM2187 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary



binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30498] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2187 correlate with, and may be deduced from, the identity of the target genes which GAM2187 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[30499] Nucleotide sequences of the GAM2187 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2187 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2187 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2187 are further described hereinbelow with reference to Table 1.

[30500] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2187 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[30501] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2188 (GAM2188) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[30502] GAM2188 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2188 was detected is described hereinabove with reference to Figs. 2-8.

[30503] GAM2188 gene, herein designated GAM GENE, and GAM2188 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[30504] GAM2188 gene, herein designated GAM GENE, encodes a GAM2188 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2188 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2188 precursor RNA is designated SEQ ID:2165, and is provided hereinbelow with reference to the sequence listing part.

[30505] GAM2188 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2188 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30506] An enzyme complex designated DICER COMPLEX, dices the GAM2188 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2188 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of GAM2188 RNA is designated SEQ ID:4779, and is provided hereinbelow with reference to the sequence listing part.

[30507] GAM2188 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2188 target RNA, herein designated GAM TARGET RNA. GAM2188 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30508] GAM2188 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2188 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2188 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2188 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2188 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30509] The complementary binding of GAM2188 RNA, herein designated GAM RNA, to target binding sites on GAM2188 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2188 target RNA, herein designated GAM TARGET RNA, into GAM2188 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[30510] It is appreciated that GAM2188 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2188 target genes. The mRNA of each one of this plurality of GAM2188 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2188 RNA, herein designated GAM RNA, and which when bound by GAM2188 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2188 target proteins.

[30511] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2188 gene, herein designated GAM GENE, on one or more GAM2188 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30512] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2188 correlate with, and may be deduced from, the identity of the target genes which GAM2188 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[30513] Nucleotide sequences of the GAM2188 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2188 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2188 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2188 are further described hereinbelow with reference to Table 1.

[30514] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2188 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

[30515] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2189 (GAM2189) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[30516] GAM2189 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2189 was detected is described hereinabove with reference to Figs. 2-8.

[30517] GAM2189 gene, herein designated GAM GENE, and GAM2189 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[30518] GAM2189 gene, herein designated GAM GENE, encodes a GAM2189 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2189 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2189 precursor RNA is designated SEQ ID:2166, and is provided hereinbelow with reference to the sequence listing part.

[30519] GAM2189 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2189 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30520] An enzyme complex designated DICER COMPLEX, dices the GAM2189 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2189 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 78%) nucleotide sequence of GAM2189 RNA is designated SEQ ID:4780, and is provided hereinbelow with reference to the sequence listing part.

[30521] GAM2189 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2189 target RNA, herein designated GAM TARGET RNA. GAM2189 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30522] GAM2189 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2189 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2189 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2189 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2189 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30523] The complementary binding of GAM2189 RNA, herein designated GAM RNA, to target binding sites on GAM2189 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2189 target RNA, herein designated GAM TARGET RNA, into GAM2189 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[30524] It is appreciated that GAM2189 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2189 target genes. The mRNA of each one of this plurality of GAM2189 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2189 RNA, herein designated GAM RNA, and which when bound by GAM2189 RNA, herein designated GAM RNA,



causes inhibition of translation of respective one or more GAM2189 target proteins.

[30525] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2189 gene, herein designated GAM GENE, on one or more GAM2189 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30526] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2189 correlate with, and may be deduced from, the identity of the target genes which GAM2189 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[30527] Nucleotide sequences of the GAM2189 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2189 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2189 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2189 are further described hereinbelow with reference to Table 1.

[30528] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2189 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[30529] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2190 (GAM2190) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[30530] GAM2190 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2190 was detected is described hereinabove with reference to Figs. 2-8.

[30531] GAM2190 gene, herein designated GAM GENE, and GAM2190 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[30532] GAM2190 gene, herein designated GAM GENE, encodes a GAM2190 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2190 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2190 precursor RNA is designated SEQ ID:2167, and is provided hereinbelow with reference to the sequence listing part.

[30533] GAM2190 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2190 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30534] An enzyme complex designated DICER COMPLEX, dices the GAM2190 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2190 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2190 RNA is designated SEQ ID:4781, and is provided hereinbelow with reference to the sequence listing part.

[30535] GAM2190 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2190 target RNA, herein designated GAM TARGET RNA. GAM2190 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30536] GAM2190 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2190 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2190 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2190 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2190 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30537] The complementary binding of GAM2190 RNA, herein designated GAM RNA, to target binding sites on GAM2190 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2190 target RNA, herein designated GAM TARGET RNA, into GAM2190 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[30538] It is appreciated that GAM2190 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2190 target genes. The

mRNA of each one of this plurality of GAM2190 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2190 RNA, herein designated GAM RNA, and which when bound by GAM2190 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2190 target proteins.

[30539] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2190 gene, herein designated GAM GENE, on one or more GAM2190 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30540] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2190 correlate with, and may be deduced from, the identity of the target genes which GAM2190 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[30541] Nucleotide sequences of the GAM2190 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2190 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2190 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2190 are further described hereinbelow with reference to Table 1.

[30542] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2190 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[30543] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2191 (GAM2191) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[30544] GAM2191 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2191 was detected is described hereinabove with reference to Figs. 2-8.

[30545] GAM2191 gene, herein designated GAM GENE, and GAM2191 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[30546] GAM2191 gene, herein designated GAM GENE, encodes a GAM2191 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2191 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2191 precursor RNA is designated SEQ ID:2168, and is provided hereinbelow with reference to the sequence listing part.

[30547] GAM2191 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2191 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30548] An enzyme complex designated DICER COMPLEX, dices the GAM2191 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2191 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2191 RNA is designated SEQ ID:4782, and is provided hereinbelow with reference to the sequence listing part.

[30549] GAM2191 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2191 target RNA, herein designated GAM TARGET RNA. GAM2191 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30550] GAM2191 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2191 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2191 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2191 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2191 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30551] The complementary binding of GAM2191 RNA, herein designated GAM RNA, to target binding sites on GAM2191 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2191 target RNA, herein designated GAM TARGET RNA, into GAM2191 target protein, herein



designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[30552] It is appreciated that GAM2191 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2191 target genes. The mRNA of each one of this plurality of GAM2191 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2191 RNA, herein designated GAM RNA, and which when bound by GAM2191 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2191 target proteins.

[30553] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2191 gene, herein designated GAM GENE, on one or more GAM2191 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30554] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2191 correlate with, and may be deduced from, the identity of the target

genes which GAM2191 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[30555] Nucleotide sequences of the GAM2191 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2191 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2191 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2191 are further described hereinbelow with reference to Table 1.

[30556] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2191 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[30557] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2192 (GAM2192) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[30558] GAM2192 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2192 was detected is described hereinabove with reference to Figs. 2-8.

[30559] GAM2192 gene, herein designated GAM GENE, and GAM2192 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

[30560] GAM2192 gene, herein designated GAM GENE, encodes a GAM2192 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2192 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2192 precursor RNA is designated SEQ ID:2169, and is provided hereinbelow with reference to the sequence listing part.

[30561] GAM2192 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2192 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30562] An enzyme complex designated DICER COMPLEX, dices the GAM2192 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2192 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 25%) nucleotide sequence of GAM2192 RNA is designated SEQ ID:4783, and is provided

hereinbelow with reference to the sequence listing part.

[30563] GAM2192 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2192 target RNA, herein designated GAM TARGET RNA. GAM2192 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30564] GAM2192 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2192 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2192 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2192 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2192 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30565] The complementary binding of GAM2192 RNA, herein designated GAM RNA, to target binding sites on GAM2192 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2192 target RNA, herein designated GAM TARGET RNA, into GAM2192 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[30566] It is appreciated that GAM2192 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2192 target genes. The mRNA of each one of this plurality of GAM2192 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2192 RNA, herein designated GAM RNA, and which when bound by GAM2192 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2192 target proteins.

[30567] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2192 gene, herein designated GAM GENE, on one or more GAM2192 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30568] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2192 correlate with, and may be deduced from, the identity of the target genes which GAM2192 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[30569] Nucleotide sequences of the GAM2192 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2192 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2192 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2192 are further described hereinbelow with reference to Table 1.

[30570] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2192 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[30571] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2193 (GAM2193) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[30572] GAM2193 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2193 was detected is described hereinabove with reference to Figs. 2-8.

[30573] GAM2193 gene, herein designated GAM GENE, and GAM2193 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[30574] GAM2193 gene, herein designated GAM GENE, encodes a GAM2193 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2193 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2193 precursor RNA is designated SEQ ID:2170, and is provided hereinbelow with reference to the sequence listing part.

[30575] GAM2193 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2193 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30576] An enzyme complex designated DICER COMPLEX, dices the GAM2193 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2193 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2193 RNA is designated SEQ ID:4785, and is provided hereinbelow with reference to the sequence listing part.

[30577] GAM2193 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2193 target RNA, herein designated GAM TARGET RNA. GAM2193 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30578] GAM2193 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2193 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2193 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2193 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2193 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target



binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30579] The complementary binding of GAM2193 RNA, herein designated GAM RNA, to target binding sites on GAM2193 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2193 target RNA, herein designated GAM TARGET RNA, into GAM2193 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[30580] It is appreciated that GAM2193 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2193 target genes. The mRNA of each one of this plurality of GAM2193 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2193 RNA, herein designated GAM RNA, and which when bound by GAM2193 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2193 target proteins.

[30581] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2193 gene, herein designated GAM GENE, on one or more GAM2193 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30582] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2193 correlate with, and may be deduced from, the identity of the target genes which GAM2193 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[30583] Nucleotide sequences of the GAM2193 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2193 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2193 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2193 are further described hereinbelow with reference to Table 1.

[30584] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2193 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[30585] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2194 (GAM2194) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[30586] GAM2194 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2194 was detected is described hereinabove with reference to Figs. 2-8.

[30587] GAM2194 gene, herein designated GAM GENE, and GAM2194 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[30588] GAM2194 gene, herein designated GAM GENE, encodes a GAM2194 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2194 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2194 precursor RNA is designated SEQ ID:2171, and is provided hereinbelow with reference to the sequence listing part.

[30589] GAM2194 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2194 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30590] An enzyme complex designated DICER COMPLEX, dices the GAM2194 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2194 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2194 RNA is designated SEQ ID:4784, and is provided hereinbelow with reference to the sequence listing part.

[30591] GAM2194 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2194 target RNA, herein designated GAM TARGET RNA. GAM2194 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30592] GAM2194 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2194 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2194 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2194 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2194 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30593] The complementary binding of GAM2194 RNA, herein designated GAM RNA, to target binding sites on GAM2194 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2194 target RNA, herein designated GAM TARGET RNA, into GAM2194 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[30594] It is appreciated that GAM2194 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2194 target genes. The mRNA of each one of this plurality of GAM2194 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2194 RNA, herein designated GAM RNA, and which when bound by GAM2194 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2194 target proteins.

[30595] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2194 gene, herein designated GAM GENE, on one or more GAM2194 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30596] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2194 correlate with, and may be deduced from, the identity of the target genes which GAM2194 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[30597] Nucleotide sequences of the GAM2194 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2194 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2194 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2194 are further described hereinbelow with reference to Table 1.

[30598] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2194 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[30599] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2195 (GAM2195) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[30600] GAM2195 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2195 was detected is described hereinabove with reference to Figs. 2-8.

[30601] GAM2195 gene, herein designated GAM GENE, and GAM2195 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[30602] GAM2195 gene, herein designated GAM GENE, encodes a GAM2195 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2195 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2195 precursor RNA is designated SEQ ID:2172, and is provided hereinbelow with reference to the sequence listing part.

[30603] GAM2195 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2195 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30604] An enzyme complex designated DICER COMPLEX, dices the GAM2195 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2195 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer



together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2195 RNA is designated SEQ ID:4787, and is provided hereinbelow with reference to the sequence listing part.

[30605] GAM2195 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2195 target RNA, herein designated GAM TARGET RNA. GAM2195 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30606] GAM2195 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2195 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2195 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2195 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2195 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or

in both 3UTR and 5UTR regions.

[30607] The complementary binding of GAM2195 RNA, herein designated GAM RNA, to target binding sites on GAM2195 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2195 target RNA, herein designated GAM TARGET RNA, into GAM2195 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[30608] It is appreciated that GAM2195 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2195 target genes. The mRNA of each one of this plurality of GAM2195 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2195 RNA, herein designated GAM RNA, and which when bound by GAM2195 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2195 target proteins.

[30609] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2195 gene, herein designated GAM GENE, on one or more GAM2195 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes

are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30610] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2195 correlate with, and may be deduced from, the identity of the target genes which GAM2195 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[30611] Nucleotide sequences of the GAM2195 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2195 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2195 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2195 are further described hereinbelow with reference to Table 1.

[30612] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2195 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[30613] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2196 (GAM2196) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

- [30614] GAM2196 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2196 was detected is described hereinabove with reference to Figs. 2-8.
- [30615] GAM2196 gene, herein designated GAM GENE, and GAM2196 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.
- [30616] GAM2196 gene, herein designated GAM GENE, encodes a GAM2196 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2196 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2196 precursor RNA is designated SEQ ID:2173, and is provided hereinbelow with reference to the sequence listing part.
- [30617] GAM2196 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2196 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.
- [30618] An enzyme complex designated DICER COMPLEX, dices the GAM2196 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2196 RNA, herein designated GAM RNA, a single stranded

~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 78%) nucleotide sequence of GAM2196 RNA is designated SEQ ID:4786, and is provided hereinbelow with reference to the sequence listing part.

[30619] GAM2196 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2196 target RNA, herein designated GAM TARGET RNA. GAM2196 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30620] GAM2196 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2196 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2196 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2196 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2196 target RNA, herein designated GAM

TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30621] The complementary binding of GAM2196 RNA, herein designated GAM RNA, to target binding sites on GAM2196 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2196 target RNA, herein designated GAM TARGET RNA, into GAM2196 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[30622] It is appreciated that GAM2196 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2196 target genes. The mRNA of each one of this plurality of GAM2196 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2196 RNA, herein designated GAM RNA, and which when bound by GAM2196 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2196 target proteins.

[30623] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2196 gene, herein designated GAM GENE, on one or more GAM2196 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with

reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30624] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2196 correlate with, and may be deduced from, the identity of the target genes which GAM2196 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[30625] Nucleotide sequences of the GAM2196 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2196 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2196 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2196 are further described hereinbelow with reference to Table 1.

[30626] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2196 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[30627] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as

Genomic Address Messenger 2197 (GAM2197) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[30628] GAM2197 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2197 was detected is described hereinabove with reference to Figs. 2-8.

[30629] GAM2197 gene, herein designated GAM GENE, and GAM2197 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[30630] GAM2197 gene, herein designated GAM GENE, encodes a GAM2197 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2197 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2197 precursor RNA is designated SEQ ID:2174, and is provided hereinbelow with reference to the sequence listing part.

[30631] GAM2197 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2197 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.



- [30632] An enzyme complex designated DICER COMPLEX, dices the GAM2197 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2197 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 83%) nucleotide sequence of GAM2197 RNA is designated SEQ ID:4788, and is provided hereinbelow with reference to the sequence listing part.
- [30633] GAM2197 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2197 target RNA, herein designated GAM TARGET RNA. GAM2197 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [30634] GAM2197 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2197 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2197 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2197 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2197 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30635] The complementary binding of GAM2197 RNA, herein designated GAM RNA, to target binding sites on GAM2197 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2197 target RNA, herein designated GAM TARGET RNA, into GAM2197 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[30636] It is appreciated that GAM2197 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2197 target genes. The mRNA of each one of this plurality of GAM2197 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2197 RNA, herein designated GAM RNA, and which when bound by GAM2197 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2197 target proteins.

[30637] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2197 gene, herein designated GAM GENE, on one or more GAM2197 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30638] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2197 correlate with, and may be deduced from, the identity of the target genes which GAM2197 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[30639] Nucleotide sequences of the GAM2197 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2197 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2197 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2197 are further described hereinbelow with reference to Table 1.

[30640] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2197 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

[30641] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2198 (GAM2198) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[30642] GAM2198 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2198 was detected is described hereinabove with reference to Figs. 2-8.

[30643] GAM2198 gene, herein designated GAM GENE, and GAM2198 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[30644] GAM2198 gene, herein designated GAM GENE, encodes a GAM2198 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2198 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2198 precursor RNA is designated SEQ ID:2175, and is provided hereinbelow with reference to the sequence listing part.

[30645] GAM2198 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2198 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30646] An enzyme complex designated DICER COMPLEX, dices the GAM2198 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2198 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of GAM2198 RNA is designated SEQ ID:4789, and is provided hereinbelow with reference to the sequence listing part.

[30647] GAM2198 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2198 target RNA, herein designated GAM TARGET RNA. GAM2198 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30648] GAM2198 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2198 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2198 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2198 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2198 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30649] The complementary binding of GAM2198 RNA, herein designated GAM RNA, to target binding sites on GAM2198 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2198 target RNA, herein designated GAM TARGET RNA, into GAM2198 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[30650] It is appreciated that GAM2198 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2198 target genes. The mRNA of each one of this plurality of GAM2198 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2198 RNA, herein designated GAM RNA, and which when bound by GAM2198 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2198 target proteins.

[30651] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2198 gene, herein designated GAM GENE, on one or more GAM2198 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30652] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2198 correlate with, and may be deduced from, the identity of the target genes which GAM2198 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[30653] Nucleotide sequences of the GAM2198 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2198 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2198 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2198 are further described hereinbelow with reference to Table 1.

[30654] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2198 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[30655] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2199 (GAM2199) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[30656] GAM2199 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2199 was detected is described hereinabove with reference to Figs. 2-8.

[30657] GAM2199 gene, herein designated GAM GENE, and GAM2199 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[30658] GAM2199 gene, herein designated GAM GENE, encodes a GAM2199 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2199 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2199 precursor RNA is designated SEQ ID:2176, and is provided hereinbelow with reference to the sequence listing part.



[30659] GAM2199 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2199 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30660] An enzyme complex designated DICER COMPLEX, dices the GAM2199 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2199 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 88%) nucleotide sequence of GAM2199 RNA is designated SEQ ID:4790, and is provided hereinbelow with reference to the sequence listing part.

[30661] GAM2199 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2199 target RNA, herein designated GAM TARGET RNA. GAM2199 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30662] GAM2199 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2199 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2199 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2199 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2199 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30663] The complementary binding of GAM2199 RNA, herein designated GAM RNA, to target binding sites on GAM2199 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2199 target RNA, herein designated GAM TARGET RNA, into GAM2199 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[30664] It is appreciated that GAM2199 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2199 target genes. The

mRNA of each one of this plurality of GAM2199 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2199 RNA, herein designated GAM RNA, and which when bound by GAM2199 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2199 target proteins.

[30665] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2199 gene, herein designated GAM GENE, on one or more GAM2199 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30666] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2199 correlate with, and may be deduced from, the identity of the target genes which GAM2199 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[30667] Nucleotide sequences of the GAM2199 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2199 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2199 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2199 are further described hereinbelow with reference to Table 1.

[30668] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2199 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[30669] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2200 (GAM2200) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[30670] GAM2200 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2200 was detected is described hereinabove with reference to Figs. 2-8.

[30671] GAM2200 gene, herein designated GAM GENE, and GAM2200 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[30672] GAM2200 gene, herein designated GAM GENE, encodes a GAM2200 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2200 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2200 precursor RNA is designated SEQ ID:2177, and is provided hereinbelow with reference to the sequence listing part.

[30673] GAM2200 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2200 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30674] An enzyme complex designated DICER COMPLEX, dices the GAM2200 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2200 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 78%) nucleotide sequence of GAM2200 RNA is designated SEQ ID:4791, and is provided hereinbelow with reference to the sequence listing part.

[30675] GAM2200 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2200 target RNA, herein designated GAM TARGET RNA. GAM2200 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30676] GAM2200 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2200 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2200 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2200 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2200 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30677] The complementary binding of GAM2200 RNA, herein designated GAM RNA, to target binding sites on GAM2200 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2200 target RNA, herein designated GAM TARGET RNA, into GAM2200 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[30678] It is appreciated that GAM2200 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2200 target genes. The mRNA of each one of this plurality of GAM2200 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2200 RNA, herein designated GAM RNA, and which when bound by GAM2200 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2200 target proteins.

[30679] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2200 gene, herein designated GAM GENE, on one or more GAM2200 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30680] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2200 correlate with, and may be deduced from, the identity of the target

genes which GAM2200 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[30681] Nucleotide sequences of the GAM2200 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2200 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2200 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2200 are further described hereinbelow with reference to Table 1.

[30682] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2200 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[30683] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2201 (GAM2201) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[30684] GAM2201 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2201 was detected is described hereinabove with reference to Figs. 2-8.

[30685] GAM2201 gene, herein designated GAM GENE, and GAM2201 target gene, herein designated GAM TARGET GENE, are human genes contained in the



human genome.

[30686] GAM2201 gene, herein designated GAM GENE, encodes a GAM2201 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2201 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2201 precursor RNA is designated SEQ ID:2178, and is provided hereinbelow with reference to the sequence listing part.

[30687] GAM2201 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2201 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30688] An enzyme complex designated DICER COMPLEX, dices the GAM2201 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2201 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 85%) nucleotide sequence of GAM2201 RNA is designated SEQ ID:4792, and is provided

hereinbelow with reference to the sequence listing part.

[30689] GAM2201 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2201 target RNA, herein designated GAM TARGET RNA. GAM2201 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30690] GAM2201 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2201 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2201 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2201 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2201 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30691] The complementary binding of GAM2201 RNA, herein designated GAM RNA, to target binding sites on GAM2201 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2201 target RNA, herein designated GAM TARGET RNA, into GAM2201 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[30692] It is appreciated that GAM2201 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2201 target genes. The mRNA of each one of this plurality of GAM2201 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2201 RNA, herein designated GAM RNA, and which when bound by GAM2201 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2201 target proteins.

[30693] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2201 gene, herein designated GAM GENE, on one or more GAM2201 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30694] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2201 correlate with, and may be deduced from, the identity of the target genes which GAM2201 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[30695] Nucleotide sequences of the GAM2201 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2201 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2201 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2201 are further described hereinbelow with reference to Table 1.

[30696] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2201 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[30697] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2202 (GAM2202) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[30698] GAM2202 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2202 was detected is described hereinabove with reference to Figs. 2-8.

[30699] GAM2202 gene, herein designated GAM GENE, and GAM2202 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[30700] GAM2202 gene, herein designated GAM GENE, encodes a GAM2202 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2202 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2202 precursor RNA is designated SEQ ID:2179, and is provided hereinbelow with reference to the sequence listing part.

[30701] GAM2202 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2202 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30702] An enzyme complex designated DICER COMPLEX, dices the GAM2202 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2202 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of GAM2202 RNA is designated SEQ ID:4793, and is provided hereinbelow with reference to the sequence listing part.

[30703] GAM2202 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2202 target RNA, herein designated GAM TARGET RNA. GAM2202 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30704] GAM2202 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2202 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2202 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2202 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2202 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30705] The complementary binding of GAM2202 RNA, herein designated GAM RNA, to target binding sites on GAM2202 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2202 target RNA, herein designated GAM TARGET RNA, into GAM2202 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[30706] It is appreciated that GAM2202 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2202 target genes. The mRNA of each one of this plurality of GAM2202 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2202 RNA, herein designated GAM RNA, and which when bound by GAM2202 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2202 target proteins.

[30707] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2202 gene, herein designated GAM GENE, on one or more GAM2202 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30708] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2202 correlate with, and may be deduced from, the identity of the target genes which GAM2202 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[30709] Nucleotide sequences of the GAM2202 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2202 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2202 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2202 are further described hereinbelow with reference to Table 1.

[30710] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2202 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[30711] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2203 (GAM2203) gene, which modulates



expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[30712] GAM2203 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2203 was detected is described hereinabove with reference to Figs. 2-8.

[30713] GAM2203 gene, herein designated GAM GENE, and GAM2203 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[30714] GAM2203 gene, herein designated GAM GENE, encodes a GAM2203 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2203 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2203 precursor RNA is designated SEQ ID:2180, and is provided hereinbelow with reference to the sequence listing part.

[30715] GAM2203 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2203 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

- [30716] An enzyme complex designated DICER COMPLEX, dices the GAM2203 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2203 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 83%) nucleotide sequence of GAM2203 RNA is designated SEQ ID:4794, and is provided hereinbelow with reference to the sequence listing part.
- [30717] GAM2203 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2203 target RNA, herein designated GAM TARGET RNA. GAM2203 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [30718] GAM2203 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2203 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2203 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2203 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2203 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30719] The complementary binding of GAM2203 RNA, herein designated GAM RNA, to target binding sites on GAM2203 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2203 target RNA, herein designated GAM TARGET RNA, into GAM2203 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[30720] It is appreciated that GAM2203 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2203 target genes. The mRNA of each one of this plurality of GAM2203 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2203 RNA, herein designated GAM RNA, and which when bound by GAM2203 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2203 target proteins.

[30721] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2203 gene, herein designated GAM GENE, on one or more GAM2203 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30722] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2203 correlate with, and may be deduced from, the identity of the target genes which GAM2203 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[30723] Nucleotide sequences of the GAM2203 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2203 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2203 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2203 are further described hereinbelow with reference to Table 1.

[30724] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2203 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

- [30725] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2204 (GAM2204) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.
- [30726] GAM2204 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2204 was detected is described hereinabove with reference to Figs. 2-8.
- [30727] GAM2204 gene, herein designated GAM GENE, and GAM2204 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.
- [30728] GAM2204 gene, herein designated GAM GENE, encodes a GAM2204 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2204 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2204 precursor RNA is designated SEQ ID:2181, and is provided hereinbelow with reference to the sequence listing part.
- [30729] GAM2204 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2204 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30730] An enzyme complex designated DICER COMPLEX, dices the GAM2204 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2204 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2204 RNA is designated SEQ ID:4795, and is provided hereinbelow with reference to the sequence listing part.

[30731] GAM2204 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2204 target RNA, herein designated GAM TARGET RNA. GAM2204 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30732] GAM2204 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2204 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2204 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2204 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2204 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30733] The complementary binding of GAM2204 RNA, herein designated GAM RNA, to target binding sites on GAM2204 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2204 target RNA, herein designated GAM TARGET RNA, into GAM2204 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[30734] It is appreciated that GAM2204 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2204 target genes. The mRNA of each one of this plurality of GAM2204 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2204 RNA, herein designated GAM RNA, and which when bound by GAM2204 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2204 target proteins.

[30735] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2204 gene, herein designated GAM GENE, on one or more GAM2204 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30736] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2204 correlate with, and may be deduced from, the identity of the target genes which GAM2204 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[30737] Nucleotide sequences of the GAM2204 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2204 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2204 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2204 are further described hereinbelow with reference to Table 1.



[30738] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2204 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[30739] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2205 (GAM2205) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[30740] GAM2205 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2205 was detected is described hereinabove with reference to Figs. 2-8.

[30741] GAM2205 gene, herein designated GAM GENE, and GAM2205 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[30742] GAM2205 gene, herein designated GAM GENE, encodes a GAM2205 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2205 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2205 precursor RNA is designated SEQ ID:2182, and is provided hereinbelow with reference to the sequence listing part.

[30743] GAM2205 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2205 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30744] An enzyme complex designated DICER COMPLEX, dices the GAM2205 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2205 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of GAM2205 RNA is designated SEQ ID:4796, and is provided hereinbelow with reference to the sequence listing part.

[30745] GAM2205 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2205 target RNA, herein designated GAM TARGET RNA. GAM2205 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30746] GAM2205 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2205 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2205 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2205 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2205 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30747] The complementary binding of GAM2205 RNA, herein designated GAM RNA, to target binding sites on GAM2205 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2205 target RNA, herein designated GAM TARGET RNA, into GAM2205 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[30748] It is appreciated that GAM2205 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2205 target genes. The

mRNA of each one of this plurality of GAM2205 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2205 RNA, herein designated GAM RNA, and which when bound by GAM2205 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2205 target proteins.

[30749] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2205 gene, herein designated GAM GENE, on one or more GAM2205 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30750] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2205 correlate with, and may be deduced from, the identity of the target genes which GAM2205 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[30751] Nucleotide sequences of the GAM2205 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2205 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2205 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2205 are further described hereinbelow with reference to Table 1.

[30752] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2205 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[30753] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2206 (GAM2206) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[30754] GAM2206 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2206 was detected is described hereinabove with reference to Figs. 2-8.

[30755] GAM2206 gene, herein designated GAM GENE, and GAM2206 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[30756] GAM2206 gene, herein designated GAM GENE, encodes a GAM2206 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2206 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2206 precursor RNA is designated SEQ ID:2183, and is provided hereinbelow with reference to the sequence listing part.

[30757] GAM2206 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2206 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30758] An enzyme complex designated DICER COMPLEX, dices the GAM2206 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2206 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of GAM2206 RNA is designated SEQ ID:4797, and is provided hereinbelow with reference to the sequence listing part.

[30759] GAM2206 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2206 target RNA, herein designated GAM TARGET RNA. GAM2206 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30760] GAM2206 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2206 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2206 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2206 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2206 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30761] The complementary binding of GAM2206 RNA, herein designated GAM RNA, to target binding sites on GAM2206 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2206 target RNA, herein designated GAM TARGET RNA, into GAM2206 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[30762] It is appreciated that GAM2206 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2206 target genes. The mRNA of each one of this plurality of GAM2206 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2206 RNA, herein designated GAM RNA, and which when bound by GAM2206 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2206 target proteins.

[30763] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2206 gene, herein designated GAM GENE, on one or more GAM2206 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30764] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2206 correlate with, and may be deduced from, the identity of the target



genes which GAM2206 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[30765] Nucleotide sequences of the GAM2206 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2206 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2206 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2206 are further described hereinbelow with reference to Table 1.

[30766] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2206 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[30767] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2207 (GAM2207) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[30768] GAM2207 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2207 was detected is described hereinabove with reference to Figs. 2-8.

[30769] GAM2207 gene, herein designated GAM GENE, and GAM2207 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

[30770] GAM2207 gene, herein designated GAM GENE, encodes a GAM2207 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2207 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2207 precursor RNA is designated SEQ ID:2184, and is provided hereinbelow with reference to the sequence listing part.

[30771] GAM2207 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2207 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30772] An enzyme complex designated DICER COMPLEX, dices the GAM2207 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2207 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 86%) nucleotide sequence of GAM2207 RNA is designated SEQ ID:4798, and is provided

hereinbelow with reference to the sequence listing part.

[30773] GAM2207 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2207 target RNA, herein designated GAM TARGET RNA. GAM2207 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30774] GAM2207 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2207 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2207 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2207 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2207 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30775] The complementary binding of GAM2207 RNA, herein designated GAM RNA, to target binding sites on GAM2207 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2207 target RNA, herein designated GAM TARGET RNA, into GAM2207 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[30776] It is appreciated that GAM2207 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2207 target genes. The mRNA of each one of this plurality of GAM2207 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2207 RNA, herein designated GAM RNA, and which when bound by GAM2207 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2207 target proteins.

[30777] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2207 gene, herein designated GAM GENE, on one or more GAM2207 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30778] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2207 correlate with, and may be deduced from, the identity of the target genes which GAM2207 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[30779] Nucleotide sequences of the GAM2207 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2207 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2207 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2207 are further described hereinbelow with reference to Table 1.

[30780] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2207 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[30781] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2208 (GAM2208) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[30782] GAM2208 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2208 was detected is described hereinabove with reference to Figs. 2-8.

[30783] GAM2208 gene, herein designated GAM GENE, and GAM2208 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[30784] GAM2208 gene, herein designated GAM GENE, encodes a GAM2208 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2208 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2208 precursor RNA is designated SEQ ID:2185, and is provided hereinbelow with reference to the sequence listing part.

[30785] GAM2208 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2208 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30786] An enzyme complex designated DICER COMPLEX, dices the GAM2208 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2208 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 91%) nucleotide sequence of GAM2208 RNA is designated SEQ ID:4799, and is provided hereinbelow with reference to the sequence listing part.

[30787] GAM2208 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2208 target RNA, herein designated GAM TARGET RNA. GAM2208 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30788] GAM2208 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2208 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2208 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2208 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2208 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30789] The complementary binding of GAM2208 RNA, herein designated GAM RNA, to target binding sites on GAM2208 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2208 target RNA, herein designated GAM TARGET RNA, into GAM2208 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[30790] It is appreciated that GAM2208 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2208 target genes. The mRNA of each one of this plurality of GAM2208 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2208 RNA, herein designated GAM RNA, and which when bound by GAM2208 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2208 target proteins.

[30791] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2208 gene, herein designated GAM GENE, on one or more GAM2208 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary



binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30792] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2208 correlate with, and may be deduced from, the identity of the target genes which GAM2208 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[30793] Nucleotide sequences of the GAM2208 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2208 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2208 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2208 are further described hereinbelow with reference to Table 1.

[30794] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2208 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[30795] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2209 (GAM2209) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[30796] GAM2209 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2209 was detected is described hereinabove with reference to Figs. 2-8.

[30797] GAM2209 gene, herein designated GAM GENE, and GAM2209 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[30798] GAM2209 gene, herein designated GAM GENE, encodes a GAM2209 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2209 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2209 precursor RNA is designated SEQ ID:2186, and is provided hereinbelow with reference to the sequence listing part.

[30799] GAM2209 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2209 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30800] An enzyme complex designated DICER COMPLEX, dices the GAM2209 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2209 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of GAM2209 RNA is designated SEQ ID:4800, and is provided hereinbelow with reference to the sequence listing part.

[30801] GAM2209 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2209 target RNA, herein designated GAM TARGET RNA. GAM2209 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30802] GAM2209 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2209 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2209 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2209 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2209 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30803] The complementary binding of GAM2209 RNA, herein designated GAM RNA, to target binding sites on GAM2209 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2209 target RNA, herein designated GAM TARGET RNA, into GAM2209 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[30804] It is appreciated that GAM2209 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2209 target genes. The mRNA of each one of this plurality of GAM2209 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2209 RNA, herein designated GAM RNA, and which when bound by GAM2209 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2209 target proteins.

[30805] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2209 gene, herein designated GAM GENE, on one or more GAM2209 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30806] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2209 correlate with, and may be deduced from, the identity of the target genes which GAM2209 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[30807] Nucleotide sequences of the GAM2209 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2209 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2209 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2209 are further described hereinbelow with reference to Table 1.

[30808] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2209 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

[30809] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2210 (GAM2210) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[30810] GAM2210 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2210 was detected is described hereinabove with reference to Figs. 2-8.

[30811] GAM2210 gene, herein designated GAM GENE, and GAM2210 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[30812] GAM2210 gene, herein designated GAM GENE, encodes a GAM2210 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2210 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2210 precursor RNA is designated SEQ ID:2187, and is provided hereinbelow with reference to the sequence listing part.

[30813] GAM2210 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2210 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30814] An enzyme complex designated DICER COMPLEX, dices the GAM2210 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2210 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2210 RNA is designated SEQ ID:4801, and is provided hereinbelow with reference to the sequence listing part.

[30815] GAM2210 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2210 target RNA, herein designated GAM TARGET RNA. GAM2210 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30816] GAM2210 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2210 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2210 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2210 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2210 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30817] The complementary binding of GAM2210 RNA, herein designated GAM RNA, to target binding sites on GAM2210 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2210 target RNA, herein designated GAM TARGET RNA, into GAM2210 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[30818] It is appreciated that GAM2210 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2210 target genes. The mRNA of each one of this plurality of GAM2210 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2210 RNA, herein designated GAM RNA, and which when bound by GAM2210 RNA, herein designated GAM RNA,



causes inhibition of translation of respective one or more GAM2210 target proteins.

[30819] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2210 gene, herein designated GAM GENE, on one or more GAM2210 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30820] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2210 correlate with, and may be deduced from, the identity of the target genes which GAM2210 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[30821] Nucleotide sequences of the GAM2210 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2210 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2210 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2210 are further described hereinbelow with reference to Table 1.

[30822] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2210 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[30823] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2211 (GAM2211) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[30824] GAM2211 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2211 was detected is described hereinabove with reference to Figs. 2-8.

[30825] GAM2211 gene, herein designated GAM GENE, and GAM2211 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[30826] GAM2211 gene, herein designated GAM GENE, encodes a GAM2211 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2211 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2211 precursor RNA is designated SEQ ID:2188, and is provided hereinbelow with reference to the sequence listing part.

[30827] GAM2211 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2211 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30828] An enzyme complex designated DICER COMPLEX, dices the GAM2211 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2211 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2211 RNA is designated SEQ ID:4802, and is provided hereinbelow with reference to the sequence listing part.

[30829] GAM2211 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2211 target RNA, herein designated GAM TARGET RNA. GAM2211 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30830] GAM2211 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2211 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2211 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2211 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2211 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30831] The complementary binding of GAM2211 RNA, herein designated GAM RNA, to target binding sites on GAM2211 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2211 target RNA, herein designated GAM TARGET RNA, into GAM2211 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[30832] It is appreciated that GAM2211 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2211 target genes. The

mRNA of each one of this plurality of GAM2211 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2211 RNA, herein designated GAM RNA, and which when bound by GAM2211 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2211 target proteins.

[30833] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2211 gene, herein designated GAM GENE, on one or more GAM2211 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30834] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2211 correlate with, and may be deduced from, the identity of the target genes which GAM2211 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[30835] Nucleotide sequences of the GAM2211 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2211 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2211 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2211 are further described hereinbelow with reference to Table 1.

[30836] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2211 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[30837] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2212 (GAM2212) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[30838] GAM2212 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2212 was detected is described hereinabove with reference to Figs. 2-8.

[30839] GAM2212 gene, herein designated GAM GENE, and GAM2212 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[30840] GAM2212 gene, herein designated GAM GENE, encodes a GAM2212 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2212 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2212 precursor RNA is designated SEQ ID:2189, and is provided hereinbelow with reference to the sequence listing part.

[30841] GAM2212 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2212 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30842] An enzyme complex designated DICER COMPLEX, dices the GAM2212 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2212 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 78%) nucleotide sequence of GAM2212 RNA is designated SEQ ID:4803, and is provided hereinbelow with reference to the sequence listing part.

[30843] GAM2212 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2212 target RNA, herein designated GAM TARGET RNA. GAM2212 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30844] GAM2212 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2212 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2212 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2212 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2212 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30845] The complementary binding of GAM2212 RNA, herein designated GAM RNA, to target binding sites on GAM2212 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2212 target RNA, herein designated GAM TARGET RNA, into GAM2212 target protein, herein



designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[30846] It is appreciated that GAM2212 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2212 target genes. The mRNA of each one of this plurality of GAM2212 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2212 RNA, herein designated GAM RNA, and which when bound by GAM2212 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2212 target proteins.

[30847] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2212 gene, herein designated GAM GENE, on one or more GAM2212 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30848] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2212 correlate with, and may be deduced from, the identity of the target

genes which GAM2212 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[30849] Nucleotide sequences of the GAM2212 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2212 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2212 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2212 are further described hereinbelow with reference to Table 1.

[30850] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2212 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[30851] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2213 (GAM2213) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[30852] GAM2213 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2213 was detected is described hereinabove with reference to Figs. 2-8.

[30853] GAM2213 gene, herein designated GAM GENE, and GAM2213 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

[30854] GAM2213 gene, herein designated GAM GENE, encodes a GAM2213 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2213 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2213 precursor RNA is designated SEQ ID:2190, and is provided hereinbelow with reference to the sequence listing part.

[30855] GAM2213 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2213 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30856] An enzyme complex designated DICER COMPLEX, dices the GAM2213 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2213 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of GAM2213 RNA is designated SEQ ID:4805, and is provided

hereinbelow with reference to the sequence listing part.

[30857] GAM2213 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2213 target RNA, herein designated GAM TARGET RNA. GAM2213 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30858] GAM2213 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2213 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2213 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2213 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2213 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30859] The complementary binding of GAM2213 RNA, herein designated GAM RNA, to target binding sites on GAM2213 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2213 target RNA, herein designated GAM TARGET RNA, into GAM2213 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[30860] It is appreciated that GAM2213 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2213 target genes. The mRNA of each one of this plurality of GAM2213 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2213 RNA, herein designated GAM RNA, and which when bound by GAM2213 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2213 target proteins.

[30861] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2213 gene, herein designated GAM GENE, on one or more GAM2213 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30862] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2213 correlate with, and may be deduced from, the identity of the target genes which GAM2213 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[30863] Nucleotide sequences of the GAM2213 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2213 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2213 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2213 are further described hereinbelow with reference to Table 1.

[30864] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2213 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[30865] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2214 (GAM2214) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[30866] GAM2214 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2214 was detected is described hereinabove with reference to Figs. 2-8.

[30867] GAM2214 gene, herein designated GAM GENE, and GAM2214 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[30868] GAM2214 gene, herein designated GAM GENE, encodes a GAM2214 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2214 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2214 precursor RNA is designated SEQ ID:2191, and is provided hereinbelow with reference to the sequence listing part.

[30869] GAM2214 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2214 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30870] An enzyme complex designated DICER COMPLEX, dices the GAM2214 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2214 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 91%) nucleotide sequence of GAM2214 RNA is designated SEQ ID:4804, and is provided hereinbelow with reference to the sequence listing part.

[30871] GAM2214 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2214 target RNA, herein designated GAM TARGET RNA. GAM2214 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30872] GAM2214 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2214 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2214 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2214 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2214 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target



binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30873] The complementary binding of GAM2214 RNA, herein designated GAM RNA, to target binding sites on GAM2214 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2214 target RNA, herein designated GAM TARGET RNA, into GAM2214 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[30874] It is appreciated that GAM2214 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2214 target genes. The mRNA of each one of this plurality of GAM2214 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2214 RNA, herein designated GAM RNA, and which when bound by GAM2214 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2214 target proteins.

[30875] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2214 gene, herein designated GAM GENE, on one or more GAM2214 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30876] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2214 correlate with, and may be deduced from, the identity of the target genes which GAM2214 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[30877] Nucleotide sequences of the GAM2214 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2214 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2214 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2214 are further described hereinbelow with reference to Table 1.

[30878] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2214 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[30879] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2215 (GAM2215) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[30880] GAM2215 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2215 was detected is described hereinabove with reference to Figs. 2-8.

[30881] GAM2215 gene, herein designated GAM GENE, and GAM2215 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[30882] GAM2215 gene, herein designated GAM GENE, encodes a GAM2215 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2215 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2215 precursor RNA is designated SEQ ID:2192, and is provided hereinbelow with reference to the sequence listing part.

[30883] GAM2215 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2215 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

- [30884] An enzyme complex designated DICER COMPLEX, dices the GAM2215 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2215 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 83%) nucleotide sequence of GAM2215 RNA is designated SEQ ID:4806, and is provided hereinbelow with reference to the sequence listing part.
- [30885] GAM2215 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2215 target RNA, herein designated GAM TARGET RNA. GAM2215 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [30886] GAM2215 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2215 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2215 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2215 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2215 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30887] The complementary binding of GAM2215 RNA, herein designated GAM RNA, to target binding sites on GAM2215 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2215 target RNA, herein designated GAM TARGET RNA, into GAM2215 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[30888] It is appreciated that GAM2215 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2215 target genes. The mRNA of each one of this plurality of GAM2215 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2215 RNA, herein designated GAM RNA, and which when bound by GAM2215 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2215 target proteins.

[30889] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2215 gene, herein designated GAM GENE, on one or more GAM2215 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30890] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2215 correlate with, and may be deduced from, the identity of the target genes which GAM2215 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[30891] Nucleotide sequences of the GAM2215 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2215 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2215 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2215 are further described hereinbelow with reference to Table 1.

[30892] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2215 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

[30893] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2216 (GAM2216) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[30894] GAM2216 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2216 was detected is described hereinabove with reference to Figs. 2-8.

[30895] GAM2216 gene, herein designated GAM GENE, and GAM2216 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[30896] GAM2216 gene, herein designated GAM GENE, encodes a GAM2216 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2216 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2216 precursor RNA is designated SEQ ID:2193, and is provided hereinbelow with reference to the sequence listing part.

[30897] GAM2216 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2216 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30898] An enzyme complex designated DICER COMPLEX, dices the GAM2216 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2216 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 78%) nucleotide sequence of GAM2216 RNA is designated SEQ ID:4807, and is provided hereinbelow with reference to the sequence listing part.

[30899] GAM2216 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2216 target RNA, herein designated GAM TARGET RNA. GAM2216 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30900] GAM2216 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2216 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2216 RNA,



herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2216 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2216 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30901] The complementary binding of GAM2216 RNA, herein designated GAM RNA, to target binding sites on GAM2216 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2216 target RNA, herein designated GAM TARGET RNA, into GAM2216 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[30902] It is appreciated that GAM2216 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2216 target genes. The mRNA of each one of this plurality of GAM2216 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2216 RNA, herein designated GAM RNA, and which when bound by GAM2216 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2216 target proteins.

[30903] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2216 gene, herein designated GAM GENE, on one or more GAM2216 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30904] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2216 correlate with, and may be deduced from, the identity of the target genes which GAM2216 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[30905] Nucleotide sequences of the GAM2216 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2216 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2216 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2216 are further described hereinbelow with reference to Table 1.

[30906] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2216 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[30907] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2217 (GAM2217) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[30908] GAM2217 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2217 was detected is described hereinabove with reference to Figs. 2-8.

[30909] GAM2217 gene, herein designated GAM GENE, and GAM2217 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[30910] GAM2217 gene, herein designated GAM GENE, encodes a GAM2217 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2217 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2217 precursor RNA is designated SEQ ID:2194, and is provided hereinbelow with reference to the sequence listing part.

[30911] GAM2217 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2217 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30912] An enzyme complex designated DICER COMPLEX, dices the GAM2217 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2217 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 92%) nucleotide sequence of GAM2217 RNA is designated SEQ ID:4808, and is provided hereinbelow with reference to the sequence listing part.

[30913] GAM2217 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2217 target RNA, herein designated GAM TARGET RNA. GAM2217 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30914] GAM2217 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2217 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2217 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2217 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2217 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30915] The complementary binding of GAM2217 RNA, herein designated GAM RNA, to target binding sites on GAM2217 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2217 target RNA, herein designated GAM TARGET RNA, into GAM2217 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[30916] It is appreciated that GAM2217 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2217 target genes. The

mRNA of each one of this plurality of GAM2217 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2217 RNA, herein designated GAM RNA, and which when bound by GAM2217 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2217 target proteins.

[30917] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2217 gene, herein designated GAM GENE, on one or more GAM2217 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30918] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2217 correlate with, and may be deduced from, the identity of the target genes which GAM2217 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[30919] Nucleotide sequences of the GAM2217 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2217 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2217 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2217 are further described hereinbelow with reference to Table 1.

[30920] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2217 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[30921] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2218 (GAM2218) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[30922] GAM2218 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2218 was detected is described hereinabove with reference to Figs. 2-8.

[30923] GAM2218 gene, herein designated GAM GENE, and GAM2218 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[30924] GAM2218 gene, herein designated GAM GENE, encodes a GAM2218 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2218 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2218 precursor RNA is designated SEQ ID:2195, and is provided hereinbelow with reference to the sequence listing part.

[30925] GAM2218 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2218 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30926] An enzyme complex designated DICER COMPLEX, dices the GAM2218 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2218 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 78%) nucleotide sequence of GAM2218 RNA is designated SEQ ID:4809, and is provided hereinbelow with reference to the sequence listing part.

[30927] GAM2218 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2218 target RNA, herein designated GAM TARGET RNA. GAM2218 target RNA, herein designated GAM



TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30928] GAM2218 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2218 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2218 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2218 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2218 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30929] The complementary binding of GAM2218 RNA, herein designated GAM RNA, to target binding sites on GAM2218 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2218 target RNA, herein designated GAM TARGET RNA, into GAM2218 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[30930] It is appreciated that GAM2218 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2218 target genes. The mRNA of each one of this plurality of GAM2218 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2218 RNA, herein designated GAM RNA, and which when bound by GAM2218 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2218 target proteins.

[30931] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2218 gene, herein designated GAM GENE, on one or more GAM2218 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30932] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2218 correlate with, and may be deduced from, the identity of the target

genes which GAM2218 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[30933] Nucleotide sequences of the GAM2218 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2218 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2218 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2218 are further described hereinbelow with reference to Table 1.

[30934] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2218 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[30935] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2219 (GAM2219) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[30936] GAM2219 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2219 was detected is described hereinabove with reference to Figs. 2-8.

[30937] GAM2219 gene, herein designated GAM GENE, and GAM2219 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

[30938] GAM2219 gene, herein designated GAM GENE, encodes a GAM2219 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2219 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2219 precursor RNA is designated SEQ ID:2196, and is provided hereinbelow with reference to the sequence listing part.

[30939] GAM2219 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2219 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30940] An enzyme complex designated DICER COMPLEX, dices the GAM2219 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2219 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of GAM2219 RNA is designated SEQ ID:4810, and is provided

hereinbelow with reference to the sequence listing part.

[30941] GAM2219 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2219 target RNA, herein designated GAM TARGET RNA. GAM2219 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30942] GAM2219 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2219 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2219 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2219 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2219 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30943] The complementary binding of GAM2219 RNA, herein designated GAM RNA, to target binding sites on GAM2219 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2219 target RNA, herein designated GAM TARGET RNA, into GAM2219 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[30944] It is appreciated that GAM2219 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2219 target genes. The mRNA of each one of this plurality of GAM2219 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2219 RNA, herein designated GAM RNA, and which when bound by GAM2219 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2219 target proteins.

[30945] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2219 gene, herein designated GAM GENE, on one or more GAM2219 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30946] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2219 correlate with, and may be deduced from, the identity of the target genes which GAM2219 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[30947] Nucleotide sequences of the GAM2219 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2219 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2219 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2219 are further described hereinbelow with reference to Table 1.

[30948] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2219 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[30949] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2220 (GAM2220) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[30950] GAM2220 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2220 was detected is described hereinabove with reference to Figs. 2-8.

[30951] GAM2220 gene, herein designated GAM GENE, and GAM2220 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[30952] GAM2220 gene, herein designated GAM GENE, encodes a GAM2220 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2220 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2220 precursor RNA is designated SEQ ID:2197, and is provided hereinbelow with reference to the sequence listing part.

[30953] GAM2220 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2220 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30954] An enzyme complex designated DICER COMPLEX, dices the GAM2220 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2220 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin



structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 84%) nucleotide sequence of GAM2220 RNA is designated SEQ ID:4811, and is provided hereinbelow with reference to the sequence listing part.

[30955] GAM2220 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2220 target RNA, herein designated GAM TARGET RNA. GAM2220 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30956] GAM2220 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2220 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2220 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2220 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2220 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30957] The complementary binding of GAM2220 RNA, herein designated GAM RNA, to target binding sites on GAM2220 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2220 target RNA, herein designated GAM TARGET RNA, into GAM2220 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[30958] It is appreciated that GAM2220 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2220 target genes. The mRNA of each one of this plurality of GAM2220 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2220 RNA, herein designated GAM RNA, and which when bound by GAM2220 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2220 target proteins.

[30959] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2220 gene, herein designated GAM GENE, on one or more GAM2220 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30960] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2220 correlate with, and may be deduced from, the identity of the target genes which GAM2220 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[30961] Nucleotide sequences of the GAM2220 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2220 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2220 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2220 are further described hereinbelow with reference to Table 1.

[30962] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2220 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[30963] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2221 (GAM2221) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[30964] GAM2221 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2221 was detected is described hereinabove with reference to Figs. 2-8.

[30965] GAM2221 gene, herein designated GAM GENE, and GAM2221 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[30966] GAM2221 gene, herein designated GAM GENE, encodes a GAM2221 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2221 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2221 precursor RNA is designated SEQ ID:2198, and is provided hereinbelow with reference to the sequence listing part.

[30967] GAM2221 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2221 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

- [30968] An enzyme complex designated DICER COMPLEX, dices the GAM2221 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2221 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of GAM2221 RNA is designated SEQ ID:4812, and is provided hereinbelow with reference to the sequence listing part.
- [30969] GAM2221 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2221 target RNA, herein designated GAM TARGET RNA. GAM2221 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [30970] GAM2221 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2221 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2221 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2221 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2221 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30971] The complementary binding of GAM2221 RNA, herein designated GAM RNA, to target binding sites on GAM2221 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2221 target RNA, herein designated GAM TARGET RNA, into GAM2221 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[30972] It is appreciated that GAM2221 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2221 target genes. The mRNA of each one of this plurality of GAM2221 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2221 RNA, herein designated GAM RNA, and which when bound by GAM2221 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2221 target proteins.

[30973] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2221 gene, herein designated GAM GENE, on one or more GAM2221 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30974] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2221 correlate with, and may be deduced from, the identity of the target genes which GAM2221 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[30975] Nucleotide sequences of the GAM2221 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2221 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2221 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2221 are further described hereinbelow with reference to Table 1.

[30976] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2221 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

[30977] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2222 (GAM2222) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[30978] GAM2222 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2222 was detected is described hereinabove with reference to Figs. 2-8.

[30979] GAM2222 gene, herein designated GAM GENE, and GAM2222 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[30980] GAM2222 gene, herein designated GAM GENE, encodes a GAM2222 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2222 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2222 precursor RNA is designated SEQ ID:2199, and is provided hereinbelow with reference to the sequence listing part.

[30981] GAM2222 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2222 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA



encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30982] An enzyme complex designated DICER COMPLEX, dices the GAM2222 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2222 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 83%) nucleotide sequence of GAM2222 RNA is designated SEQ ID:4813, and is provided hereinbelow with reference to the sequence listing part.

[30983] GAM2222 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2222 target RNA, herein designated GAM TARGET RNA. GAM2222 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30984] GAM2222 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2222 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2222 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2222 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2222 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30985] The complementary binding of GAM2222 RNA, herein designated GAM RNA, to target binding sites on GAM2222 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2222 target RNA, herein designated GAM TARGET RNA, into GAM2222 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[30986] It is appreciated that GAM2222 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2222 target genes. The mRNA of each one of this plurality of GAM2222 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2222 RNA, herein designated GAM RNA, and which when bound by GAM2222 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2222 target proteins.

[30987] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2222 gene, herein designated GAM GENE, on one or more GAM2222 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[30988] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2222 correlate with, and may be deduced from, the identity of the target genes which GAM2222 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[30989] Nucleotide sequences of the GAM2222 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2222 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2222 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2222 are further described hereinbelow with reference to Table 1.

[30990] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2222 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[30991] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2223 (GAM2223) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[30992] GAM2223 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2223 was detected is described hereinabove with reference to Figs. 2-8.

[30993] GAM2223 gene, herein designated GAM GENE, and GAM2223 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[30994] GAM2223 gene, herein designated GAM GENE, encodes a GAM2223 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2223 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2223 precursor RNA is designated SEQ ID:2200, and is provided hereinbelow with reference to the sequence listing part.

[30995] GAM2223 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2223 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[30996] An enzyme complex designated DICER COMPLEX, dices the GAM2223 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2223 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2223 RNA is designated SEQ ID:4814, and is provided hereinbelow with reference to the sequence listing part.

[30997] GAM2223 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2223 target RNA, herein designated GAM TARGET RNA. GAM2223 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[30998] GAM2223 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2223 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2223 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2223 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2223 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[30999] The complementary binding of GAM2223 RNA, herein designated GAM RNA, to target binding sites on GAM2223 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2223 target RNA, herein designated GAM TARGET RNA, into GAM2223 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31000] It is appreciated that GAM2223 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2223 target genes. The

mRNA of each one of this plurality of GAM2223 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2223 RNA, herein designated GAM RNA, and which when bound by GAM2223 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2223 target proteins.

[31001] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2223 gene, herein designated GAM GENE, on one or more GAM2223 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31002] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2223 correlate with, and may be deduced from, the identity of the target genes which GAM2223 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31003] Nucleotide sequences of the GAM2223 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2223 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2223 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2223 are further described hereinbelow with reference to Table 1.

[31004] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2223 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[31005] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2224 (GAM2224) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31006] GAM2224 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2224 was detected is described hereinabove with reference to Figs. 2-8.

[31007] GAM2224 gene, herein designated GAM GENE, and GAM2224 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[31008] GAM2224 gene, herein designated GAM GENE, encodes a GAM2224 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2224 precursor RNA,



herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2224 precursor RNA is designated SEQ ID:2201, and is provided hereinbelow with reference to the sequence listing part.

[31009] GAM2224 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2224 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31010] An enzyme complex designated DICER COMPLEX, dices the GAM2224 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2224 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of GAM2224 RNA is designated SEQ ID:4815, and is provided hereinbelow with reference to the sequence listing part.

[31011] GAM2224 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2224 target RNA, herein designated GAM TARGET RNA. GAM2224 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31012] GAM2224 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2224 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2224 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2224 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2224 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31013] The complementary binding of GAM2224 RNA, herein designated GAM RNA, to target binding sites on GAM2224 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2224 target RNA, herein designated GAM TARGET RNA, into GAM2224 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31014] It is appreciated that GAM2224 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2224 target genes. The mRNA of each one of this plurality of GAM2224 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2224 RNA, herein designated GAM RNA, and which when bound by GAM2224 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2224 target proteins.

[31015] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2224 gene, herein designated GAM GENE, on one or more GAM2224 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31016] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2224 correlate with, and may be deduced from, the identity of the target

genes which GAM2224 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31017] Nucleotide sequences of the GAM2224 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2224 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2224 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2224 are further described hereinbelow with reference to Table 1.

[31018] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2224 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[31019] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2225 (GAM2225) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31020] GAM2225 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2225 was detected is described hereinabove with reference to Figs. 2-8.

[31021] GAM2225 gene, herein designated GAM GENE, and GAM2225 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

[31022] GAM2225 gene, herein designated GAM GENE, encodes a GAM2225 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2225 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2225 precursor RNA is designated SEQ ID:2202, and is provided hereinbelow with reference to the sequence listing part.

[31023] GAM2225 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2225 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31024] An enzyme complex designated DICER COMPLEX, dices the GAM2225 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2225 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 76%) nucleotide sequence of GAM2225 RNA is designated SEQ ID:4816, and is provided

hereinbelow with reference to the sequence listing part.

[31025] GAM2225 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2225 target RNA, herein designated GAM TARGET RNA. GAM2225 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31026] GAM2225 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2225 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2225 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2225 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2225 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31027] The complementary binding of GAM2225 RNA, herein designated GAM RNA, to target binding sites on GAM2225 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2225 target RNA, herein designated GAM TARGET RNA, into GAM2225 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31028] It is appreciated that GAM2225 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2225 target genes. The mRNA of each one of this plurality of GAM2225 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2225 RNA, herein designated GAM RNA, and which when bound by GAM2225 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2225 target proteins.

[31029] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2225 gene, herein designated GAM GENE, on one or more GAM2225 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31030] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2225 correlate with, and may be deduced from, the identity of the target genes which GAM2225 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31031] Nucleotide sequences of the GAM2225 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2225 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2225 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2225 are further described hereinbelow with reference to Table 1.

[31032] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2225 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[31033] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2226 (GAM2226) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31034] GAM2226 is a novel bioinformatically detected regulatory, non protein



coding, micro RNA (miRNA) gene. The method by which GAM2226 was detected is described hereinabove with reference to Figs. 2-8.

[31035] GAM2226 gene, herein designated GAM GENE, and GAM2226 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[31036] GAM2226 gene, herein designated GAM GENE, encodes a GAM2226 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2226 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2226 precursor RNA is designated SEQ ID:2203, and is provided hereinbelow with reference to the sequence listing part.

[31037] GAM2226 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2226 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31038] An enzyme complex designated DICER COMPLEX, dices the GAM2226 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2226 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 85%) nucleotide sequence of GAM2226 RNA is designated SEQ ID:4817, and is provided hereinbelow with reference to the sequence listing part.

[31039] GAM2226 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2226 target RNA, herein designated GAM TARGET RNA. GAM2226 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31040] GAM2226 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2226 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2226 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2226 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2226 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31041] The complementary binding of GAM2226 RNA, herein designated GAM RNA, to target binding sites on GAM2226 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2226 target RNA, herein designated GAM TARGET RNA, into GAM2226 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31042] It is appreciated that GAM2226 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2226 target genes. The mRNA of each one of this plurality of GAM2226 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2226 RNA, herein designated GAM RNA, and which when bound by GAM2226 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2226 target proteins.

[31043] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2226 gene, herein designated GAM GENE, on one or more GAM2226 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31044] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2226 correlate with, and may be deduced from, the identity of the target genes which GAM2226 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31045] Nucleotide sequences of the GAM2226 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2226 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2226 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2226 are further described hereinbelow with reference to Table 1.

[31046] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2226 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[31047] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2227 (GAM2227) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31048] GAM2227 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2227 was detected is described hereinabove with reference to Figs. 2-8.

[31049] GAM2227 gene, herein designated GAM GENE, and GAM2227 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[31050] GAM2227 gene, herein designated GAM GENE, encodes a GAM2227 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2227 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2227 precursor RNA is designated SEQ ID:2204, and is provided hereinbelow with reference to the sequence listing part.

[31051] GAM2227 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2227 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

- [31052] An enzyme complex designated DICER COMPLEX, dices the GAM2227 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2227 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2227 RNA is designated SEQ ID:4818, and is provided hereinbelow with reference to the sequence listing part.
- [31053] GAM2227 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2227 target RNA, herein designated GAM TARGET RNA. GAM2227 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [31054] GAM2227 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2227 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2227 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2227 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2227 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31055] The complementary binding of GAM2227 RNA, herein designated GAM RNA, to target binding sites on GAM2227 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2227 target RNA, herein designated GAM TARGET RNA, into GAM2227 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31056] It is appreciated that GAM2227 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2227 target genes. The mRNA of each one of this plurality of GAM2227 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2227 RNA, herein designated GAM RNA, and which when bound by GAM2227 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2227 target proteins.

[31057] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2227 gene, herein designated GAM GENE, on one or more GAM2227 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31058] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2227 correlate with, and may be deduced from, the identity of the target genes which GAM2227 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31059] Nucleotide sequences of the GAM2227 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2227 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2227 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2227 are further described hereinbelow with reference to Table 1.

[31060] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2227 RNA, herein designated GAM RNA, are described hereinbelow



with reference to Table 2.

[31061] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2228 (GAM2228) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31062] GAM2228 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2228 was detected is described hereinabove with reference to Figs. 2-8.

[31063] GAM2228 gene, herein designated GAM GENE, and GAM2228 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[31064] GAM2228 gene, herein designated GAM GENE, encodes a GAM2228 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2228 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2228 precursor RNA is designated SEQ ID:2205, and is provided hereinbelow with reference to the sequence listing part.

[31065] GAM2228 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2228 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31066] An enzyme complex designated DICER COMPLEX, dices the GAM2228 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2228 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 25%) nucleotide sequence of GAM2228 RNA is designated SEQ ID:4820, and is provided hereinbelow with reference to the sequence listing part.

[31067] GAM2228 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2228 target RNA, herein designated GAM TARGET RNA. GAM2228 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31068] GAM2228 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2228 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2228 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2228 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2228 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31069] The complementary binding of GAM2228 RNA, herein designated GAM RNA, to target binding sites on GAM2228 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2228 target RNA, herein designated GAM TARGET RNA, into GAM2228 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31070] It is appreciated that GAM2228 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2228 target genes. The mRNA of each one of this plurality of GAM2228 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2228 RNA, herein designated GAM RNA, and which when bound by GAM2228 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2228 target proteins.

[31071] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2228 gene, herein designated GAM GENE, on one or more GAM2228 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31072] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2228 correlate with, and may be deduced from, the identity of the target genes which GAM2228 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31073] Nucleotide sequences of the GAM2228 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2228 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2228 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2228 are further described hereinbelow with reference to Table 1.

[31074] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2228 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[31075] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2229 (GAM2229) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31076] GAM2229 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2229 was detected is described hereinabove with reference to Figs. 2-8.

[31077] GAM2229 gene, herein designated GAM GENE, and GAM2229 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[31078] GAM2229 gene, herein designated GAM GENE, encodes a GAM2229 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2229 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2229 precursor RNA is designated SEQ ID:2206, and is provided hereinbelow with reference to the sequence listing part.

[31079] GAM2229 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2229 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31080] An enzyme complex designated DICER COMPLEX, dices the GAM2229 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2229 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of GAM2229 RNA is designated SEQ ID:4819, and is provided hereinbelow with reference to the sequence listing part.

[31081] GAM2229 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2229 target RNA, herein designated GAM TARGET RNA. GAM2229 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31082] GAM2229 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2229 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2229 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2229 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2229 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31083] The complementary binding of GAM2229 RNA, herein designated GAM RNA, to target binding sites on GAM2229 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2229 target RNA, herein designated GAM TARGET RNA, into GAM2229 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31084] It is appreciated that GAM2229 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2229 target genes. The

mRNA of each one of this plurality of GAM2229 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2229 RNA, herein designated GAM RNA, and which when bound by GAM2229 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2229 target proteins.

[31085] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2229 gene, herein designated GAM GENE, on one or more GAM2229 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31086] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2229 correlate with, and may be deduced from, the identity of the target genes which GAM2229 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31087] Nucleotide sequences of the GAM2229 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2229 RNA, herein



designated GAM RNA, and a schematic representation of the secondary folding of GAM2229 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2229 are further described hereinbelow with reference to Table 1.

[31088] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2229 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[31089] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2230 (GAM2230) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31090] GAM2230 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2230 was detected is described hereinabove with reference to Figs. 2-8.

[31091] GAM2230 gene, herein designated GAM GENE, and GAM2230 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[31092] GAM2230 gene, herein designated GAM GENE, encodes a GAM2230 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2230 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2230 precursor RNA is designated SEQ ID:2207, and is provided hereinbelow with reference to the sequence listing part.

[31093] GAM2230 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2230 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31094] An enzyme complex designated DICER COMPLEX, dices the GAM2230 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2230 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 25%) nucleotide sequence of GAM2230 RNA is designated SEQ ID:4821, and is provided hereinbelow with reference to the sequence listing part.

[31095] GAM2230 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2230 target RNA, herein designated GAM TARGET RNA. GAM2230 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31096] GAM2230 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2230 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2230 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2230 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2230 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31097] The complementary binding of GAM2230 RNA, herein designated GAM RNA, to target binding sites on GAM2230 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2230 target RNA, herein designated GAM TARGET RNA, into GAM2230 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31098] It is appreciated that GAM2230 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2230 target genes. The mRNA of each one of this plurality of GAM2230 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2230 RNA, herein designated GAM RNA, and which when bound by GAM2230 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2230 target proteins.

[31099] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2230 gene, herein designated GAM GENE, on one or more GAM2230 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31100] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2230 correlate with, and may be deduced from, the identity of the target

genes which GAM2230 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31101] Nucleotide sequences of the GAM2230 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2230 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2230 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2230 are further described hereinbelow with reference to Table 1.

[31102] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2230 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[31103] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2231 (GAM2231) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31104] GAM2231 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2231 was detected is described hereinabove with reference to Figs. 2-8.

[31105] GAM2231 gene, herein designated GAM GENE, and GAM2231 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

- [31106] GAM2231 gene, herein designated GAM GENE, encodes a GAM2231 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2231 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2231 precursor RNA is designated SEQ ID:2208, and is provided hereinbelow with reference to the sequence listing part.
- [31107] GAM2231 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2231 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.
- [31108] An enzyme complex designated DICER COMPLEX, dices the GAM2231 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2231 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 84%) nucleotide sequence of GAM2231 RNA is designated SEQ ID:4822, and is provided

hereinbelow with reference to the sequence listing part.

[31109] GAM2231 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2231 target RNA, herein designated GAM TARGET RNA. GAM2231 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31110] GAM2231 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2231 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2231 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2231 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2231 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31111] The complementary binding of GAM2231 RNA, herein designated GAM RNA, to target binding sites on GAM2231 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2231 target RNA, herein designated GAM TARGET RNA, into GAM2231 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31112] It is appreciated that GAM2231 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2231 target genes. The mRNA of each one of this plurality of GAM2231 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2231 RNA, herein designated GAM RNA, and which when bound by GAM2231 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2231 target proteins.

[31113] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2231 gene, herein designated GAM GENE, on one or more GAM2231 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding



sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31114] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2231 correlate with, and may be deduced from, the identity of the target genes which GAM2231 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31115] Nucleotide sequences of the GAM2231 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2231 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2231 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2231 are further described hereinbelow with reference to Table 1.

[31116] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2231 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[31117] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2232 (GAM2232) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31118] GAM2232 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2232 was detected is described hereinabove with reference to Figs. 2-8.

[31119] GAM2232 gene, herein designated GAM GENE, and GAM2232 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[31120] GAM2232 gene, herein designated GAM GENE, encodes a GAM2232 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2232 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2232 precursor RNA is designated SEQ ID:2209, and is provided hereinbelow with reference to the sequence listing part.

[31121] GAM2232 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2232 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31122] An enzyme complex designated DICER COMPLEX, dices the GAM2232 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2232 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of GAM2232 RNA is designated SEQ ID:4823, and is provided hereinbelow with reference to the sequence listing part.

[31123] GAM2232 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2232 target RNA, herein designated GAM TARGET RNA. GAM2232 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31124] GAM2232 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2232 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2232 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2232 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2232 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31125] The complementary binding of GAM2232 RNA, herein designated GAM RNA, to target binding sites on GAM2232 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2232 target RNA, herein designated GAM TARGET RNA, into GAM2232 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31126] It is appreciated that GAM2232 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2232 target genes. The mRNA of each one of this plurality of GAM2232 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2232 RNA, herein designated GAM RNA, and which when bound by GAM2232 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2232 target proteins.

[31127] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2232 gene, herein designated GAM GENE, on one or more GAM2232 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31128] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2232 correlate with, and may be deduced from, the identity of the target genes which GAM2232 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31129] Nucleotide sequences of the GAM2232 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2232 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2232 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2232 are further described hereinbelow with reference to Table 1.

[31130] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2232 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[31131] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2233 (GAM2233) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31132] GAM2233 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2233 was detected is described hereinabove with reference to Figs. 2-8.

[31133] GAM2233 gene, herein designated GAM GENE, and GAM2233 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[31134] GAM2233 gene, herein designated GAM GENE, encodes a GAM2233 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2233 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2233 precursor RNA is designated SEQ ID:2210, and is provided hereinbelow with reference to the sequence listing part.

[31135] GAM2233 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2233 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

- [31136] An enzyme complex designated DICER COMPLEX, dices the GAM2233 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2233 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 93%) nucleotide sequence of GAM2233 RNA is designated SEQ ID:4824, and is provided hereinbelow with reference to the sequence listing part.
- [31137] GAM2233 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2233 target RNA, herein designated GAM TARGET RNA. GAM2233 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [31138] GAM2233 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2233 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2233 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2233 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2233 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31139] The complementary binding of GAM2233 RNA, herein designated GAM RNA, to target binding sites on GAM2233 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2233 target RNA, herein designated GAM TARGET RNA, into GAM2233 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31140] It is appreciated that GAM2233 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2233 target genes. The mRNA of each one of this plurality of GAM2233 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2233 RNA, herein designated GAM RNA, and which when bound by GAM2233 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2233 target proteins.

[31141] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition



exerted by GAM2233 gene, herein designated GAM GENE, on one or more GAM2233 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31142] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2233 correlate with, and may be deduced from, the identity of the target genes which GAM2233 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31143] Nucleotide sequences of the GAM2233 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2233 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2233 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2233 are further described hereinbelow with reference to Table 1.

[31144] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2233 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

- [31145] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2234 (GAM2234) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.
- [31146] GAM2234 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2234 was detected is described hereinabove with reference to Figs. 2-8.
- [31147] GAM2234 gene, herein designated GAM GENE, and GAM2234 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.
- [31148] GAM2234 gene, herein designated GAM GENE, encodes a GAM2234 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2234 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2234 precursor RNA is designated SEQ ID:2211, and is provided hereinbelow with reference to the sequence listing part.
- [31149] GAM2234 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2234 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31150] An enzyme complex designated DICER COMPLEX, dices the GAM2234 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2234 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 25%) nucleotide sequence of GAM2234 RNA is designated SEQ ID:4825, and is provided hereinbelow with reference to the sequence listing part.

[31151] GAM2234 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2234 target RNA, herein designated GAM TARGET RNA. GAM2234 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31152] GAM2234 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2234 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2234 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2234 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2234 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31153] The complementary binding of GAM2234 RNA, herein designated GAM RNA, to target binding sites on GAM2234 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2234 target RNA, herein designated GAM TARGET RNA, into GAM2234 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31154] It is appreciated that GAM2234 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2234 target genes. The mRNA of each one of this plurality of GAM2234 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2234 RNA, herein designated GAM RNA, and which when bound by GAM2234 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2234 target proteins.

[31155] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2234 gene, herein designated GAM GENE, on one or more GAM2234 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31156] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2234 correlate with, and may be deduced from, the identity of the target genes which GAM2234 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31157] Nucleotide sequences of the GAM2234 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2234 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2234 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2234 are further described hereinbelow with reference to Table 1.

[31158] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2234 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[31159] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2235 (GAM2235) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31160] GAM2235 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2235 was detected is described hereinabove with reference to Figs. 2-8.

[31161] GAM2235 gene, herein designated GAM GENE, and GAM2235 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[31162] GAM2235 gene, herein designated GAM GENE, encodes a GAM2235 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2235 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2235 precursor RNA is designated SEQ ID:2212, and is provided hereinbelow with reference to the sequence listing part.

[31163] GAM2235 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2235 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31164] An enzyme complex designated DICER COMPLEX, dices the GAM2235 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2235 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of GAM2235 RNA is designated SEQ ID:4826, and is provided hereinbelow with reference to the sequence listing part.

[31165] GAM2235 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2235 target RNA, herein designated GAM TARGET RNA. GAM2235 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31166] GAM2235 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2235 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2235 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2235 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2235 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31167] The complementary binding of GAM2235 RNA, herein designated GAM RNA, to target binding sites on GAM2235 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2235 target RNA, herein designated GAM TARGET RNA, into GAM2235 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31168] It is appreciated that GAM2235 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2235 target genes. The



mRNA of each one of this plurality of GAM2235 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2235 RNA, herein designated GAM RNA, and which when bound by GAM2235 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2235 target proteins.

[31169] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2235 gene, herein designated GAM GENE, on one or more GAM2235 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31170] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2235 correlate with, and may be deduced from, the identity of the target genes which GAM2235 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31171] Nucleotide sequences of the GAM2235 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2235 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2235 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2235 are further described hereinbelow with reference to Table 1.

[31172] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2235 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[31173] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2236 (GAM2236) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31174] GAM2236 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2236 was detected is described hereinabove with reference to Figs. 2-8.

[31175] GAM2236 gene, herein designated GAM GENE, and GAM2236 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[31176] GAM2236 gene, herein designated GAM GENE, encodes a GAM2236 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2236 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2236 precursor RNA is designated SEQ ID:2213, and is provided hereinbelow with reference to the sequence listing part.

[31177] GAM2236 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2236 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31178] An enzyme complex designated DICER COMPLEX, dices the GAM2236 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2236 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of GAM2236 RNA is designated SEQ ID:4827, and is provided hereinbelow with reference to the sequence listing part.

[31179] GAM2236 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2236 target RNA, herein designated GAM TARGET RNA. GAM2236 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31180] GAM2236 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2236 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2236 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2236 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2236 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31181] The complementary binding of GAM2236 RNA, herein designated GAM RNA, to target binding sites on GAM2236 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2236 target RNA, herein designated GAM TARGET RNA, into GAM2236 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31182] It is appreciated that GAM2236 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2236 target genes. The mRNA of each one of this plurality of GAM2236 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2236 RNA, herein designated GAM RNA, and which when bound by GAM2236 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2236 target proteins.

[31183] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2236 gene, herein designated GAM GENE, on one or more GAM2236 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31184] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2236 correlate with, and may be deduced from, the identity of the target

genes which GAM2236 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31185] Nucleotide sequences of the GAM2236 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2236 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2236 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2236 are further described hereinbelow with reference to Table 1.

[31186] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2236 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[31187] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2237 (GAM2237) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31188] GAM2237 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2237 was detected is described hereinabove with reference to Figs. 2-8.

[31189] GAM2237 gene, herein designated GAM GENE, and GAM2237 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

[31190] GAM2237 gene, herein designated GAM GENE, encodes a GAM2237 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2237 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2237 precursor RNA is designated SEQ ID:2214, and is provided hereinbelow with reference to the sequence listing part.

[31191] GAM2237 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2237 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31192] An enzyme complex designated DICER COMPLEX, dices the GAM2237 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2237 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 86%) nucleotide sequence of GAM2237 RNA is designated SEQ ID:4828, and is provided

hereinbelow with reference to the sequence listing part.

[31193] GAM2237 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2237 target RNA, herein designated GAM TARGET RNA. GAM2237 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31194] GAM2237 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2237 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2237 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2237 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2237 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.



[31195] The complementary binding of GAM2237 RNA, herein designated GAM RNA, to target binding sites on GAM2237 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2237 target RNA, herein designated GAM TARGET RNA, into GAM2237 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31196] It is appreciated that GAM2237 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2237 target genes. The mRNA of each one of this plurality of GAM2237 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2237 RNA, herein designated GAM RNA, and which when bound by GAM2237 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2237 target proteins.

[31197] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2237 gene, herein designated GAM GENE, on one or more GAM2237 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31198] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2237 correlate with, and may be deduced from, the identity of the target genes which GAM2237 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31199] Nucleotide sequences of the GAM2237 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2237 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2237 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2237 are further described hereinbelow with reference to Table 1.

[31200] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2237 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[31201] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2238 (GAM2238) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31202] GAM2238 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2238 was detected is described hereinabove with reference to Figs. 2-8.

[31203] GAM2238 gene, herein designated GAM GENE, and GAM2238 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[31204] GAM2238 gene, herein designated GAM GENE, encodes a GAM2238 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2238 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2238 precursor RNA is designated SEQ ID:2215, and is provided hereinbelow with reference to the sequence listing part.

[31205] GAM2238 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2238 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31206] An enzyme complex designated DICER COMPLEX, dices the GAM2238 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2238 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 83%) nucleotide sequence of GAM2238 RNA is designated SEQ ID:4830, and is provided hereinbelow with reference to the sequence listing part.

[31207] GAM2238 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2238 target RNA, herein designated GAM TARGET RNA. GAM2238 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31208] GAM2238 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2238 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2238 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2238 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2238 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31209] The complementary binding of GAM2238 RNA, herein designated GAM RNA, to target binding sites on GAM2238 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2238 target RNA, herein designated GAM TARGET RNA, into GAM2238 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31210] It is appreciated that GAM2238 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2238 target genes. The mRNA of each one of this plurality of GAM2238 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2238 RNA, herein designated GAM RNA, and which when bound by GAM2238 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2238 target proteins.

[31211] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2238 gene, herein designated GAM GENE, on one or more GAM2238 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31212] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2238 correlate with, and may be deduced from, the identity of the target genes which GAM2238 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31213] Nucleotide sequences of the GAM2238 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2238 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2238 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2238 are further described hereinbelow with reference to Table 1.

[31214] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2238 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[31215] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2239 (GAM2239) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31216] GAM2239 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2239 was detected is described hereinabove with reference to Figs. 2-8.

[31217] GAM2239 gene, herein designated GAM GENE, and GAM2239 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[31218] GAM2239 gene, herein designated GAM GENE, encodes a GAM2239 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2239 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2239 precursor RNA is designated SEQ ID:2216, and is provided hereinbelow with reference to the sequence listing part.

[31219] GAM2239 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2239 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

- [31220] An enzyme complex designated DICER COMPLEX, dices the GAM2239 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2239 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 85%) nucleotide sequence of GAM2239 RNA is designated SEQ ID:4829, and is provided hereinbelow with reference to the sequence listing part.
- [31221] GAM2239 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2239 target RNA, herein designated GAM TARGET RNA. GAM2239 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [31222] GAM2239 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2239 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2239 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an



illustration only, and is not meant to be limiting GAM2239 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2239 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31223] The complementary binding of GAM2239 RNA, herein designated GAM RNA, to target binding sites on GAM2239 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2239 target RNA, herein designated GAM TARGET RNA, into GAM2239 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31224] It is appreciated that GAM2239 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2239 target genes. The mRNA of each one of this plurality of GAM2239 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2239 RNA, herein designated GAM RNA, and which when bound by GAM2239 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2239 target proteins.

[31225] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2239 gene, herein designated GAM GENE, on one or more GAM2239 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31226] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2239 correlate with, and may be deduced from, the identity of the target genes which GAM2239 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31227] Nucleotide sequences of the GAM2239 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2239 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2239 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2239 are further described hereinbelow with reference to Table 1.

[31228] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2239 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

[31229] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2240 (GAM2240) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31230] GAM2240 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2240 was detected is described hereinabove with reference to Figs. 2-8.

[31231] GAM2240 gene, herein designated GAM GENE, and GAM2240 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[31232] GAM2240 gene, herein designated GAM GENE, encodes a GAM2240 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2240 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2240 precursor RNA is designated SEQ ID:2217, and is provided hereinbelow with reference to the sequence listing part.

[31233] GAM2240 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2240 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31234] An enzyme complex designated DICER COMPLEX, dices the GAM2240 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2240 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 84%) nucleotide sequence of GAM2240 RNA is designated SEQ ID:4831, and is provided hereinbelow with reference to the sequence listing part.

[31235] GAM2240 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2240 target RNA, herein designated GAM TARGET RNA. GAM2240 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31236] GAM2240 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2240 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2240 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2240 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2240 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31237] The complementary binding of GAM2240 RNA, herein designated GAM RNA, to target binding sites on GAM2240 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2240 target RNA, herein designated GAM TARGET RNA, into GAM2240 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31238] It is appreciated that GAM2240 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2240 target genes. The mRNA of each one of this plurality of GAM2240 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2240 RNA, herein designated GAM RNA, and which when bound by GAM2240 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2240 target proteins.

[31239] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2240 gene, herein designated GAM GENE, on one or more GAM2240 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31240] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2240 correlate with, and may be deduced from, the identity of the target genes which GAM2240 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31241] Nucleotide sequences of the GAM2240 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2240 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2240 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2240 are further described hereinbelow with reference to Table 1.

[31242] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2240 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[31243] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2241 (GAM2241) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31244] GAM2241 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2241 was detected is described hereinabove with reference to Figs. 2-8.

[31245] GAM2241 gene, herein designated GAM GENE, and GAM2241 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[31246] GAM2241 gene, herein designated GAM GENE, encodes a GAM2241 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2241 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2241 precursor RNA is designated SEQ ID:2218, and is provided hereinbelow with reference to the sequence listing part.

[31247] GAM2241 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2241 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31248] An enzyme complex designated DICER COMPLEX, dices the GAM2241 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2241 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 83%) nucleotide sequence of GAM2241 RNA is designated SEQ ID:4832, and is provided hereinbelow with reference to the sequence listing part.

[31249] GAM2241 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2241 target RNA, herein designated GAM TARGET RNA. GAM2241 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.



[31250] GAM2241 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2241 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2241 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2241 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2241 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31251] The complementary binding of GAM2241 RNA, herein designated GAM RNA, to target binding sites on GAM2241 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2241 target RNA, herein designated GAM TARGET RNA, into GAM2241 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31252] It is appreciated that GAM2241 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2241 target genes. The

mRNA of each one of this plurality of GAM2241 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2241 RNA, herein designated GAM RNA, and which when bound by GAM2241 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2241 target proteins.

[31253] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2241 gene, herein designated GAM GENE, on one or more GAM2241 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31254] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2241 correlate with, and may be deduced from, the identity of the target genes which GAM2241 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31255] Nucleotide sequences of the GAM2241 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2241 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2241 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2241 are further described hereinbelow with reference to Table 1.

[31256] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2241 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[31257] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2242 (GAM2242) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31258] GAM2242 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2242 was detected is described hereinabove with reference to Figs. 2-8.

[31259] GAM2242 gene, herein designated GAM GENE, and GAM2242 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[31260] GAM2242 gene, herein designated GAM GENE, encodes a GAM2242 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2242 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2242 precursor RNA is designated SEQ ID:2219, and is provided hereinbelow with reference to the sequence listing part.

[31261] GAM2242 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2242 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31262] An enzyme complex designated DICER COMPLEX, dices the GAM2242 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2242 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of GAM2242 RNA is designated SEQ ID:4833, and is provided hereinbelow with reference to the sequence listing part.

[31263] GAM2242 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2242 target RNA, herein designated GAM TARGET RNA. GAM2242 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31264] GAM2242 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2242 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2242 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2242 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2242 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31265] The complementary binding of GAM2242 RNA, herein designated GAM RNA, to target binding sites on GAM2242 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2242 target RNA, herein designated GAM TARGET RNA, into GAM2242 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31266] It is appreciated that GAM2242 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2242 target genes. The mRNA of each one of this plurality of GAM2242 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2242 RNA, herein designated GAM RNA, and which when bound by GAM2242 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2242 target proteins.

[31267] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2242 gene, herein designated GAM GENE, on one or more GAM2242 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31268] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2242 correlate with, and may be deduced from, the identity of the target

genes which GAM2242 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31269] Nucleotide sequences of the GAM2242 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2242 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2242 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2242 are further described hereinbelow with reference to Table 1.

[31270] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2242 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[31271] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2243 (GAM2243) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31272] GAM2243 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2243 was detected is described hereinabove with reference to Figs. 2-8.

[31273] GAM2243 gene, herein designated GAM GENE, and GAM2243 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

[31274] GAM2243 gene, herein designated GAM GENE, encodes a GAM2243 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2243 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2243 precursor RNA is designated SEQ ID:2220, and is provided hereinbelow with reference to the sequence listing part.

[31275] GAM2243 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2243 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31276] An enzyme complex designated DICER COMPLEX, dices the GAM2243 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2243 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 84%) nucleotide sequence of GAM2243 RNA is designated SEQ ID:4834, and is provided



hereinbelow with reference to the sequence listing part.

[31277] GAM2243 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2243 target RNA, herein designated GAM TARGET RNA. GAM2243 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31278] GAM2243 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2243 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2243 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2243 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2243 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31279] The complementary binding of GAM2243 RNA, herein designated GAM RNA, to target binding sites on GAM2243 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2243 target RNA, herein designated GAM TARGET RNA, into GAM2243 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31280] It is appreciated that GAM2243 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2243 target genes. The mRNA of each one of this plurality of GAM2243 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2243 RNA, herein designated GAM RNA, and which when bound by GAM2243 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2243 target proteins.

[31281] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2243 gene, herein designated GAM GENE, on one or more GAM2243 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31282] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2243 correlate with, and may be deduced from, the identity of the target genes which GAM2243 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31283] Nucleotide sequences of the GAM2243 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2243 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2243 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2243 are further described hereinbelow with reference to Table 1.

[31284] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2243 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[31285] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2244 (GAM2244) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31286] GAM2244 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2244 was detected is described hereinabove with reference to Figs. 2-8.

[31287] GAM2244 gene, herein designated GAM GENE, and GAM2244 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[31288] GAM2244 gene, herein designated GAM GENE, encodes a GAM2244 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2244 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2244 precursor RNA is designated SEQ ID:2221, and is provided hereinbelow with reference to the sequence listing part.

[31289] GAM2244 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2244 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31290] An enzyme complex designated DICER COMPLEX, dices the GAM2244 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2244 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 87%) nucleotide sequence of GAM2244 RNA is designated SEQ ID:4835, and is provided hereinbelow with reference to the sequence listing part.

[31291] GAM2244 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2244 target RNA, herein designated GAM TARGET RNA. GAM2244 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31292] GAM2244 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2244 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2244 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2244 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2244 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31293] The complementary binding of GAM2244 RNA, herein designated GAM RNA, to target binding sites on GAM2244 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2244 target RNA, herein designated GAM TARGET RNA, into GAM2244 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31294] It is appreciated that GAM2244 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2244 target genes. The mRNA of each one of this plurality of GAM2244 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2244 RNA, herein designated GAM RNA, and which when bound by GAM2244 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2244 target proteins.

[31295] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2244 gene, herein designated GAM GENE, on one or more GAM2244 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31296] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2244 correlate with, and may be deduced from, the identity of the target genes which GAM2244 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31297] Nucleotide sequences of the GAM2244 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2244 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2244 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2244 are further described hereinbelow with reference to Table 1.

[31298] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2244 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[31299] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2245 (GAM2245) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31300] GAM2245 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2245 was detected is described hereinabove with reference to Figs. 2-8.

[31301] GAM2245 gene, herein designated GAM GENE, and GAM2245 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[31302] GAM2245 gene, herein designated GAM GENE, encodes a GAM2245 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2245 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2245 precursor RNA is designated SEQ ID:2222, and is provided hereinbelow with reference to the sequence listing part.

[31303] GAM2245 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2245 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.



- [31304] An enzyme complex designated DICER COMPLEX, dices the GAM2245 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2245 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of GAM2245 RNA is designated SEQ ID:4836, and is provided hereinbelow with reference to the sequence listing part.
- [31305] GAM2245 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2245 target RNA, herein designated GAM TARGET RNA. GAM2245 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [31306] GAM2245 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2245 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2245 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2245 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2245 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31307] The complementary binding of GAM2245 RNA, herein designated GAM RNA, to target binding sites on GAM2245 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2245 target RNA, herein designated GAM TARGET RNA, into GAM2245 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31308] It is appreciated that GAM2245 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2245 target genes. The mRNA of each one of this plurality of GAM2245 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2245 RNA, herein designated GAM RNA, and which when bound by GAM2245 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2245 target proteins.

[31309] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2245 gene, herein designated GAM GENE, on one or more GAM2245 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31310] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2245 correlate with, and may be deduced from, the identity of the target genes which GAM2245 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31311] Nucleotide sequences of the GAM2245 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2245 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2245 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2245 are further described hereinbelow with reference to Table 1.

[31312] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2245 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

[31313] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2246 (GAM2246) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31314] GAM2246 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2246 was detected is described hereinabove with reference to Figs. 2-8.

[31315] GAM2246 gene, herein designated GAM GENE, and GAM2246 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[31316] GAM2246 gene, herein designated GAM GENE, encodes a GAM2246 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2246 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2246 precursor RNA is designated SEQ ID:2223, and is provided hereinbelow with reference to the sequence listing part.

[31317] GAM2246 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2246 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31318] An enzyme complex designated DICER COMPLEX, dices the GAM2246 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2246 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of GAM2246 RNA is designated SEQ ID:4837, and is provided hereinbelow with reference to the sequence listing part.

[31319] GAM2246 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2246 target RNA, herein designated GAM TARGET RNA. GAM2246 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31320] GAM2246 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2246 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2246 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2246 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2246 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31321] The complementary binding of GAM2246 RNA, herein designated GAM RNA, to target binding sites on GAM2246 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2246 target RNA, herein designated GAM TARGET RNA, into GAM2246 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31322] It is appreciated that GAM2246 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2246 target genes. The mRNA of each one of this plurality of GAM2246 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2246 RNA, herein designated GAM RNA, and which when bound by GAM2246 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2246 target proteins.

[31323] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2246 gene, herein designated GAM GENE, on one or more GAM2246 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31324] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2246 correlate with, and may be deduced from, the identity of the target genes which GAM2246 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31325] Nucleotide sequences of the GAM2246 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2246 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2246 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2246 are further described hereinbelow with reference to Table 1.

[31326] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2246 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[31327] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2247 (GAM2247) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31328] GAM2247 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2247 was detected is described hereinabove with reference to Figs. 2-8.

[31329] GAM2247 gene, herein designated GAM GENE, and GAM2247 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[31330] GAM2247 gene, herein designated GAM GENE, encodes a GAM2247 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2247 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2247 precursor RNA is designated SEQ ID:2224, and is provided hereinbelow with reference to the sequence listing part.



[31331] GAM2247 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2247 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31332] An enzyme complex designated DICER COMPLEX, dices the GAM2247 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2247 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 78%) nucleotide sequence of GAM2247 RNA is designated SEQ ID:4838, and is provided hereinbelow with reference to the sequence listing part.

[31333] GAM2247 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2247 target RNA, herein designated GAM TARGET RNA. GAM2247 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31334] GAM2247 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2247 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2247 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2247 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2247 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31335] The complementary binding of GAM2247 RNA, herein designated GAM RNA, to target binding sites on GAM2247 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2247 target RNA, herein designated GAM TARGET RNA, into GAM2247 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31336] It is appreciated that GAM2247 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2247 target genes. The

mRNA of each one of this plurality of GAM2247 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2247 RNA, herein designated GAM RNA, and which when bound by GAM2247 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2247 target proteins.

[31337] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2247 gene, herein designated GAM GENE, on one or more GAM2247 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31338] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2247 correlate with, and may be deduced from, the identity of the target genes which GAM2247 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31339] Nucleotide sequences of the GAM2247 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2247 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2247 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2247 are further described hereinbelow with reference to Table 1.

[31340] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2247 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[31341] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2248 (GAM2248) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31342] GAM2248 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2248 was detected is described hereinabove with reference to Figs. 2-8.

[31343] GAM2248 gene, herein designated GAM GENE, and GAM2248 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[31344] GAM2248 gene, herein designated GAM GENE, encodes a GAM2248 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2248 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2248 precursor RNA is designated SEQ ID:2225, and is provided hereinbelow with reference to the sequence listing part.

[31345] GAM2248 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2248 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31346] An enzyme complex designated DICER COMPLEX, dices the GAM2248 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2248 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 90%) nucleotide sequence of GAM2248 RNA is designated SEQ ID:4839, and is provided hereinbelow with reference to the sequence listing part.

[31347] GAM2248 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2248 target RNA, herein designated GAM TARGET RNA. GAM2248 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31348] GAM2248 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2248 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2248 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2248 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2248 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31349] The complementary binding of GAM2248 RNA, herein designated GAM RNA, to target binding sites on GAM2248 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2248 target RNA, herein designated GAM TARGET RNA, into GAM2248 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31350] It is appreciated that GAM2248 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2248 target genes. The mRNA of each one of this plurality of GAM2248 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2248 RNA, herein designated GAM RNA, and which when bound by GAM2248 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2248 target proteins.

[31351] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2248 gene, herein designated GAM GENE, on one or more GAM2248 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31352] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2248 correlate with, and may be deduced from, the identity of the target

genes which GAM2248 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31353] Nucleotide sequences of the GAM2248 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2248 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2248 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2248 are further described hereinbelow with reference to Table 1.

[31354] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2248 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[31355] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2249 (GAM2249) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31356] GAM2249 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2249 was detected is described hereinabove with reference to Figs. 2-8.

[31357] GAM2249 gene, herein designated GAM GENE, and GAM2249 target gene, herein designated GAM TARGET GENE, are human genes contained in the



human genome.

[31358] GAM2249 gene, herein designated GAM GENE, encodes a GAM2249 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2249 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2249 precursor RNA is designated SEQ ID:2226, and is provided hereinbelow with reference to the sequence listing part.

[31359] GAM2249 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2249 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31360] An enzyme complex designated DICER COMPLEX, dices the GAM2249 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2249 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 84%) nucleotide sequence of GAM2249 RNA is designated SEQ ID:4840, and is provided

hereinbelow with reference to the sequence listing part.

[31361] GAM2249 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2249 target RNA, herein designated GAM TARGET RNA. GAM2249 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31362] GAM2249 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2249 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2249 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2249 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2249 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31363] The complementary binding of GAM2249 RNA, herein designated GAM RNA, to target binding sites on GAM2249 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2249 target RNA, herein designated GAM TARGET RNA, into GAM2249 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31364] It is appreciated that GAM2249 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2249 target genes. The mRNA of each one of this plurality of GAM2249 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2249 RNA, herein designated GAM RNA, and which when bound by GAM2249 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2249 target proteins.

[31365] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2249 gene, herein designated GAM GENE, on one or more GAM2249 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31366] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2249 correlate with, and may be deduced from, the identity of the target genes which GAM2249 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31367] Nucleotide sequences of the GAM2249 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2249 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2249 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2249 are further described hereinbelow with reference to Table 1.

[31368] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2249 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[31369] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2250 (GAM2250) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31370] GAM2250 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2250 was detected is described hereinabove with reference to Figs. 2-8.

[31371] GAM2250 gene, herein designated GAM GENE, and GAM2250 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[31372] GAM2250 gene, herein designated GAM GENE, encodes a GAM2250 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2250 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2250 precursor RNA is designated SEQ ID:2227, and is provided hereinbelow with reference to the sequence listing part.

[31373] GAM2250 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2250 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31374] An enzyme complex designated DICER COMPLEX, dices the GAM2250 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2250 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2250 RNA is designated SEQ ID:4841, and is provided hereinbelow with reference to the sequence listing part.

[31375] GAM2250 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2250 target RNA, herein designated GAM TARGET RNA. GAM2250 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31376] GAM2250 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2250 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2250 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2250 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2250 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31377] The complementary binding of GAM2250 RNA, herein designated GAM RNA, to target binding sites on GAM2250 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2250 target RNA, herein designated GAM TARGET RNA, into GAM2250 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31378] It is appreciated that GAM2250 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2250 target genes. The mRNA of each one of this plurality of GAM2250 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2250 RNA, herein designated GAM RNA, and which when bound by GAM2250 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2250 target proteins.

[31379] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2250 gene, herein designated GAM GENE, on one or more GAM2250 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31380] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2250 correlate with, and may be deduced from, the identity of the target genes which GAM2250 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31381] Nucleotide sequences of the GAM2250 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2250 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2250 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2250 are further described hereinbelow with reference to Table 1.

[31382] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2250 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[31383] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2251 (GAM2251) gene, which modulates



expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31384] GAM2251 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2251 was detected is described hereinabove with reference to Figs. 2-8.

[31385] GAM2251 gene, herein designated GAM GENE, and GAM2251 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[31386] GAM2251 gene, herein designated GAM GENE, encodes a GAM2251 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2251 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2251 precursor RNA is designated SEQ ID:2228, and is provided hereinbelow with reference to the sequence listing part.

[31387] GAM2251 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2251 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

- [31388] An enzyme complex designated DICER COMPLEX, dices the GAM2251 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2251 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 84%) nucleotide sequence of GAM2251 RNA is designated SEQ ID:4842, and is provided hereinbelow with reference to the sequence listing part.
- [31389] GAM2251 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2251 target RNA, herein designated GAM TARGET RNA. GAM2251 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [31390] GAM2251 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2251 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2251 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2251 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2251 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31391] The complementary binding of GAM2251 RNA, herein designated GAM RNA, to target binding sites on GAM2251 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2251 target RNA, herein designated GAM TARGET RNA, into GAM2251 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31392] It is appreciated that GAM2251 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2251 target genes. The mRNA of each one of this plurality of GAM2251 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2251 RNA, herein designated GAM RNA, and which when bound by GAM2251 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2251 target proteins.

[31393] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2251 gene, herein designated GAM GENE, on one or more GAM2251 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31394] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2251 correlate with, and may be deduced from, the identity of the target genes which GAM2251 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31395] Nucleotide sequences of the GAM2251 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2251 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2251 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2251 are further described hereinbelow with reference to Table 1.

[31396] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2251 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

[31397] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2252 (GAM2252) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31398] GAM2252 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2252 was detected is described hereinabove with reference to Figs. 2-8.

[31399] GAM2252 gene, herein designated GAM GENE, and GAM2252 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[31400] GAM2252 gene, herein designated GAM GENE, encodes a GAM2252 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2252 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2252 precursor RNA is designated SEQ ID:2229, and is provided hereinbelow with reference to the sequence listing part.

[31401] GAM2252 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2252 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31402] An enzyme complex designated DICER COMPLEX, dices the GAM2252 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2252 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 84%) nucleotide sequence of GAM2252 RNA is designated SEQ ID:4843, and is provided hereinbelow with reference to the sequence listing part.

[31403] GAM2252 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2252 target RNA, herein designated GAM TARGET RNA. GAM2252 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31404] GAM2252 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2252 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2252 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2252 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2252 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31405] The complementary binding of GAM2252 RNA, herein designated GAM RNA, to target binding sites on GAM2252 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2252 target RNA, herein designated GAM TARGET RNA, into GAM2252 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31406] It is appreciated that GAM2252 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2252 target genes. The mRNA of each one of this plurality of GAM2252 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2252 RNA, herein designated GAM RNA, and which when bound by GAM2252 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2252 target proteins.

[31407] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2252 gene, herein designated GAM GENE, on one or more GAM2252 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31408] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2252 correlate with, and may be deduced from, the identity of the target genes which GAM2252 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31409] Nucleotide sequences of the GAM2252 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2252 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2252 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2252 are further described hereinbelow with reference to Table 1.



- [31410] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2252 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.
- [31411] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2253 (GAM2253) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.
- [31412] GAM2253 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2253 was detected is described hereinabove with reference to Figs. 2-8.
- [31413] GAM2253 gene, herein designated GAM GENE, and GAM2253 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.
- [31414] GAM2253 gene, herein designated GAM GENE, encodes a GAM2253 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2253 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2253 precursor RNA is designated SEQ ID:2230, and is provided hereinbelow with reference to the sequence listing part.

[31415] GAM2253 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2253 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31416] An enzyme complex designated DICER COMPLEX, dices the GAM2253 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2253 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of GAM2253 RNA is designated SEQ ID:4844, and is provided hereinbelow with reference to the sequence listing part.

[31417] GAM2253 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2253 target RNA, herein designated GAM TARGET RNA. GAM2253 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31418] GAM2253 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2253 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2253 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2253 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2253 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31419] The complementary binding of GAM2253 RNA, herein designated GAM RNA, to target binding sites on GAM2253 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2253 target RNA, herein designated GAM TARGET RNA, into GAM2253 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31420] It is appreciated that GAM2253 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2253 target genes. The

mRNA of each one of this plurality of GAM2253 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2253 RNA, herein designated GAM RNA, and which when bound by GAM2253 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2253 target proteins.

[31421] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2253 gene, herein designated GAM GENE, on one or more GAM2253 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31422] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2253 correlate with, and may be deduced from, the identity of the target genes which GAM2253 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31423] Nucleotide sequences of the GAM2253 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2253 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2253 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2253 are further described hereinbelow with reference to Table 1.

[31424] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2253 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[31425] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2254 (GAM2254) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31426] GAM2254 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2254 was detected is described hereinabove with reference to Figs. 2-8.

[31427] GAM2254 gene, herein designated GAM GENE, and GAM2254 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[31428] GAM2254 gene, herein designated GAM GENE, encodes a GAM2254 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2254 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2254 precursor RNA is designated SEQ ID:2231, and is provided hereinbelow with reference to the sequence listing part.

[31429] GAM2254 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2254 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31430] An enzyme complex designated DICER COMPLEX, dices the GAM2254 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2254 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM2254 RNA is designated SEQ ID:4845, and is provided hereinbelow with reference to the sequence listing part.

[31431] GAM2254 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2254 target RNA, herein designated GAM TARGET RNA. GAM2254 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31432] GAM2254 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2254 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2254 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2254 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2254 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31433] The complementary binding of GAM2254 RNA, herein designated GAM RNA, to target binding sites on GAM2254 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2254 target RNA, herein designated GAM TARGET RNA, into GAM2254 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31434] It is appreciated that GAM2254 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2254 target genes. The mRNA of each one of this plurality of GAM2254 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2254 RNA, herein designated GAM RNA, and which when bound by GAM2254 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2254 target proteins.

[31435] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2254 gene, herein designated GAM GENE, on one or more GAM2254 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31436] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2254 correlate with, and may be deduced from, the identity of the target



genes which GAM2254 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31437] Nucleotide sequences of the GAM2254 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2254 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2254 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2254 are further described hereinbelow with reference to Table 1.

[31438] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2254 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[31439] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2255 (GAM2255) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31440] GAM2255 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2255 was detected is described hereinabove with reference to Figs. 2-8.

[31441] GAM2255 gene, herein designated GAM GENE, and GAM2255 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

[31442] GAM2255 gene, herein designated GAM GENE, encodes a GAM2255 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2255 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2255 precursor RNA is designated SEQ ID:2232, and is provided hereinbelow with reference to the sequence listing part.

[31443] GAM2255 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2255 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31444] An enzyme complex designated DICER COMPLEX, dices the GAM2255 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2255 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2255 RNA is designated SEQ ID:4846, and is provided

hereinbelow with reference to the sequence listing part.

[31445] GAM2255 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2255 target RNA, herein designated GAM TARGET RNA. GAM2255 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31446] GAM2255 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2255 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2255 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2255 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2255 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31447] The complementary binding of GAM2255 RNA, herein designated GAM RNA, to target binding sites on GAM2255 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2255 target RNA, herein designated GAM TARGET RNA, into GAM2255 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31448] It is appreciated that GAM2255 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2255 target genes. The mRNA of each one of this plurality of GAM2255 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2255 RNA, herein designated GAM RNA, and which when bound by GAM2255 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2255 target proteins.

[31449] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2255 gene, herein designated GAM GENE, on one or more GAM2255 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31450] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2255 correlate with, and may be deduced from, the identity of the target genes which GAM2255 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31451] Nucleotide sequences of the GAM2255 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2255 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2255 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2255 are further described hereinbelow with reference to Table 1.

[31452] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2255 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[31453] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2256 (GAM2256) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31454] GAM2256 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2256 was detected is described hereinabove with reference to Figs. 2-8.

[31455] GAM2256 gene, herein designated GAM GENE, and GAM2256 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[31456] GAM2256 gene, herein designated GAM GENE, encodes a GAM2256 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2256 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2256 precursor RNA is designated SEQ ID:2233, and is provided hereinbelow with reference to the sequence listing part.

[31457] GAM2256 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2256 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31458] An enzyme complex designated DICER COMPLEX, dices the GAM2256 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2256 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 78%) nucleotide sequence of GAM2256 RNA is designated SEQ ID:4847, and is provided hereinbelow with reference to the sequence listing part.

[31459] GAM2256 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2256 target RNA, herein designated GAM TARGET RNA. GAM2256 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31460] GAM2256 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2256 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2256 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2256 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2256 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31461] The complementary binding of GAM2256 RNA, herein designated GAM RNA, to target binding sites on GAM2256 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2256 target RNA, herein designated GAM TARGET RNA, into GAM2256 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31462] It is appreciated that GAM2256 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2256 target genes. The mRNA of each one of this plurality of GAM2256 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2256 RNA, herein designated GAM RNA, and which when bound by GAM2256 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2256 target proteins.

[31463] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2256 gene, herein designated GAM GENE, on one or more GAM2256 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary



binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31464] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2256 correlate with, and may be deduced from, the identity of the target genes which GAM2256 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31465] Nucleotide sequences of the GAM2256 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2256 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2256 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2256 are further described hereinbelow with reference to Table 1.

[31466] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2256 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[31467] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2257 (GAM2257) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31468] GAM2257 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2257 was detected is described hereinabove with reference to Figs. 2-8.

[31469] GAM2257 gene, herein designated GAM GENE, and GAM2257 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[31470] GAM2257 gene, herein designated GAM GENE, encodes a GAM2257 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2257 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2257 precursor RNA is designated SEQ ID:2234, and is provided hereinbelow with reference to the sequence listing part.

[31471] GAM2257 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2257 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

- [31472] An enzyme complex designated DICER COMPLEX, dices the GAM2257 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2257 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 88%) nucleotide sequence of GAM2257 RNA is designated SEQ ID:4848, and is provided hereinbelow with reference to the sequence listing part.
- [31473] GAM2257 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2257 target RNA, herein designated GAM TARGET RNA. GAM2257 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [31474] GAM2257 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2257 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2257 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2257 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2257 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31475] The complementary binding of GAM2257 RNA, herein designated GAM RNA, to target binding sites on GAM2257 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2257 target RNA, herein designated GAM TARGET RNA, into GAM2257 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31476] It is appreciated that GAM2257 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2257 target genes. The mRNA of each one of this plurality of GAM2257 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2257 RNA, herein designated GAM RNA, and which when bound by GAM2257 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2257 target proteins.

[31477] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2257 gene, herein designated GAM GENE, on one or more GAM2257 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31478] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2257 correlate with, and may be deduced from, the identity of the target genes which GAM2257 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31479] Nucleotide sequences of the GAM2257 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2257 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2257 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2257 are further described hereinbelow with reference to Table 1.

[31480] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2257 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

[31481] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2258 (GAM2258) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31482] GAM2258 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2258 was detected is described hereinabove with reference to Figs. 2-8.

[31483] GAM2258 gene, herein designated GAM GENE, and GAM2258 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[31484] GAM2258 gene, herein designated GAM GENE, encodes a GAM2258 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2258 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2258 precursor RNA is designated SEQ ID:2235, and is provided hereinbelow with reference to the sequence listing part.

[31485] GAM2258 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2258 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31486] An enzyme complex designated DICER COMPLEX, dices the GAM2258 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2258 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of GAM2258 RNA is designated SEQ ID:4849, and is provided hereinbelow with reference to the sequence listing part.

[31487] GAM2258 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2258 target RNA, herein designated GAM TARGET RNA. GAM2258 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31488] GAM2258 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2258 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2258 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2258 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2258 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31489] The complementary binding of GAM2258 RNA, herein designated GAM RNA, to target binding sites on GAM2258 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2258 target RNA, herein designated GAM TARGET RNA, into GAM2258 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31490] It is appreciated that GAM2258 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2258 target genes. The mRNA of each one of this plurality of GAM2258 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2258 RNA, herein designated GAM RNA, and which when bound by GAM2258 RNA, herein designated GAM RNA,



causes inhibition of translation of respective one or more GAM2258 target proteins.

[31491] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2258 gene, herein designated GAM GENE, on one or more GAM2258 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31492] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2258 correlate with, and may be deduced from, the identity of the target genes which GAM2258 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31493] Nucleotide sequences of the GAM2258 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2258 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2258 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2258 are further described hereinbelow with reference to Table 1.

- [31494] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2258 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.
- [31495] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2259 (GAM2259) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.
- [31496] GAM2259 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2259 was detected is described hereinabove with reference to Figs. 2-8.
- [31497] GAM2259 gene, herein designated GAM GENE, and GAM2259 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.
- [31498] GAM2259 gene, herein designated GAM GENE, encodes a GAM2259 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2259 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2259 precursor RNA is designated SEQ ID:2236, and is provided hereinbelow with reference to the sequence listing part.

[31499] GAM2259 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2259 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31500] An enzyme complex designated DICER COMPLEX, dices the GAM2259 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2259 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of GAM2259 RNA is designated SEQ ID:4851, and is provided hereinbelow with reference to the sequence listing part.

[31501] GAM2259 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2259 target RNA, herein designated GAM TARGET RNA. GAM2259 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31502] GAM2259 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2259 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2259 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2259 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2259 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31503] The complementary binding of GAM2259 RNA, herein designated GAM RNA, to target binding sites on GAM2259 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2259 target RNA, herein designated GAM TARGET RNA, into GAM2259 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31504] It is appreciated that GAM2259 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2259 target genes. The

mRNA of each one of this plurality of GAM2259 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2259 RNA, herein designated GAM RNA, and which when bound by GAM2259 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2259 target proteins.

[31505] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2259 gene, herein designated GAM GENE, on one or more GAM2259 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31506] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2259 correlate with, and may be deduced from, the identity of the target genes which GAM2259 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31507] Nucleotide sequences of the GAM2259 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2259 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2259 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2259 are further described hereinbelow with reference to Table 1.

[31508] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2259 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[31509] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2260 (GAM2260) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31510] GAM2260 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2260 was detected is described hereinabove with reference to Figs. 2-8.

[31511] GAM2260 gene, herein designated GAM GENE, and GAM2260 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[31512] GAM2260 gene, herein designated GAM GENE, encodes a GAM2260 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2260 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2260 precursor RNA is designated SEQ ID:2237, and is provided hereinbelow with reference to the sequence listing part.

[31513] GAM2260 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2260 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31514] An enzyme complex designated DICER COMPLEX, dices the GAM2260 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2260 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of GAM2260 RNA is designated SEQ ID:4850, and is provided hereinbelow with reference to the sequence listing part.

[31515] GAM2260 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2260 target RNA, herein designated GAM TARGET RNA. GAM2260 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31516] GAM2260 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2260 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2260 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2260 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2260 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31517] The complementary binding of GAM2260 RNA, herein designated GAM RNA, to target binding sites on GAM2260 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2260 target RNA, herein designated GAM TARGET RNA, into GAM2260 target protein, herein



designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31518] It is appreciated that GAM2260 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2260 target genes. The mRNA of each one of this plurality of GAM2260 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2260 RNA, herein designated GAM RNA, and which when bound by GAM2260 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2260 target proteins.

[31519] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2260 gene, herein designated GAM GENE, on one or more GAM2260 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31520] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2260 correlate with, and may be deduced from, the identity of the target

genes which GAM2260 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31521] Nucleotide sequences of the GAM2260 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2260 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2260 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2260 are further described hereinbelow with reference to Table 1.

[31522] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2260 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[31523] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2261 (GAM2261) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31524] GAM2261 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2261 was detected is described hereinabove with reference to Figs. 2-8.

[31525] GAM2261 gene, herein designated GAM GENE, and GAM2261 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

[31526] GAM2261 gene, herein designated GAM GENE, encodes a GAM2261 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2261 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2261 precursor RNA is designated SEQ ID:2238, and is provided hereinbelow with reference to the sequence listing part.

[31527] GAM2261 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2261 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31528] An enzyme complex designated DICER COMPLEX, dices the GAM2261 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2261 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of GAM2261 RNA is designated SEQ ID:4852, and is provided

hereinbelow with reference to the sequence listing part.

[31529] GAM2261 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2261 target RNA, herein designated GAM TARGET RNA. GAM2261 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31530] GAM2261 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2261 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2261 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2261 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2261 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31531] The complementary binding of GAM2261 RNA, herein designated GAM RNA, to target binding sites on GAM2261 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2261 target RNA, herein designated GAM TARGET RNA, into GAM2261 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31532] It is appreciated that GAM2261 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2261 target genes. The mRNA of each one of this plurality of GAM2261 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2261 RNA, herein designated GAM RNA, and which when bound by GAM2261 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2261 target proteins.

[31533] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2261 gene, herein designated GAM GENE, on one or more GAM2261 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31534] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2261 correlate with, and may be deduced from, the identity of the target genes which GAM2261 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31535] Nucleotide sequences of the GAM2261 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2261 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2261 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2261 are further described hereinbelow with reference to Table 1.

[31536] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2261 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[31537] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2262 (GAM2262) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31538] GAM2262 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2262 was detected is described hereinabove with reference to Figs. 2-8.

[31539] GAM2262 gene, herein designated GAM GENE, and GAM2262 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[31540] GAM2262 gene, herein designated GAM GENE, encodes a GAM2262 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2262 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2262 precursor RNA is designated SEQ ID:2239, and is provided hereinbelow with reference to the sequence listing part.

[31541] GAM2262 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2262 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31542] An enzyme complex designated DICER COMPLEX, dices the GAM2262 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2262 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 87%) nucleotide sequence of GAM2262 RNA is designated SEQ ID:4853, and is provided hereinbelow with reference to the sequence listing part.

[31543] GAM2262 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2262 target RNA, herein designated GAM TARGET RNA. GAM2262 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31544] GAM2262 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2262 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2262 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2262 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2262 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target



binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31545] The complementary binding of GAM2262 RNA, herein designated GAM RNA, to target binding sites on GAM2262 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2262 target RNA, herein designated GAM TARGET RNA, into GAM2262 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31546] It is appreciated that GAM2262 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2262 target genes. The mRNA of each one of this plurality of GAM2262 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2262 RNA, herein designated GAM RNA, and which when bound by GAM2262 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2262 target proteins.

[31547] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2262 gene, herein designated GAM GENE, on one or more GAM2262 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31548] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2262 correlate with, and may be deduced from, the identity of the target genes which GAM2262 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31549] Nucleotide sequences of the GAM2262 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2262 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2262 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2262 are further described hereinbelow with reference to Table 1.

[31550] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2262 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[31551] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2263 (GAM2263) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31552] GAM2263 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2263 was detected is described hereinabove with reference to Figs. 2-8.

[31553] GAM2263 gene, herein designated GAM GENE, and GAM2263 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[31554] GAM2263 gene, herein designated GAM GENE, encodes a GAM2263 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2263 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2263 precursor RNA is designated SEQ ID:2240, and is provided hereinbelow with reference to the sequence listing part.

[31555] GAM2263 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2263 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

- [31556] An enzyme complex designated DICER COMPLEX, dices the GAM2263 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2263 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 84%) nucleotide sequence of GAM2263 RNA is designated SEQ ID:4854, and is provided hereinbelow with reference to the sequence listing part.
- [31557] GAM2263 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2263 target RNA, herein designated GAM TARGET RNA. GAM2263 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [31558] GAM2263 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2263 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2263 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2263 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2263 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31559] The complementary binding of GAM2263 RNA, herein designated GAM RNA, to target binding sites on GAM2263 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2263 target RNA, herein designated GAM TARGET RNA, into GAM2263 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31560] It is appreciated that GAM2263 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2263 target genes. The mRNA of each one of this plurality of GAM2263 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2263 RNA, herein designated GAM RNA, and which when bound by GAM2263 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2263 target proteins.

[31561] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2263 gene, herein designated GAM GENE, on one or more GAM2263 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31562] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2263 correlate with, and may be deduced from, the identity of the target genes which GAM2263 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31563] Nucleotide sequences of the GAM2263 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2263 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2263 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2263 are further described hereinbelow with reference to Table 1.

[31564] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2263 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

[31565] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2264 (GAM2264) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31566] GAM2264 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2264 was detected is described hereinabove with reference to Figs. 2-8.

[31567] GAM2264 gene, herein designated GAM GENE, and GAM2264 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[31568] GAM2264 gene, herein designated GAM GENE, encodes a GAM2264 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2264 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2264 precursor RNA is designated SEQ ID:2241, and is provided hereinbelow with reference to the sequence listing part.

[31569] GAM2264 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2264 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31570] An enzyme complex designated DICER COMPLEX, dices the GAM2264 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2264 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of GAM2264 RNA is designated SEQ ID:4856, and is provided hereinbelow with reference to the sequence listing part.

[31571] GAM2264 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2264 target RNA, herein designated GAM TARGET RNA. GAM2264 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31572] GAM2264 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2264 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2264 RNA,



herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2264 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2264 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31573] The complementary binding of GAM2264 RNA, herein designated GAM RNA, to target binding sites on GAM2264 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2264 target RNA, herein designated GAM TARGET RNA, into GAM2264 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31574] It is appreciated that GAM2264 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2264 target genes. The mRNA of each one of this plurality of GAM2264 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2264 RNA, herein designated GAM RNA, and which when bound by GAM2264 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2264 target proteins.

[31575] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2264 gene, herein designated GAM GENE, on one or more GAM2264 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31576] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2264 correlate with, and may be deduced from, the identity of the target genes which GAM2264 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31577] Nucleotide sequences of the GAM2264 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2264 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2264 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2264 are further described hereinbelow with reference to Table 1.

[31578] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2264 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[31579] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2265 (GAM2265) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31580] GAM2265 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2265 was detected is described hereinabove with reference to Figs. 2-8.

[31581] GAM2265 gene, herein designated GAM GENE, and GAM2265 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[31582] GAM2265 gene, herein designated GAM GENE, encodes a GAM2265 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2265 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2265 precursor RNA is designated SEQ ID:2242, and is provided hereinbelow with reference to the sequence listing part.

[31583] GAM2265 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2265 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31584] An enzyme complex designated DICER COMPLEX, dices the GAM2265 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2265 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 83%) nucleotide sequence of GAM2265 RNA is designated SEQ ID:4855, and is provided hereinbelow with reference to the sequence listing part.

[31585] GAM2265 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2265 target RNA, herein designated GAM TARGET RNA. GAM2265 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31586] GAM2265 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2265 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2265 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2265 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2265 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31587] The complementary binding of GAM2265 RNA, herein designated GAM RNA, to target binding sites on GAM2265 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2265 target RNA, herein designated GAM TARGET RNA, into GAM2265 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31588] It is appreciated that GAM2265 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2265 target genes. The

mRNA of each one of this plurality of GAM2265 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2265 RNA, herein designated GAM RNA, and which when bound by GAM2265 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2265 target proteins.

[31589] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2265 gene, herein designated GAM GENE, on one or more GAM2265 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31590] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2265 correlate with, and may be deduced from, the identity of the target genes which GAM2265 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31591] Nucleotide sequences of the GAM2265 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2265 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2265 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2265 are further described hereinbelow with reference to Table 1.

[31592] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2265 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[31593] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2266 (GAM2266) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31594] GAM2266 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2266 was detected is described hereinabove with reference to Figs. 2-8.

[31595] GAM2266 gene, herein designated GAM GENE, and GAM2266 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[31596] GAM2266 gene, herein designated GAM GENE, encodes a GAM2266 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2266 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2266 precursor RNA is designated SEQ ID:2243, and is provided hereinbelow with reference to the sequence listing part.

[31597] GAM2266 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2266 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31598] An enzyme complex designated DICER COMPLEX, dices the GAM2266 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2266 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 84%) nucleotide sequence of GAM2266 RNA is designated SEQ ID:4857, and is provided hereinbelow with reference to the sequence listing part.

[31599] GAM2266 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2266 target RNA, herein designated GAM TARGET RNA. GAM2266 target RNA, herein designated GAM



TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31600] GAM2266 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2266 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2266 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2266 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2266 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31601] The complementary binding of GAM2266 RNA, herein designated GAM RNA, to target binding sites on GAM2266 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2266 target RNA, herein designated GAM TARGET RNA, into GAM2266 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31602] It is appreciated that GAM2266 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2266 target genes. The mRNA of each one of this plurality of GAM2266 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2266 RNA, herein designated GAM RNA, and which when bound by GAM2266 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2266 target proteins.

[31603] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2266 gene, herein designated GAM GENE, on one or more GAM2266 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31604] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2266 correlate with, and may be deduced from, the identity of the target

genes which GAM2266 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31605] Nucleotide sequences of the GAM2266 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2266 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2266 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2266 are further described hereinbelow with reference to Table 1.

[31606] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2266 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[31607] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2267 (GAM2267) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31608] GAM2267 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2267 was detected is described hereinabove with reference to Figs. 2-8.

[31609] GAM2267 gene, herein designated GAM GENE, and GAM2267 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

[31610] GAM2267 gene, herein designated GAM GENE, encodes a GAM2267 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2267 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2267 precursor RNA is designated SEQ ID:2244, and is provided hereinbelow with reference to the sequence listing part.

[31611] GAM2267 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2267 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31612] An enzyme complex designated DICER COMPLEX, dices the GAM2267 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2267 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of GAM2267 RNA is designated SEQ ID:4858, and is provided

hereinbelow with reference to the sequence listing part.

[31613] GAM2267 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2267 target RNA, herein designated GAM TARGET RNA. GAM2267 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31614] GAM2267 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2267 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2267 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2267 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2267 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31615] The complementary binding of GAM2267 RNA, herein designated GAM RNA, to target binding sites on GAM2267 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2267 target RNA, herein designated GAM TARGET RNA, into GAM2267 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31616] It is appreciated that GAM2267 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2267 target genes. The mRNA of each one of this plurality of GAM2267 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2267 RNA, herein designated GAM RNA, and which when bound by GAM2267 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2267 target proteins.

[31617] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2267 gene, herein designated GAM GENE, on one or more GAM2267 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31618] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2267 correlate with, and may be deduced from, the identity of the target genes which GAM2267 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31619] Nucleotide sequences of the GAM2267 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2267 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2267 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2267 are further described hereinbelow with reference to Table 1.

[31620] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2267 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[31621] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2268 (GAM2268) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31622] GAM2268 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2268 was detected is described hereinabove with reference to Figs. 2-8.

[31623] GAM2268 gene, herein designated GAM GENE, and GAM2268 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[31624] GAM2268 gene, herein designated GAM GENE, encodes a GAM2268 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2268 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2268 precursor RNA is designated SEQ ID:2245, and is provided hereinbelow with reference to the sequence listing part.

[31625] GAM2268 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2268 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31626] An enzyme complex designated DICER COMPLEX, dices the GAM2268 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2268 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin



structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2268 RNA is designated SEQ ID:4859, and is provided hereinbelow with reference to the sequence listing part.

[31627] GAM2268 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2268 target RNA, herein designated GAM TARGET RNA. GAM2268 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31628] GAM2268 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2268 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2268 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2268 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2268 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31629] The complementary binding of GAM2268 RNA, herein designated GAM RNA, to target binding sites on GAM2268 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2268 target RNA, herein designated GAM TARGET RNA, into GAM2268 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31630] It is appreciated that GAM2268 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2268 target genes. The mRNA of each one of this plurality of GAM2268 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2268 RNA, herein designated GAM RNA, and which when bound by GAM2268 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2268 target proteins.

[31631] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2268 gene, herein designated GAM GENE, on one or more GAM2268 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31632] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2268 correlate with, and may be deduced from, the identity of the target genes which GAM2268 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31633] Nucleotide sequences of the GAM2268 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2268 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2268 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2268 are further described hereinbelow with reference to Table 1.

[31634] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2268 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[31635] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2269 (GAM2269) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31636] GAM2269 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2269 was detected is described hereinabove with reference to Figs. 2-8.

[31637] GAM2269 gene, herein designated GAM GENE, and GAM2269 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[31638] GAM2269 gene, herein designated GAM GENE, encodes a GAM2269 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2269 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2269 precursor RNA is designated SEQ ID:2246, and is provided hereinbelow with reference to the sequence listing part.

[31639] GAM2269 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2269 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

- [31640] An enzyme complex designated DICER COMPLEX, dices the GAM2269 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2269 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2269 RNA is designated SEQ ID:4860, and is provided hereinbelow with reference to the sequence listing part.
- [31641] GAM2269 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2269 target RNA, herein designated GAM TARGET RNA. GAM2269 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [31642] GAM2269 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2269 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2269 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2269 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2269 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31643] The complementary binding of GAM2269 RNA, herein designated GAM RNA, to target binding sites on GAM2269 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2269 target RNA, herein designated GAM TARGET RNA, into GAM2269 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31644] It is appreciated that GAM2269 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2269 target genes. The mRNA of each one of this plurality of GAM2269 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2269 RNA, herein designated GAM RNA, and which when bound by GAM2269 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2269 target proteins.

[31645] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2269 gene, herein designated GAM GENE, on one or more GAM2269 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31646] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2269 correlate with, and may be deduced from, the identity of the target genes which GAM2269 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31647] Nucleotide sequences of the GAM2269 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2269 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2269 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2269 are further described hereinbelow with reference to Table 1.

[31648] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2269 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

[31649] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2270 (GAM2270) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31650] GAM2270 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2270 was detected is described hereinabove with reference to Figs. 2-8.

[31651] GAM2270 gene, herein designated GAM GENE, and GAM2270 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[31652] GAM2270 gene, herein designated GAM GENE, encodes a GAM2270 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2270 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2270 precursor RNA is designated SEQ ID:2247, and is provided hereinbelow with reference to the sequence listing part.

[31653] GAM2270 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2270 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA



encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31654] An enzyme complex designated DICER COMPLEX, dices the GAM2270 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2270 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 83%) nucleotide sequence of GAM2270 RNA is designated SEQ ID:4861, and is provided hereinbelow with reference to the sequence listing part.

[31655] GAM2270 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2270 target RNA, herein designated GAM TARGET RNA. GAM2270 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31656] GAM2270 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2270 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2270 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2270 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2270 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31657] The complementary binding of GAM2270 RNA, herein designated GAM RNA, to target binding sites on GAM2270 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2270 target RNA, herein designated GAM TARGET RNA, into GAM2270 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31658] It is appreciated that GAM2270 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2270 target genes. The mRNA of each one of this plurality of GAM2270 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2270 RNA, herein designated GAM RNA, and which when bound by GAM2270 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2270 target proteins.

[31659] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2270 gene, herein designated GAM GENE, on one or more GAM2270 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31660] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2270 correlate with, and may be deduced from, the identity of the target genes which GAM2270 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31661] Nucleotide sequences of the GAM2270 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2270 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2270 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2270 are further described hereinbelow with reference to Table 1.

[31662] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2270 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[31663] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2271 (GAM2271) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31664] GAM2271 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2271 was detected is described hereinabove with reference to Figs. 2-8.

[31665] GAM2271 gene, herein designated GAM GENE, and GAM2271 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[31666] GAM2271 gene, herein designated GAM GENE, encodes a GAM2271 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2271 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2271 precursor RNA is designated SEQ ID:2248, and is provided hereinbelow with reference to the sequence listing part.

[31667] GAM2271 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2271 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31668] An enzyme complex designated DICER COMPLEX, dices the GAM2271 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2271 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2271 RNA is designated SEQ ID:4862, and is provided hereinbelow with reference to the sequence listing part.

[31669] GAM2271 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2271 target RNA, herein designated GAM TARGET RNA. GAM2271 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31670] GAM2271 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2271 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2271 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2271 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2271 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31671] The complementary binding of GAM2271 RNA, herein designated GAM RNA, to target binding sites on GAM2271 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2271 target RNA, herein designated GAM TARGET RNA, into GAM2271 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31672] It is appreciated that GAM2271 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2271 target genes. The

mRNA of each one of this plurality of GAM2271 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2271 RNA, herein designated GAM RNA, and which when bound by GAM2271 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2271 target proteins.

[31673] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2271 gene, herein designated GAM GENE, on one or more GAM2271 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31674] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2271 correlate with, and may be deduced from, the identity of the target genes which GAM2271 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31675] Nucleotide sequences of the GAM2271 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2271 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2271 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2271 are further described hereinbelow with reference to Table 1.

[31676] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2271 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[31677] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2272 (GAM2272) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31678] GAM2272 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2272 was detected is described hereinabove with reference to Figs. 2-8.

[31679] GAM2272 gene, herein designated GAM GENE, and GAM2272 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[31680] GAM2272 gene, herein designated GAM GENE, encodes a GAM2272 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2272 precursor RNA,



herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2272 precursor RNA is designated SEQ ID:2249, and is provided hereinbelow with reference to the sequence listing part.

[31681] GAM2272 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2272 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31682] An enzyme complex designated DICER COMPLEX, dices the GAM2272 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2272 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 85%) nucleotide sequence of GAM2272 RNA is designated SEQ ID:4863, and is provided hereinbelow with reference to the sequence listing part.

[31683] GAM2272 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2272 target RNA, herein designated GAM TARGET RNA. GAM2272 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31684] GAM2272 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2272 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2272 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2272 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2272 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31685] The complementary binding of GAM2272 RNA, herein designated GAM RNA, to target binding sites on GAM2272 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2272 target RNA, herein designated GAM TARGET RNA, into GAM2272 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31686] It is appreciated that GAM2272 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2272 target genes. The mRNA of each one of this plurality of GAM2272 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2272 RNA, herein designated GAM RNA, and which when bound by GAM2272 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2272 target proteins.

[31687] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2272 gene, herein designated GAM GENE, on one or more GAM2272 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31688] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2272 correlate with, and may be deduced from, the identity of the target

genes which GAM2272 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31689] Nucleotide sequences of the GAM2272 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2272 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2272 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2272 are further described hereinbelow with reference to Table 1.

[31690] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2272 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[31691] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2273 (GAM2273) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31692] GAM2273 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2273 was detected is described hereinabove with reference to Figs. 2-8.

[31693] GAM2273 gene, herein designated GAM GENE, and GAM2273 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

[31694] GAM2273 gene, herein designated GAM GENE, encodes a GAM2273 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2273 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2273 precursor RNA is designated SEQ ID:2250, and is provided hereinbelow with reference to the sequence listing part.

[31695] GAM2273 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2273 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31696] An enzyme complex designated DICER COMPLEX, dices the GAM2273 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2273 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 88%) nucleotide sequence of GAM2273 RNA is designated SEQ ID:4864, and is provided

hereinbelow with reference to the sequence listing part.

[31697] GAM2273 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2273 target RNA, herein designated GAM TARGET RNA. GAM2273 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31698] GAM2273 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2273 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2273 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2273 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2273 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31699] The complementary binding of GAM2273 RNA, herein designated GAM RNA, to target binding sites on GAM2273 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2273 target RNA, herein designated GAM TARGET RNA, into GAM2273 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31700] It is appreciated that GAM2273 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2273 target genes. The mRNA of each one of this plurality of GAM2273 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2273 RNA, herein designated GAM RNA, and which when bound by GAM2273 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2273 target proteins.

[31701] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2273 gene, herein designated GAM GENE, on one or more GAM2273 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31702] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2273 correlate with, and may be deduced from, the identity of the target genes which GAM2273 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31703] Nucleotide sequences of the GAM2273 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2273 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2273 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2273 are further described hereinbelow with reference to Table 1.

[31704] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2273 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[31705] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2274 (GAM2274) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31706] GAM2274 is a novel bioinformatically detected regulatory, non protein



coding, micro RNA (miRNA) gene. The method by which GAM2274 was detected is described hereinabove with reference to Figs. 2-8.

[31707] GAM2274 gene, herein designated GAM GENE, and GAM2274 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[31708] GAM2274 gene, herein designated GAM GENE, encodes a GAM2274 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2274 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2274 precursor RNA is designated SEQ ID:2251, and is provided hereinbelow with reference to the sequence listing part.

[31709] GAM2274 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2274 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31710] An enzyme complex designated DICER COMPLEX, dices the GAM2274 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2274 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 88%) nucleotide sequence of GAM2274 RNA is designated SEQ ID:4865, and is provided hereinbelow with reference to the sequence listing part.

[31711] GAM2274 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2274 target RNA, herein designated GAM TARGET RNA. GAM2274 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31712] GAM2274 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2274 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2274 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2274 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2274 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31713] The complementary binding of GAM2274 RNA, herein designated GAM RNA, to target binding sites on GAM2274 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2274 target RNA, herein designated GAM TARGET RNA, into GAM2274 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31714] It is appreciated that GAM2274 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2274 target genes. The mRNA of each one of this plurality of GAM2274 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2274 RNA, herein designated GAM RNA, and which when bound by GAM2274 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2274 target proteins.

[31715] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2274 gene, herein designated GAM GENE, on one or more GAM2274 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31716] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2274 correlate with, and may be deduced from, the identity of the target genes which GAM2274 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31717] Nucleotide sequences of the GAM2274 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2274 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2274 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2274 are further described hereinbelow with reference to Table 1.

[31718] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2274 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[31719] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2275 (GAM2275) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31720] GAM2275 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2275 was detected is described hereinabove with reference to Figs. 2-8.

[31721] GAM2275 gene, herein designated GAM GENE, and GAM2275 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[31722] GAM2275 gene, herein designated GAM GENE, encodes a GAM2275 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2275 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2275 precursor RNA is designated SEQ ID:2252, and is provided hereinbelow with reference to the sequence listing part.

[31723] GAM2275 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2275 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

- [31724] An enzyme complex designated DICER COMPLEX, dices the GAM2275 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2275 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of GAM2275 RNA is designated SEQ ID:4866, and is provided hereinbelow with reference to the sequence listing part.
- [31725] GAM2275 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2275 target RNA, herein designated GAM TARGET RNA. GAM2275 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [31726] GAM2275 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2275 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2275 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2275 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2275 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31727] The complementary binding of GAM2275 RNA, herein designated GAM RNA, to target binding sites on GAM2275 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2275 target RNA, herein designated GAM TARGET RNA, into GAM2275 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31728] It is appreciated that GAM2275 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2275 target genes. The mRNA of each one of this plurality of GAM2275 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2275 RNA, herein designated GAM RNA, and which when bound by GAM2275 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2275 target proteins.

[31729] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2275 gene, herein designated GAM GENE, on one or more GAM2275 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31730] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2275 correlate with, and may be deduced from, the identity of the target genes which GAM2275 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31731] Nucleotide sequences of the GAM2275 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2275 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2275 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2275 are further described hereinbelow with reference to Table 1.

[31732] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2275 RNA, herein designated GAM RNA, are described hereinbelow



with reference to Table 2.

[31733] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2276 (GAM2276) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31734] GAM2276 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2276 was detected is described hereinabove with reference to Figs. 2-8.

[31735] GAM2276 gene, herein designated GAM GENE, and GAM2276 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[31736] GAM2276 gene, herein designated GAM GENE, encodes a GAM2276 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2276 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2276 precursor RNA is designated SEQ ID:2253, and is provided hereinbelow with reference to the sequence listing part.

[31737] GAM2276 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2276 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31738] An enzyme complex designated DICER COMPLEX, dices the GAM2276 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2276 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of GAM2276 RNA is designated SEQ ID:4868, and is provided hereinbelow with reference to the sequence listing part.

[31739] GAM2276 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2276 target RNA, herein designated GAM TARGET RNA. GAM2276 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31740] GAM2276 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2276 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2276 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2276 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2276 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31741] The complementary binding of GAM2276 RNA, herein designated GAM RNA, to target binding sites on GAM2276 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2276 target RNA, herein designated GAM TARGET RNA, into GAM2276 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31742] It is appreciated that GAM2276 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2276 target genes. The mRNA of each one of this plurality of GAM2276 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2276 RNA, herein designated GAM RNA, and which when bound by GAM2276 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2276 target proteins.

[31743] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2276 gene, herein designated GAM GENE, on one or more GAM2276 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31744] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2276 correlate with, and may be deduced from, the identity of the target genes which GAM2276 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31745] Nucleotide sequences of the GAM2276 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2276 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2276 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2276 are further described hereinbelow with reference to Table 1.

[31746] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2276 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[31747] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2277 (GAM2277) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31748] GAM2277 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2277 was detected is described hereinabove with reference to Figs. 2-8.

[31749] GAM2277 gene, herein designated GAM GENE, and GAM2277 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[31750] GAM2277 gene, herein designated GAM GENE, encodes a GAM2277 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2277 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2277 precursor RNA is designated SEQ ID:2254, and is provided hereinbelow with reference to the sequence listing part.

[31751] GAM2277 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2277 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31752] An enzyme complex designated DICER COMPLEX, dices the GAM2277 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2277 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 84%) nucleotide sequence of GAM2277 RNA is designated SEQ ID:4867, and is provided hereinbelow with reference to the sequence listing part.

[31753] GAM2277 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2277 target RNA, herein designated GAM TARGET RNA. GAM2277 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31754] GAM2277 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2277 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2277 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2277 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2277 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31755] The complementary binding of GAM2277 RNA, herein designated GAM RNA, to target binding sites on GAM2277 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2277 target RNA, herein designated GAM TARGET RNA, into GAM2277 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31756] It is appreciated that GAM2277 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2277 target genes. The

mRNA of each one of this plurality of GAM2277 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2277 RNA, herein designated GAM RNA, and which when bound by GAM2277 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2277 target proteins.

[31757] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2277 gene, herein designated GAM GENE, on one or more GAM2277 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31758] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2277 correlate with, and may be deduced from, the identity of the target genes which GAM2277 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31759] Nucleotide sequences of the GAM2277 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2277 RNA, herein



designated GAM RNA, and a schematic representation of the secondary folding of GAM2277 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2277 are further described hereinbelow with reference to Table 1.

[31760] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2277 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[31761] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2278 (GAM2278) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31762] GAM2278 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2278 was detected is described hereinabove with reference to Figs. 2-8.

[31763] GAM2278 gene, herein designated GAM GENE, and GAM2278 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[31764] GAM2278 gene, herein designated GAM GENE, encodes a GAM2278 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2278 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2278 precursor RNA is designated SEQ ID:2255, and is provided hereinbelow with reference to the sequence listing part.

[31765] GAM2278 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2278 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31766] An enzyme complex designated DICER COMPLEX, dices the GAM2278 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2278 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 92%) nucleotide sequence of GAM2278 RNA is designated SEQ ID:4869, and is provided hereinbelow with reference to the sequence listing part.

[31767] GAM2278 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2278 target RNA, herein designated GAM TARGET RNA. GAM2278 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31768] GAM2278 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2278 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2278 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2278 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2278 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31769] The complementary binding of GAM2278 RNA, herein designated GAM RNA, to target binding sites on GAM2278 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2278 target RNA, herein designated GAM TARGET RNA, into GAM2278 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31770] It is appreciated that GAM2278 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2278 target genes. The mRNA of each one of this plurality of GAM2278 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2278 RNA, herein designated GAM RNA, and which when bound by GAM2278 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2278 target proteins.

[31771] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2278 gene, herein designated GAM GENE, on one or more GAM2278 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31772] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2278 correlate with, and may be deduced from, the identity of the target

genes which GAM2278 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31773] Nucleotide sequences of the GAM2278 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2278 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2278 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2278 are further described hereinbelow with reference to Table 1.

[31774] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2278 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[31775] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2279 (GAM2279) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31776] GAM2279 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2279 was detected is described hereinabove with reference to Figs. 2-8.

[31777] GAM2279 gene, herein designated GAM GENE, and GAM2279 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

[31778] GAM2279 gene, herein designated GAM GENE, encodes a GAM2279 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2279 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2279 precursor RNA is designated SEQ ID:2256, and is provided hereinbelow with reference to the sequence listing part.

[31779] GAM2279 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2279 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31780] An enzyme complex designated DICER COMPLEX, dices the GAM2279 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2279 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2279 RNA is designated SEQ ID:4870, and is provided

hereinbelow with reference to the sequence listing part.

[31781] GAM2279 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2279 target RNA, herein designated GAM TARGET RNA. GAM2279 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31782] GAM2279 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2279 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2279 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2279 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2279 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31783] The complementary binding of GAM2279 RNA, herein designated GAM RNA, to target binding sites on GAM2279 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2279 target RNA, herein designated GAM TARGET RNA, into GAM2279 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31784] It is appreciated that GAM2279 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2279 target genes. The mRNA of each one of this plurality of GAM2279 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2279 RNA, herein designated GAM RNA, and which when bound by GAM2279 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2279 target proteins.

[31785] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2279 gene, herein designated GAM GENE, on one or more GAM2279 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding



sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31786] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2279 correlate with, and may be deduced from, the identity of the target genes which GAM2279 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31787] Nucleotide sequences of the GAM2279 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2279 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2279 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2279 are further described hereinbelow with reference to Table 1.

[31788] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2279 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[31789] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2280 (GAM2280) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31790] GAM2280 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2280 was detected is described hereinabove with reference to Figs. 2-8.

[31791] GAM2280 gene, herein designated GAM GENE, and GAM2280 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[31792] GAM2280 gene, herein designated GAM GENE, encodes a GAM2280 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2280 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2280 precursor RNA is designated SEQ ID:2257, and is provided hereinbelow with reference to the sequence listing part.

[31793] GAM2280 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2280 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31794] An enzyme complex designated DICER COMPLEX, dices the GAM2280 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2280 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2280 RNA is designated SEQ ID:4871, and is provided hereinbelow with reference to the sequence listing part.

[31795] GAM2280 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2280 target RNA, herein designated GAM TARGET RNA. GAM2280 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31796] GAM2280 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2280 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2280 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2280 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2280 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31797] The complementary binding of GAM2280 RNA, herein designated GAM RNA, to target binding sites on GAM2280 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2280 target RNA, herein designated GAM TARGET RNA, into GAM2280 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31798] It is appreciated that GAM2280 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2280 target genes. The mRNA of each one of this plurality of GAM2280 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2280 RNA, herein designated GAM RNA, and which when bound by GAM2280 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2280 target proteins.

[31799] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2280 gene, herein designated GAM GENE, on one or more GAM2280 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31800] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2280 correlate with, and may be deduced from, the identity of the target genes which GAM2280 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31801] Nucleotide sequences of the GAM2280 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2280 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2280 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2280 are further described hereinbelow with reference to Table 1.

[31802] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2280 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[31803] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2281 (GAM2281) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31804] GAM2281 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2281 was detected is described hereinabove with reference to Figs. 2-8.

[31805] GAM2281 gene, herein designated GAM GENE, and GAM2281 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[31806] GAM2281 gene, herein designated GAM GENE, encodes a GAM2281 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2281 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2281 precursor RNA is designated SEQ ID:2258, and is provided hereinbelow with reference to the sequence listing part.

[31807] GAM2281 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2281 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

- [31808] An enzyme complex designated DICER COMPLEX, dices the GAM2281 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2281 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 78%) nucleotide sequence of GAM2281 RNA is designated SEQ ID:4872, and is provided hereinbelow with reference to the sequence listing part.
- [31809] GAM2281 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2281 target RNA, herein designated GAM TARGET RNA. GAM2281 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [31810] GAM2281 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2281 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2281 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2281 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2281 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31811] The complementary binding of GAM2281 RNA, herein designated GAM RNA, to target binding sites on GAM2281 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2281 target RNA, herein designated GAM TARGET RNA, into GAM2281 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31812] It is appreciated that GAM2281 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2281 target genes. The mRNA of each one of this plurality of GAM2281 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2281 RNA, herein designated GAM RNA, and which when bound by GAM2281 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2281 target proteins.

[31813] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition



exerted by GAM2281 gene, herein designated GAM GENE, on one or more GAM2281 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31814] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2281 correlate with, and may be deduced from, the identity of the target genes which GAM2281 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31815] Nucleotide sequences of the GAM2281 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2281 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2281 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2281 are further described hereinbelow with reference to Table 1.

[31816] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2281 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

[31817] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2282 (GAM2282) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31818] GAM2282 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2282 was detected is described hereinabove with reference to Figs. 2-8.

[31819] GAM2282 gene, herein designated GAM GENE, and GAM2282 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[31820] GAM2282 gene, herein designated GAM GENE, encodes a GAM2282 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2282 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2282 precursor RNA is designated SEQ ID:2259, and is provided hereinbelow with reference to the sequence listing part.

[31821] GAM2282 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2282 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31822] An enzyme complex designated DICER COMPLEX, dices the GAM2282 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2282 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of GAM2282 RNA is designated SEQ ID:4873, and is provided hereinbelow with reference to the sequence listing part.

[31823] GAM2282 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2282 target RNA, herein designated GAM TARGET RNA. GAM2282 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31824] GAM2282 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2282 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2282 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2282 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2282 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31825] The complementary binding of GAM2282 RNA, herein designated GAM RNA, to target binding sites on GAM2282 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2282 target RNA, herein designated GAM TARGET RNA, into GAM2282 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31826] It is appreciated that GAM2282 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2282 target genes. The mRNA of each one of this plurality of GAM2282 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2282 RNA, herein designated GAM RNA, and which when bound by GAM2282 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2282 target proteins.

[31827] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2282 gene, herein designated GAM GENE, on one or more GAM2282 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31828] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2282 correlate with, and may be deduced from, the identity of the target genes which GAM2282 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31829] Nucleotide sequences of the GAM2282 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2282 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2282 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2282 are further described hereinbelow with reference to Table 1.

[31830] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2282 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[31831] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2283 (GAM2283) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31832] GAM2283 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2283 was detected is described hereinabove with reference to Figs. 2-8.

[31833] GAM2283 gene, herein designated GAM GENE, and GAM2283 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[31834] GAM2283 gene, herein designated GAM GENE, encodes a GAM2283 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2283 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2283 precursor RNA is designated SEQ ID:2260, and is provided hereinbelow with reference to the sequence listing part.

[31835] GAM2283 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2283 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31836] An enzyme complex designated DICER COMPLEX, dices the GAM2283 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2283 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of GAM2283 RNA is designated SEQ ID:4874, and is provided hereinbelow with reference to the sequence listing part.

[31837] GAM2283 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2283 target RNA, herein designated GAM TARGET RNA. GAM2283 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31838] GAM2283 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2283 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2283 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2283 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2283 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31839] The complementary binding of GAM2283 RNA, herein designated GAM RNA, to target binding sites on GAM2283 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2283 target RNA, herein designated GAM TARGET RNA, into GAM2283 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31840] It is appreciated that GAM2283 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2283 target genes. The



mRNA of each one of this plurality of GAM2283 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2283 RNA, herein designated GAM RNA, and which when bound by GAM2283 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2283 target proteins.

[31841] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2283 gene, herein designated GAM GENE, on one or more GAM2283 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31842] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2283 correlate with, and may be deduced from, the identity of the target genes which GAM2283 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31843] Nucleotide sequences of the GAM2283 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2283 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2283 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2283 are further described hereinbelow with reference to Table 1.

[31844] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2283 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[31845] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2284 (GAM2284) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31846] GAM2284 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2284 was detected is described hereinabove with reference to Figs. 2-8.

[31847] GAM2284 gene, herein designated GAM GENE, and GAM2284 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[31848] GAM2284 gene, herein designated GAM GENE, encodes a GAM2284 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2284 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2284 precursor RNA is designated SEQ ID:2261, and is provided hereinbelow with reference to the sequence listing part.

[31849] GAM2284 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2284 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31850] An enzyme complex designated DICER COMPLEX, dices the GAM2284 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2284 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 84%) nucleotide sequence of GAM2284 RNA is designated SEQ ID:4875, and is provided hereinbelow with reference to the sequence listing part.

[31851] GAM2284 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2284 target RNA, herein designated GAM TARGET RNA. GAM2284 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31852] GAM2284 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2284 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2284 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2284 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2284 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31853] The complementary binding of GAM2284 RNA, herein designated GAM RNA, to target binding sites on GAM2284 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2284 target RNA, herein designated GAM TARGET RNA, into GAM2284 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31854] It is appreciated that GAM2284 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2284 target genes. The mRNA of each one of this plurality of GAM2284 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2284 RNA, herein designated GAM RNA, and which when bound by GAM2284 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2284 target proteins.

[31855] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2284 gene, herein designated GAM GENE, on one or more GAM2284 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31856] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2284 correlate with, and may be deduced from, the identity of the target

genes which GAM2284 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31857] Nucleotide sequences of the GAM2284 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2284 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2284 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2284 are further described hereinbelow with reference to Table 1.

[31858] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2284 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[31859] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2285 (GAM2285) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31860] GAM2285 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2285 was detected is described hereinabove with reference to Figs. 2-8.

[31861] GAM2285 gene, herein designated GAM GENE, and GAM2285 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

[31862] GAM2285 gene, herein designated GAM GENE, encodes a GAM2285 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2285 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2285 precursor RNA is designated SEQ ID:2262, and is provided hereinbelow with reference to the sequence listing part.

[31863] GAM2285 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2285 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31864] An enzyme complex designated DICER COMPLEX, dices the GAM2285 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2285 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of GAM2285 RNA is designated SEQ ID:4876, and is provided

hereinbelow with reference to the sequence listing part.

[31865] GAM2285 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2285 target RNA, herein designated GAM TARGET RNA. GAM2285 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31866] GAM2285 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2285 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2285 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2285 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2285 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.



[31867] The complementary binding of GAM2285 RNA, herein designated GAM RNA, to target binding sites on GAM2285 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2285 target RNA, herein designated GAM TARGET RNA, into GAM2285 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31868] It is appreciated that GAM2285 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2285 target genes. The mRNA of each one of this plurality of GAM2285 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2285 RNA, herein designated GAM RNA, and which when bound by GAM2285 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2285 target proteins.

[31869] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2285 gene, herein designated GAM GENE, on one or more GAM2285 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31870] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2285 correlate with, and may be deduced from, the identity of the target genes which GAM2285 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31871] Nucleotide sequences of the GAM2285 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2285 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2285 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2285 are further described hereinbelow with reference to Table 1.

[31872] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2285 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[31873] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2286 (GAM2286) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31874] GAM2286 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2286 was detected is described hereinabove with reference to Figs. 2-8.

[31875] GAM2286 gene, herein designated GAM GENE, and GAM2286 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[31876] GAM2286 gene, herein designated GAM GENE, encodes a GAM2286 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2286 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2286 precursor RNA is designated SEQ ID:2263, and is provided hereinbelow with reference to the sequence listing part.

[31877] GAM2286 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2286 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31878] An enzyme complex designated DICER COMPLEX, dices the GAM2286 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2286 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of GAM2286 RNA is designated SEQ ID:4877, and is provided hereinbelow with reference to the sequence listing part.

[31879] GAM2286 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2286 target RNA, herein designated GAM TARGET RNA. GAM2286 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31880] GAM2286 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2286 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2286 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2286 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2286 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31881] The complementary binding of GAM2286 RNA, herein designated GAM RNA, to target binding sites on GAM2286 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2286 target RNA, herein designated GAM TARGET RNA, into GAM2286 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31882] It is appreciated that GAM2286 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2286 target genes. The mRNA of each one of this plurality of GAM2286 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2286 RNA, herein designated GAM RNA, and which when bound by GAM2286 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2286 target proteins.

[31883] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2286 gene, herein designated GAM GENE, on one or more GAM2286 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31884] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2286 correlate with, and may be deduced from, the identity of the target genes which GAM2286 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31885] Nucleotide sequences of the GAM2286 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2286 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2286 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2286 are further described hereinbelow with reference to Table 1.

[31886] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2286 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[31887] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2287 (GAM2287) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31888] GAM2287 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2287 was detected is described hereinabove with reference to Figs. 2-8.

[31889] GAM2287 gene, herein designated GAM GENE, and GAM2287 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[31890] GAM2287 gene, herein designated GAM GENE, encodes a GAM2287 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2287 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2287 precursor RNA is designated SEQ ID:2264, and is provided hereinbelow with reference to the sequence listing part.

[31891] GAM2287 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2287 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

- [31892] An enzyme complex designated DICER COMPLEX, dices the GAM2287 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2287 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 76%) nucleotide sequence of GAM2287 RNA is designated SEQ ID:4878, and is provided hereinbelow with reference to the sequence listing part.
- [31893] GAM2287 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2287 target RNA, herein designated GAM TARGET RNA. GAM2287 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [31894] GAM2287 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2287 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2287 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an



illustration only, and is not meant to be limiting GAM2287 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2287 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31895] The complementary binding of GAM2287 RNA, herein designated GAM RNA, to target binding sites on GAM2287 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2287 target RNA, herein designated GAM TARGET RNA, into GAM2287 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31896] It is appreciated that GAM2287 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2287 target genes. The mRNA of each one of this plurality of GAM2287 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2287 RNA, herein designated GAM RNA, and which when bound by GAM2287 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2287 target proteins.

[31897] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2287 gene, herein designated GAM GENE, on one or more GAM2287 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31898] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2287 correlate with, and may be deduced from, the identity of the target genes which GAM2287 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31899] Nucleotide sequences of the GAM2287 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2287 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2287 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2287 are further described hereinbelow with reference to Table 1.

[31900] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2287 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

[31901] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2288 (GAM2288) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31902] GAM2288 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2288 was detected is described hereinabove with reference to Figs. 2-8.

[31903] GAM2288 gene, herein designated GAM GENE, and GAM2288 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[31904] GAM2288 gene, herein designated GAM GENE, encodes a GAM2288 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2288 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2288 precursor RNA is designated SEQ ID:2265, and is provided hereinbelow with reference to the sequence listing part.

[31905] GAM2288 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2288 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31906] An enzyme complex designated DICER COMPLEX, dices the GAM2288 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2288 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 88%) nucleotide sequence of GAM2288 RNA is designated SEQ ID:4879, and is provided hereinbelow with reference to the sequence listing part.

[31907] GAM2288 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2288 target RNA, herein designated GAM TARGET RNA. GAM2288 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31908] GAM2288 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2288 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2288 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2288 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2288 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31909] The complementary binding of GAM2288 RNA, herein designated GAM RNA, to target binding sites on GAM2288 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2288 target RNA, herein designated GAM TARGET RNA, into GAM2288 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31910] It is appreciated that GAM2288 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2288 target genes. The mRNA of each one of this plurality of GAM2288 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2288 RNA, herein designated GAM RNA, and which when bound by GAM2288 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2288 target proteins.

[31911] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2288 gene, herein designated GAM GENE, on one or more GAM2288 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31912] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2288 correlate with, and may be deduced from, the identity of the target genes which GAM2288 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31913] Nucleotide sequences of the GAM2288 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2288 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2288 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2288 are further described hereinbelow with reference to Table 1.

[31914] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2288 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[31915] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2289 (GAM2289) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31916] GAM2289 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2289 was detected is described hereinabove with reference to Figs. 2-8.

[31917] GAM2289 gene, herein designated GAM GENE, and GAM2289 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[31918] GAM2289 gene, herein designated GAM GENE, encodes a GAM2289 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2289 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2289 precursor RNA is designated SEQ ID:2266, and is provided hereinbelow with reference to the sequence listing part.

[31919] GAM2289 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2289 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31920] An enzyme complex designated DICER COMPLEX, dices the GAM2289 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2289 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 88%) nucleotide sequence of GAM2289 RNA is designated SEQ ID:4880, and is provided hereinbelow with reference to the sequence listing part.

[31921] GAM2289 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2289 target RNA, herein designated GAM TARGET RNA. GAM2289 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.



[31922] GAM2289 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2289 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2289 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2289 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2289 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31923] The complementary binding of GAM2289 RNA, herein designated GAM RNA, to target binding sites on GAM2289 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2289 target RNA, herein designated GAM TARGET RNA, into GAM2289 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31924] It is appreciated that GAM2289 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2289 target genes. The

mRNA of each one of this plurality of GAM2289 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2289 RNA, herein designated GAM RNA, and which when bound by GAM2289 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2289 target proteins.

[31925] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2289 gene, herein designated GAM GENE, on one or more GAM2289 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31926] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2289 correlate with, and may be deduced from, the identity of the target genes which GAM2289 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31927] Nucleotide sequences of the GAM2289 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2289 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2289 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2289 are further described hereinbelow with reference to Table 1.

[31928] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2289 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[31929] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2290 (GAM2290) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31930] GAM2290 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2290 was detected is described hereinabove with reference to Figs. 2-8.

[31931] GAM2290 gene, herein designated GAM GENE, and GAM2290 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[31932] GAM2290 gene, herein designated GAM GENE, encodes a GAM2290 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2290 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2290 precursor RNA is designated SEQ ID:2267, and is provided hereinbelow with reference to the sequence listing part.

[31933] GAM2290 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2290 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31934] An enzyme complex designated DICER COMPLEX, dices the GAM2290 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2290 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2290 RNA is designated SEQ ID:4881, and is provided hereinbelow with reference to the sequence listing part.

[31935] GAM2290 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2290 target RNA, herein designated GAM TARGET RNA. GAM2290 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31936] GAM2290 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2290 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2290 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2290 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2290 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31937] The complementary binding of GAM2290 RNA, herein designated GAM RNA, to target binding sites on GAM2290 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2290 target RNA, herein designated GAM TARGET RNA, into GAM2290 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31938] It is appreciated that GAM2290 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2290 target genes. The mRNA of each one of this plurality of GAM2290 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2290 RNA, herein designated GAM RNA, and which when bound by GAM2290 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2290 target proteins.

[31939] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2290 gene, herein designated GAM GENE, on one or more GAM2290 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31940] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2290 correlate with, and may be deduced from, the identity of the target

genes which GAM2290 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31941] Nucleotide sequences of the GAM2290 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2290 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2290 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2290 are further described hereinbelow with reference to Table 1.

[31942] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2290 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[31943] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2291 (GAM2291) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31944] GAM2291 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2291 was detected is described hereinabove with reference to Figs. 2-8.

[31945] GAM2291 gene, herein designated GAM GENE, and GAM2291 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

[31946] GAM2291 gene, herein designated GAM GENE, encodes a GAM2291 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2291 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2291 precursor RNA is designated SEQ ID:2268, and is provided hereinbelow with reference to the sequence listing part.

[31947] GAM2291 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2291 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31948] An enzyme complex designated DICER COMPLEX, dices the GAM2291 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2291 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of GAM2291 RNA is designated SEQ ID:4882, and is provided



hereinbelow with reference to the sequence listing part.

[31949] GAM2291 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2291 target RNA, herein designated GAM TARGET RNA. GAM2291 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31950] GAM2291 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2291 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2291 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2291 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2291 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31951] The complementary binding of GAM2291 RNA, herein designated GAM RNA, to target binding sites on GAM2291 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2291 target RNA, herein designated GAM TARGET RNA, into GAM2291 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31952] It is appreciated that GAM2291 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2291 target genes. The mRNA of each one of this plurality of GAM2291 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2291 RNA, herein designated GAM RNA, and which when bound by GAM2291 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2291 target proteins.

[31953] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2291 gene, herein designated GAM GENE, on one or more GAM2291 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31954] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2291 correlate with, and may be deduced from, the identity of the target genes which GAM2291 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31955] Nucleotide sequences of the GAM2291 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2291 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2291 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2291 are further described hereinbelow with reference to Table 1.

[31956] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2291 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[31957] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2292 (GAM2292) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31958] GAM2292 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2292 was detected is described hereinabove with reference to Figs. 2-8.

[31959] GAM2292 gene, herein designated GAM GENE, and GAM2292 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[31960] GAM2292 gene, herein designated GAM GENE, encodes a GAM2292 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2292 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2292 precursor RNA is designated SEQ ID:2269, and is provided hereinbelow with reference to the sequence listing part.

[31961] GAM2292 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2292 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31962] An enzyme complex designated DICER COMPLEX, dices the GAM2292 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2292 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of GAM2292 RNA is designated SEQ ID:4883, and is provided hereinbelow with reference to the sequence listing part.

[31963] GAM2292 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2292 target RNA, herein designated GAM TARGET RNA. GAM2292 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31964] GAM2292 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2292 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2292 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2292 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2292 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31965] The complementary binding of GAM2292 RNA, herein designated GAM RNA, to target binding sites on GAM2292 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2292 target RNA, herein designated GAM TARGET RNA, into GAM2292 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31966] It is appreciated that GAM2292 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2292 target genes. The mRNA of each one of this plurality of GAM2292 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2292 RNA, herein designated GAM RNA, and which when bound by GAM2292 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2292 target proteins.

[31967] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2292 gene, herein designated GAM GENE, on one or more GAM2292 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31968] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2292 correlate with, and may be deduced from, the identity of the target genes which GAM2292 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31969] Nucleotide sequences of the GAM2292 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2292 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2292 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2292 are further described hereinbelow with reference to Table 1.

[31970] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2292 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[31971] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2293 (GAM2293) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31972] GAM2293 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2293 was detected is described hereinabove with reference to Figs. 2-8.

[31973] GAM2293 gene, herein designated GAM GENE, and GAM2293 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[31974] GAM2293 gene, herein designated GAM GENE, encodes a GAM2293 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2293 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2293 precursor RNA is designated SEQ ID:2270, and is provided hereinbelow with reference to the sequence listing part.

[31975] GAM2293 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2293 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.



- [31976] An enzyme complex designated DICER COMPLEX, dices the GAM2293 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2293 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2293 RNA is designated SEQ ID:4884, and is provided hereinbelow with reference to the sequence listing part.
- [31977] GAM2293 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2293 target RNA, herein designated GAM TARGET RNA. GAM2293 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [31978] GAM2293 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2293 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2293 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2293 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2293 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31979] The complementary binding of GAM2293 RNA, herein designated GAM RNA, to target binding sites on GAM2293 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2293 target RNA, herein designated GAM TARGET RNA, into GAM2293 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31980] It is appreciated that GAM2293 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2293 target genes. The mRNA of each one of this plurality of GAM2293 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2293 RNA, herein designated GAM RNA, and which when bound by GAM2293 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2293 target proteins.

[31981] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2293 gene, herein designated GAM GENE, on one or more GAM2293 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31982] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2293 correlate with, and may be deduced from, the identity of the target genes which GAM2293 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31983] Nucleotide sequences of the GAM2293 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2293 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2293 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2293 are further described hereinbelow with reference to Table 1.

[31984] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2293 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

- [31985] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2294 (GAM2294) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.
- [31986] GAM2294 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2294 was detected is described hereinabove with reference to Figs. 2-8.
- [31987] GAM2294 gene, herein designated GAM GENE, and GAM2294 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.
- [31988] GAM2294 gene, herein designated GAM GENE, encodes a GAM2294 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2294 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2294 precursor RNA is designated SEQ ID:2271, and is provided hereinbelow with reference to the sequence listing part.
- [31989] GAM2294 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2294 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31990] An enzyme complex designated DICER COMPLEX, dices the GAM2294 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2294 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2294 RNA is designated SEQ ID:4885, and is provided hereinbelow with reference to the sequence listing part.

[31991] GAM2294 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2294 target RNA, herein designated GAM TARGET RNA. GAM2294 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[31992] GAM2294 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2294 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2294 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2294 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2294 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[31993] The complementary binding of GAM2294 RNA, herein designated GAM RNA, to target binding sites on GAM2294 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2294 target RNA, herein designated GAM TARGET RNA, into GAM2294 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31994] It is appreciated that GAM2294 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2294 target genes. The mRNA of each one of this plurality of GAM2294 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2294 RNA, herein designated GAM RNA, and which when bound by GAM2294 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2294 target proteins.

[31995] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2294 gene, herein designated GAM GENE, on one or more GAM2294 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31996] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2294 correlate with, and may be deduced from, the identity of the target genes which GAM2294 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31997] Nucleotide sequences of the GAM2294 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2294 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2294 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2294 are further described hereinbelow with reference to Table 1.

[31998] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2294 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[31999] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2295 (GAM2295) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32000] GAM2295 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2295 was detected is described hereinabove with reference to Figs. 2-8.

[32001] GAM2295 gene, herein designated GAM GENE, and GAM2295 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[32002] GAM2295 gene, herein designated GAM GENE, encodes a GAM2295 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2295 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2295 precursor RNA is designated SEQ ID:2272, and is provided hereinbelow with reference to the sequence listing part.



[32003] GAM2295 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2295 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32004] An enzyme complex designated DICER COMPLEX, dices the GAM2295 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2295 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of GAM2295 RNA is designated SEQ ID:4886, and is provided hereinbelow with reference to the sequence listing part.

[32005] GAM2295 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2295 target RNA, herein designated GAM TARGET RNA. GAM2295 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32006] GAM2295 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2295 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2295 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2295 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2295 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32007] The complementary binding of GAM2295 RNA, herein designated GAM RNA, to target binding sites on GAM2295 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2295 target RNA, herein designated GAM TARGET RNA, into GAM2295 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32008] It is appreciated that GAM2295 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2295 target genes. The

mRNA of each one of this plurality of GAM2295 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2295 RNA, herein designated GAM RNA, and which when bound by GAM2295 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2295 target proteins.

[32009] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2295 gene, herein designated GAM GENE, on one or more GAM2295 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32010] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2295 correlate with, and may be deduced from, the identity of the target genes which GAM2295 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32011] Nucleotide sequences of the GAM2295 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2295 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2295 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2295 are further described hereinbelow with reference to Table 1.

[32012] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2295 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[32013] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2296 (GAM2296) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32014] GAM2296 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2296 was detected is described hereinabove with reference to Figs. 2-8.

[32015] GAM2296 gene, herein designated GAM GENE, and GAM2296 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[32016] GAM2296 gene, herein designated GAM GENE, encodes a GAM2296 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2296 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2296 precursor RNA is designated SEQ ID:2273, and is provided hereinbelow with reference to the sequence listing part.

[32017] GAM2296 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2296 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32018] An enzyme complex designated DICER COMPLEX, dices the GAM2296 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2296 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 78%) nucleotide sequence of GAM2296 RNA is designated SEQ ID:4887, and is provided hereinbelow with reference to the sequence listing part.

[32019] GAM2296 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2296 target RNA, herein designated GAM TARGET RNA. GAM2296 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32020] GAM2296 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2296 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2296 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2296 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2296 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32021] The complementary binding of GAM2296 RNA, herein designated GAM RNA, to target binding sites on GAM2296 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2296 target RNA, herein designated GAM TARGET RNA, into GAM2296 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32022] It is appreciated that GAM2296 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2296 target genes. The mRNA of each one of this plurality of GAM2296 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2296 RNA, herein designated GAM RNA, and which when bound by GAM2296 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2296 target proteins.

[32023] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2296 gene, herein designated GAM GENE, on one or more GAM2296 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32024] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2296 correlate with, and may be deduced from, the identity of the target

genes which GAM2296 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32025] Nucleotide sequences of the GAM2296 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2296 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2296 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2296 are further described hereinbelow with reference to Table 1.

[32026] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2296 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[32027] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2297 (GAM2297) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32028] GAM2297 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2297 was detected is described hereinabove with reference to Figs. 2-8.

[32029] GAM2297 gene, herein designated GAM GENE, and GAM2297 target gene, herein designated GAM TARGET GENE, are human genes contained in the



human genome.

[32030] GAM2297 gene, herein designated GAM GENE, encodes a GAM2297 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2297 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2297 precursor RNA is designated SEQ ID:2274, and is provided hereinbelow with reference to the sequence listing part.

[32031] GAM2297 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2297 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32032] An enzyme complex designated DICER COMPLEX, dices the GAM2297 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2297 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of GAM2297 RNA is designated SEQ ID:4888, and is provided

hereinbelow with reference to the sequence listing part.

[32033] GAM2297 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2297 target RNA, herein designated GAM TARGET RNA. GAM2297 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32034] GAM2297 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2297 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2297 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2297 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2297 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32035] The complementary binding of GAM2297 RNA, herein designated GAM RNA, to target binding sites on GAM2297 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2297 target RNA, herein designated GAM TARGET RNA, into GAM2297 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32036] It is appreciated that GAM2297 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2297 target genes. The mRNA of each one of this plurality of GAM2297 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2297 RNA, herein designated GAM RNA, and which when bound by GAM2297 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2297 target proteins.

[32037] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2297 gene, herein designated GAM GENE, on one or more GAM2297 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32038] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2297 correlate with, and may be deduced from, the identity of the target genes which GAM2297 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32039] Nucleotide sequences of the GAM2297 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2297 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2297 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2297 are further described hereinbelow with reference to Table 1.

[32040] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2297 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[32041] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2298 (GAM2298) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32042] GAM2298 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2298 was detected is described hereinabove with reference to Figs. 2-8.

[32043] GAM2298 gene, herein designated GAM GENE, and GAM2298 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[32044] GAM2298 gene, herein designated GAM GENE, encodes a GAM2298 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2298 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2298 precursor RNA is designated SEQ ID:2275, and is provided hereinbelow with reference to the sequence listing part.

[32045] GAM2298 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2298 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32046] An enzyme complex designated DICER COMPLEX, dices the GAM2298 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2298 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 88%) nucleotide sequence of GAM2298 RNA is designated SEQ ID:4889, and is provided hereinbelow with reference to the sequence listing part.

[32047] GAM2298 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2298 target RNA, herein designated GAM TARGET RNA. GAM2298 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32048] GAM2298 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2298 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2298 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2298 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2298 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32049] The complementary binding of GAM2298 RNA, herein designated GAM RNA, to target binding sites on GAM2298 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2298 target RNA, herein designated GAM TARGET RNA, into GAM2298 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32050] It is appreciated that GAM2298 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2298 target genes. The mRNA of each one of this plurality of GAM2298 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2298 RNA, herein designated GAM RNA, and which when bound by GAM2298 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2298 target proteins.

[32051] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2298 gene, herein designated GAM GENE, on one or more GAM2298 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32052] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2298 correlate with, and may be deduced from, the identity of the target genes which GAM2298 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32053] Nucleotide sequences of the GAM2298 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2298 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2298 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2298 are further described hereinbelow with reference to Table 1.

[32054] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2298 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[32055] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2299 (GAM2299) gene, which modulates



expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32056] GAM2299 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2299 was detected is described hereinabove with reference to Figs. 2-8.

[32057] GAM2299 gene, herein designated GAM GENE, and GAM2299 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[32058] GAM2299 gene, herein designated GAM GENE, encodes a GAM2299 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2299 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2299 precursor RNA is designated SEQ ID:2276, and is provided hereinbelow with reference to the sequence listing part.

[32059] GAM2299 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2299 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32060] An enzyme complex designated DICER COMPLEX, dices the GAM2299 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2299 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2299 RNA is designated SEQ ID:4890, and is provided hereinbelow with reference to the sequence listing part.

[32061] GAM2299 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2299 target RNA, herein designated GAM TARGET RNA. GAM2299 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32062] GAM2299 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2299 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2299 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2299 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2299 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32063] The complementary binding of GAM2299 RNA, herein designated GAM RNA, to target binding sites on GAM2299 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2299 target RNA, herein designated GAM TARGET RNA, into GAM2299 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32064] It is appreciated that GAM2299 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2299 target genes. The mRNA of each one of this plurality of GAM2299 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2299 RNA, herein designated GAM RNA, and which when bound by GAM2299 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2299 target proteins.

[32065] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2299 gene, herein designated GAM GENE, on one or more GAM2299 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32066] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2299 correlate with, and may be deduced from, the identity of the target genes which GAM2299 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32067] Nucleotide sequences of the GAM2299 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2299 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2299 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2299 are further described hereinbelow with reference to Table 1.

[32068] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2299 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

[32069] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2300 (GAM2300) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32070] GAM2300 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2300 was detected is described hereinabove with reference to Figs. 2-8.

[32071] GAM2300 gene, herein designated GAM GENE, and GAM2300 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[32072] GAM2300 gene, herein designated GAM GENE, encodes a GAM2300 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2300 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2300 precursor RNA is designated SEQ ID:2277, and is provided hereinbelow with reference to the sequence listing part.

[32073] GAM2300 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2300 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32074] An enzyme complex designated DICER COMPLEX, dices the GAM2300 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2300 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of GAM2300 RNA is designated SEQ ID:4891, and is provided hereinbelow with reference to the sequence listing part.

[32075] GAM2300 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2300 target RNA, herein designated GAM TARGET RNA. GAM2300 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32076] GAM2300 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2300 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2300 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2300 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2300 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32077] The complementary binding of GAM2300 RNA, herein designated GAM RNA, to target binding sites on GAM2300 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2300 target RNA, herein designated GAM TARGET RNA, into GAM2300 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32078] It is appreciated that GAM2300 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2300 target genes. The mRNA of each one of this plurality of GAM2300 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2300 RNA, herein designated GAM RNA, and which when bound by GAM2300 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2300 target proteins.

[32079] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2300 gene, herein designated GAM GENE, on one or more GAM2300 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32080] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2300 correlate with, and may be deduced from, the identity of the target genes which GAM2300 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32081] Nucleotide sequences of the GAM2300 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2300 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2300 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2300 are further described hereinbelow with reference to Table 1.



[32082] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2300 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[32083] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2301 (GAM2301) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32084] GAM2301 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2301 was detected is described hereinabove with reference to Figs. 2-8.

[32085] GAM2301 gene, herein designated GAM GENE, and GAM2301 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[32086] GAM2301 gene, herein designated GAM GENE, encodes a GAM2301 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2301 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2301 precursor RNA is designated SEQ ID:2278, and is provided hereinbelow with reference to the sequence listing part.

[32087] GAM2301 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2301 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32088] An enzyme complex designated DICER COMPLEX, dices the GAM2301 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2301 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 25%) nucleotide sequence of GAM2301 RNA is designated SEQ ID:4893, and is provided hereinbelow with reference to the sequence listing part.

[32089] GAM2301 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2301 target RNA, herein designated GAM TARGET RNA. GAM2301 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32090] GAM2301 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2301 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2301 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2301 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2301 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32091] The complementary binding of GAM2301 RNA, herein designated GAM RNA, to target binding sites on GAM2301 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2301 target RNA, herein designated GAM TARGET RNA, into GAM2301 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32092] It is appreciated that GAM2301 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2301 target genes. The

mRNA of each one of this plurality of GAM2301 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2301 RNA, herein designated GAM RNA, and which when bound by GAM2301 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2301 target proteins.

[32093] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2301 gene, herein designated GAM GENE, on one or more GAM2301 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32094] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2301 correlate with, and may be deduced from, the identity of the target genes which GAM2301 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32095] Nucleotide sequences of the GAM2301 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2301 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2301 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2301 are further described hereinbelow with reference to Table 1.

[32096] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2301 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[32097] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2302 (GAM2302) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32098] GAM2302 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2302 was detected is described hereinabove with reference to Figs. 2-8.

[32099] GAM2302 gene, herein designated GAM GENE, and GAM2302 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[32100] GAM2302 gene, herein designated GAM GENE, encodes a GAM2302 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2302 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2302 precursor RNA is designated SEQ ID:2279, and is provided hereinbelow with reference to the sequence listing part.

[32101] GAM2302 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2302 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32102] An enzyme complex designated DICER COMPLEX, dices the GAM2302 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2302 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 87%) nucleotide sequence of GAM2302 RNA is designated SEQ ID:4892, and is provided hereinbelow with reference to the sequence listing part.

[32103] GAM2302 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2302 target RNA, herein designated GAM TARGET RNA. GAM2302 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32104] GAM2302 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2302 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2302 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2302 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2302 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32105] The complementary binding of GAM2302 RNA, herein designated GAM RNA, to target binding sites on GAM2302 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2302 target RNA, herein designated GAM TARGET RNA, into GAM2302 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32106] It is appreciated that GAM2302 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2302 target genes. The mRNA of each one of this plurality of GAM2302 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2302 RNA, herein designated GAM RNA, and which when bound by GAM2302 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2302 target proteins.

[32107] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2302 gene, herein designated GAM GENE, on one or more GAM2302 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32108] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2302 correlate with, and may be deduced from, the identity of the target



genes which GAM2302 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32109] Nucleotide sequences of the GAM2302 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2302 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2302 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2302 are further described hereinbelow with reference to Table 1.

[32110] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2302 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[32111] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2303 (GAM2303) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32112] GAM2303 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2303 was detected is described hereinabove with reference to Figs. 2-8.

[32113] GAM2303 gene, herein designated GAM GENE, and GAM2303 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

- [32114] GAM2303 gene, herein designated GAM GENE, encodes a GAM2303 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2303 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2303 precursor RNA is designated SEQ ID:2280, and is provided hereinbelow with reference to the sequence listing part.
- [32115] GAM2303 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2303 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.
- [32116] An enzyme complex designated DICER COMPLEX, dices the GAM2303 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2303 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of GAM2303 RNA is designated SEQ ID:4894, and is provided

hereinbelow with reference to the sequence listing part.

[32117] GAM2303 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2303 target RNA, herein designated GAM TARGET RNA. GAM2303 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32118] GAM2303 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2303 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2303 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2303 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2303 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32119] The complementary binding of GAM2303 RNA, herein designated GAM RNA, to target binding sites on GAM2303 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2303 target RNA, herein designated GAM TARGET RNA, into GAM2303 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32120] It is appreciated that GAM2303 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2303 target genes. The mRNA of each one of this plurality of GAM2303 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2303 RNA, herein designated GAM RNA, and which when bound by GAM2303 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2303 target proteins.

[32121] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2303 gene, herein designated GAM GENE, on one or more GAM2303 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32122] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2303 correlate with, and may be deduced from, the identity of the target genes which GAM2303 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32123] Nucleotide sequences of the GAM2303 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2303 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2303 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2303 are further described hereinbelow with reference to Table 1.

[32124] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2303 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[32125] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2304 (GAM2304) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32126] GAM2304 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2304 was detected is described hereinabove with reference to Figs. 2-8.

[32127] GAM2304 gene, herein designated GAM GENE, and GAM2304 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[32128] GAM2304 gene, herein designated GAM GENE, encodes a GAM2304 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2304 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2304 precursor RNA is designated SEQ ID:2281, and is provided hereinbelow with reference to the sequence listing part.

[32129] GAM2304 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2304 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32130] An enzyme complex designated DICER COMPLEX, dices the GAM2304 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2304 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 84%) nucleotide sequence of GAM2304 RNA is designated SEQ ID:4895, and is provided hereinbelow with reference to the sequence listing part.

[32131] GAM2304 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2304 target RNA, herein designated GAM TARGET RNA. GAM2304 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32132] GAM2304 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2304 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2304 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2304 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2304 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32133] The complementary binding of GAM2304 RNA, herein designated GAM RNA, to target binding sites on GAM2304 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2304 target RNA, herein designated GAM TARGET RNA, into GAM2304 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32134] It is appreciated that GAM2304 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2304 target genes. The mRNA of each one of this plurality of GAM2304 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2304 RNA, herein designated GAM RNA, and which when bound by GAM2304 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2304 target proteins.

[32135] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2304 gene, herein designated GAM GENE, on one or more GAM2304 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary



binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32136] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2304 correlate with, and may be deduced from, the identity of the target genes which GAM2304 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32137] Nucleotide sequences of the GAM2304 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2304 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2304 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2304 are further described hereinbelow with reference to Table 1.

[32138] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2304 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[32139] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2305 (GAM2305) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32140] GAM2305 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2305 was detected is described hereinabove with reference to Figs. 2-8.

[32141] GAM2305 gene, herein designated GAM GENE, and GAM2305 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[32142] GAM2305 gene, herein designated GAM GENE, encodes a GAM2305 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2305 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2305 precursor RNA is designated SEQ ID:2282, and is provided hereinbelow with reference to the sequence listing part.

[32143] GAM2305 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2305 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

- [32144] An enzyme complex designated DICER COMPLEX, dices the GAM2305 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2305 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of GAM2305 RNA is designated SEQ ID:4896, and is provided hereinbelow with reference to the sequence listing part.
- [32145] GAM2305 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2305 target RNA, herein designated GAM TARGET RNA. GAM2305 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [32146] GAM2305 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2305 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2305 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2305 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2305 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32147] The complementary binding of GAM2305 RNA, herein designated GAM RNA, to target binding sites on GAM2305 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2305 target RNA, herein designated GAM TARGET RNA, into GAM2305 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32148] It is appreciated that GAM2305 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2305 target genes. The mRNA of each one of this plurality of GAM2305 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2305 RNA, herein designated GAM RNA, and which when bound by GAM2305 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2305 target proteins.

[32149] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2305 gene, herein designated GAM GENE, on one or more GAM2305 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32150] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2305 correlate with, and may be deduced from, the identity of the target genes which GAM2305 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32151] Nucleotide sequences of the GAM2305 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2305 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2305 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2305 are further described hereinbelow with reference to Table 1.

[32152] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2305 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

- [32153] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2306 (GAM2306) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.
- [32154] GAM2306 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2306 was detected is described hereinabove with reference to Figs. 2-8.
- [32155] GAM2306 gene, herein designated GAM GENE, and GAM2306 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.
- [32156] GAM2306 gene, herein designated GAM GENE, encodes a GAM2306 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2306 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2306 precursor RNA is designated SEQ ID:2283, and is provided hereinbelow with reference to the sequence listing part.
- [32157] GAM2306 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2306 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32158] An enzyme complex designated DICER COMPLEX, dices the GAM2306 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2306 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 78%) nucleotide sequence of GAM2306 RNA is designated SEQ ID:4897, and is provided hereinbelow with reference to the sequence listing part.

[32159] GAM2306 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2306 target RNA, herein designated GAM TARGET RNA. GAM2306 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32160] GAM2306 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2306 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2306 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2306 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2306 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32161] The complementary binding of GAM2306 RNA, herein designated GAM RNA, to target binding sites on GAM2306 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2306 target RNA, herein designated GAM TARGET RNA, into GAM2306 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32162] It is appreciated that GAM2306 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2306 target genes. The mRNA of each one of this plurality of GAM2306 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2306 RNA, herein designated GAM RNA, and which when bound by GAM2306 RNA, herein designated GAM RNA,



causes inhibition of translation of respective one or more GAM2306 target proteins.

[32163] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2306 gene, herein designated GAM GENE, on one or more GAM2306 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32164] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2306 correlate with, and may be deduced from, the identity of the target genes which GAM2306 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32165] Nucleotide sequences of the GAM2306 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2306 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2306 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2306 are further described hereinbelow with reference to Table 1.

[32166] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2306 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[32167] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2307 (GAM2307) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32168] GAM2307 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2307 was detected is described hereinabove with reference to Figs. 2-8.

[32169] GAM2307 gene, herein designated GAM GENE, and GAM2307 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[32170] GAM2307 gene, herein designated GAM GENE, encodes a GAM2307 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2307 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2307 precursor RNA is designated SEQ ID:2284, and is provided hereinbelow with reference to the sequence listing part.

[32171] GAM2307 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2307 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32172] An enzyme complex designated DICER COMPLEX, dices the GAM2307 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2307 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2307 RNA is designated SEQ ID:4898, and is provided hereinbelow with reference to the sequence listing part.

[32173] GAM2307 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2307 target RNA, herein designated GAM TARGET RNA. GAM2307 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32174] GAM2307 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2307 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2307 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2307 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2307 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32175] The complementary binding of GAM2307 RNA, herein designated GAM RNA, to target binding sites on GAM2307 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2307 target RNA, herein designated GAM TARGET RNA, into GAM2307 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32176] It is appreciated that GAM2307 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2307 target genes. The

mRNA of each one of this plurality of GAM2307 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2307 RNA, herein designated GAM RNA, and which when bound by GAM2307 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2307 target proteins.

[32177] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2307 gene, herein designated GAM GENE, on one or more GAM2307 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32178] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2307 correlate with, and may be deduced from, the identity of the target genes which GAM2307 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32179] Nucleotide sequences of the GAM2307 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2307 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2307 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2307 are further described hereinbelow with reference to Table 1.

[32180] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2307 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[32181] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2308 (GAM2308) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32182] GAM2308 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2308 was detected is described hereinabove with reference to Figs. 2-8.

[32183] GAM2308 gene, herein designated GAM GENE, and GAM2308 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[32184] GAM2308 gene, herein designated GAM GENE, encodes a GAM2308 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2308 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2308 precursor RNA is designated SEQ ID:2285, and is provided hereinbelow with reference to the sequence listing part.

[32185] GAM2308 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2308 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32186] An enzyme complex designated DICER COMPLEX, dices the GAM2308 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2308 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 84%) nucleotide sequence of GAM2308 RNA is designated SEQ ID:4899, and is provided hereinbelow with reference to the sequence listing part.

[32187] GAM2308 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2308 target RNA, herein designated GAM TARGET RNA. GAM2308 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32188] GAM2308 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2308 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2308 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2308 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2308 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32189] The complementary binding of GAM2308 RNA, herein designated GAM RNA, to target binding sites on GAM2308 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2308 target RNA, herein designated GAM TARGET RNA, into GAM2308 target protein, herein



designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32190] It is appreciated that GAM2308 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2308 target genes. The mRNA of each one of this plurality of GAM2308 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2308 RNA, herein designated GAM RNA, and which when bound by GAM2308 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2308 target proteins.

[32191] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2308 gene, herein designated GAM GENE, on one or more GAM2308 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32192] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2308 correlate with, and may be deduced from, the identity of the target

genes which GAM2308 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32193] Nucleotide sequences of the GAM2308 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2308 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2308 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2308 are further described hereinbelow with reference to Table 1.

[32194] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2308 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[32195] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2309 (GAM2309) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32196] GAM2309 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2309 was detected is described hereinabove with reference to Figs. 2-8.

[32197] GAM2309 gene, herein designated GAM GENE, and GAM2309 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

[32198] GAM2309 gene, herein designated GAM GENE, encodes a GAM2309 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2309 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2309 precursor RNA is designated SEQ ID:2286, and is provided hereinbelow with reference to the sequence listing part.

[32199] GAM2309 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2309 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32200] An enzyme complex designated DICER COMPLEX, dices the GAM2309 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2309 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 83%) nucleotide sequence of GAM2309 RNA is designated SEQ ID:4900, and is provided

hereinbelow with reference to the sequence listing part.

[32201] GAM2309 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2309 target RNA, herein designated GAM TARGET RNA. GAM2309 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32202] GAM2309 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2309 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2309 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2309 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2309 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32203] The complementary binding of GAM2309 RNA, herein designated GAM RNA, to target binding sites on GAM2309 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2309 target RNA, herein designated GAM TARGET RNA, into GAM2309 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32204] It is appreciated that GAM2309 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2309 target genes. The mRNA of each one of this plurality of GAM2309 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2309 RNA, herein designated GAM RNA, and which when bound by GAM2309 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2309 target proteins.

[32205] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2309 gene, herein designated GAM GENE, on one or more GAM2309 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32206] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2309 correlate with, and may be deduced from, the identity of the target genes which GAM2309 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32207] Nucleotide sequences of the GAM2309 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2309 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2309 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2309 are further described hereinbelow with reference to Table 1.

[32208] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2309 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[32209] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2310 (GAM2310) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32210] GAM2310 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2310 was detected is described hereinabove with reference to Figs. 2-8.

[32211] GAM2310 gene, herein designated GAM GENE, and GAM2310 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[32212] GAM2310 gene, herein designated GAM GENE, encodes a GAM2310 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2310 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2310 precursor RNA is designated SEQ ID:2287, and is provided hereinbelow with reference to the sequence listing part.

[32213] GAM2310 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2310 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32214] An enzyme complex designated DICER COMPLEX, dices the GAM2310 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2310 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of GAM2310 RNA is designated SEQ ID:4901, and is provided hereinbelow with reference to the sequence listing part.

[32215] GAM2310 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2310 target RNA, herein designated GAM TARGET RNA. GAM2310 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32216] GAM2310 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2310 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2310 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2310 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2310 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target



binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32217] The complementary binding of GAM2310 RNA, herein designated GAM RNA, to target binding sites on GAM2310 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2310 target RNA, herein designated GAM TARGET RNA, into GAM2310 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32218] It is appreciated that GAM2310 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2310 target genes. The mRNA of each one of this plurality of GAM2310 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2310 RNA, herein designated GAM RNA, and which when bound by GAM2310 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2310 target proteins.

[32219] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2310 gene, herein designated GAM GENE, on one or more GAM2310 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32220] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2310 correlate with, and may be deduced from, the identity of the target genes which GAM2310 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32221] Nucleotide sequences of the GAM2310 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2310 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2310 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2310 are further described hereinbelow with reference to Table 1.

[32222] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2310 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[32223] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2311 (GAM2311) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32224] GAM2311 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2311 was detected is described hereinabove with reference to Figs. 2-8.

[32225] GAM2311 gene, herein designated GAM GENE, and GAM2311 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[32226] GAM2311 gene, herein designated GAM GENE, encodes a GAM2311 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2311 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2311 precursor RNA is designated SEQ ID:2288, and is provided hereinbelow with reference to the sequence listing part.

[32227] GAM2311 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2311 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

- [32228] An enzyme complex designated DICER COMPLEX, dices the GAM2311 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2311 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 25%) nucleotide sequence of GAM2311 RNA is designated SEQ ID:4902, and is provided hereinbelow with reference to the sequence listing part.
- [32229] GAM2311 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2311 target RNA, herein designated GAM TARGET RNA. GAM2311 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [32230] GAM2311 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2311 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2311 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2311 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2311 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32231] The complementary binding of GAM2311 RNA, herein designated GAM RNA, to target binding sites on GAM2311 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2311 target RNA, herein designated GAM TARGET RNA, into GAM2311 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32232] It is appreciated that GAM2311 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2311 target genes. The mRNA of each one of this plurality of GAM2311 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2311 RNA, herein designated GAM RNA, and which when bound by GAM2311 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2311 target proteins.

[32233] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2311 gene, herein designated GAM GENE, on one or more GAM2311 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32234] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2311 correlate with, and may be deduced from, the identity of the target genes which GAM2311 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32235] Nucleotide sequences of the GAM2311 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2311 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2311 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2311 are further described hereinbelow with reference to Table 1.

[32236] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2311 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

[32237] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2312 (GAM2312) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32238] GAM2312 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2312 was detected is described hereinabove with reference to Figs. 2-8.

[32239] GAM2312 gene, herein designated GAM GENE, and GAM2312 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[32240] GAM2312 gene, herein designated GAM GENE, encodes a GAM2312 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2312 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2312 precursor RNA is designated SEQ ID:2289, and is provided hereinbelow with reference to the sequence listing part.

[32241] GAM2312 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2312 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32242] An enzyme complex designated DICER COMPLEX, dices the GAM2312 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2312 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 92%) nucleotide sequence of GAM2312 RNA is designated SEQ ID:4903, and is provided hereinbelow with reference to the sequence listing part.

[32243] GAM2312 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2312 target RNA, herein designated GAM TARGET RNA. GAM2312 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32244] GAM2312 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2312 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2312 RNA,



herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2312 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2312 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32245] The complementary binding of GAM2312 RNA, herein designated GAM RNA, to target binding sites on GAM2312 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2312 target RNA, herein designated GAM TARGET RNA, into GAM2312 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32246] It is appreciated that GAM2312 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2312 target genes. The mRNA of each one of this plurality of GAM2312 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2312 RNA, herein designated GAM RNA, and which when bound by GAM2312 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2312 target proteins.

[32247] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2312 gene, herein designated GAM GENE, on one or more GAM2312 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32248] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2312 correlate with, and may be deduced from, the identity of the target genes which GAM2312 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32249] Nucleotide sequences of the GAM2312 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2312 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2312 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2312 are further described hereinbelow with reference to Table 1.

[32250] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2312 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[32251] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2313 (GAM2313) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32252] GAM2313 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2313 was detected is described hereinabove with reference to Figs. 2-8.

[32253] GAM2313 gene, herein designated GAM GENE, and GAM2313 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[32254] GAM2313 gene, herein designated GAM GENE, encodes a GAM2313 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2313 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2313 precursor RNA is designated SEQ ID:2290, and is provided hereinbelow with reference to the sequence listing part.

[32255] GAM2313 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2313 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32256] An enzyme complex designated DICER COMPLEX, dices the GAM2313 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2313 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 84%) nucleotide sequence of GAM2313 RNA is designated SEQ ID:4904, and is provided hereinbelow with reference to the sequence listing part.

[32257] GAM2313 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2313 target RNA, herein designated GAM TARGET RNA. GAM2313 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32258] GAM2313 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2313 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2313 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2313 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2313 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32259] The complementary binding of GAM2313 RNA, herein designated GAM RNA, to target binding sites on GAM2313 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2313 target RNA, herein designated GAM TARGET RNA, into GAM2313 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32260] It is appreciated that GAM2313 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2313 target genes. The

mRNA of each one of this plurality of GAM2313 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2313 RNA, herein designated GAM RNA, and which when bound by GAM2313 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2313 target proteins.

[32261] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2313 gene, herein designated GAM GENE, on one or more GAM2313 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32262] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2313 correlate with, and may be deduced from, the identity of the target genes which GAM2313 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32263] Nucleotide sequences of the GAM2313 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2313 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2313 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2313 are further described hereinbelow with reference to Table 1.

[32264] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2313 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[32265] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2314 (GAM2314) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32266] GAM2314 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2314 was detected is described hereinabove with reference to Figs. 2-8.

[32267] GAM2314 gene, herein designated GAM GENE, and GAM2314 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[32268] GAM2314 gene, herein designated GAM GENE, encodes a GAM2314 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2314 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2314 precursor RNA is designated SEQ ID:2291, and is provided hereinbelow with reference to the sequence listing part.

[32269] GAM2314 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2314 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32270] An enzyme complex designated DICER COMPLEX, dices the GAM2314 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2314 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of GAM2314 RNA is designated SEQ ID:4906, and is provided hereinbelow with reference to the sequence listing part.

[32271] GAM2314 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2314 target RNA, herein designated GAM TARGET RNA. GAM2314 target RNA, herein designated GAM



TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32272] GAM2314 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2314 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2314 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2314 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2314 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32273] The complementary binding of GAM2314 RNA, herein designated GAM RNA, to target binding sites on GAM2314 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2314 target RNA, herein designated GAM TARGET RNA, into GAM2314 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32274] It is appreciated that GAM2314 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2314 target genes. The mRNA of each one of this plurality of GAM2314 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2314 RNA, herein designated GAM RNA, and which when bound by GAM2314 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2314 target proteins.

[32275] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2314 gene, herein designated GAM GENE, on one or more GAM2314 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32276] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2314 correlate with, and may be deduced from, the identity of the target

genes which GAM2314 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32277] Nucleotide sequences of the GAM2314 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2314 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2314 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2314 are further described hereinbelow with reference to Table 1.

[32278] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2314 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[32279] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2315 (GAM2315) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32280] GAM2315 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2315 was detected is described hereinabove with reference to Figs. 2-8.

[32281] GAM2315 gene, herein designated GAM GENE, and GAM2315 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

[32282] GAM2315 gene, herein designated GAM GENE, encodes a GAM2315 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2315 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2315 precursor RNA is designated SEQ ID:2292, and is provided hereinbelow with reference to the sequence listing part.

[32283] GAM2315 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2315 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32284] An enzyme complex designated DICER COMPLEX, dices the GAM2315 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2315 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of GAM2315 RNA is designated SEQ ID:4905, and is provided

hereinbelow with reference to the sequence listing part.

[32285] GAM2315 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2315 target RNA, herein designated GAM TARGET RNA. GAM2315 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32286] GAM2315 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2315 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2315 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2315 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2315 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32287] The complementary binding of GAM2315 RNA, herein designated GAM RNA, to target binding sites on GAM2315 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2315 target RNA, herein designated GAM TARGET RNA, into GAM2315 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32288] It is appreciated that GAM2315 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2315 target genes. The mRNA of each one of this plurality of GAM2315 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2315 RNA, herein designated GAM RNA, and which when bound by GAM2315 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2315 target proteins.

[32289] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2315 gene, herein designated GAM GENE, on one or more GAM2315 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32290] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2315 correlate with, and may be deduced from, the identity of the target genes which GAM2315 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32291] Nucleotide sequences of the GAM2315 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2315 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2315 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2315 are further described hereinbelow with reference to Table 1.

[32292] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2315 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[32293] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2316 (GAM2316) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32294] GAM2316 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2316 was detected is described hereinabove with reference to Figs. 2-8.

[32295] GAM2316 gene, herein designated GAM GENE, and GAM2316 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[32296] GAM2316 gene, herein designated GAM GENE, encodes a GAM2316 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2316 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2316 precursor RNA is designated SEQ ID:2293, and is provided hereinbelow with reference to the sequence listing part.

[32297] GAM2316 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2316 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32298] An enzyme complex designated DICER COMPLEX, dices the GAM2316 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2316 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin



structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2316 RNA is designated SEQ ID:4908, and is provided hereinbelow with reference to the sequence listing part.

[32299] GAM2316 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2316 target RNA, herein designated GAM TARGET RNA. GAM2316 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32300] GAM2316 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2316 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2316 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2316 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2316 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32301] The complementary binding of GAM2316 RNA, herein designated GAM RNA, to target binding sites on GAM2316 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2316 target RNA, herein designated GAM TARGET RNA, into GAM2316 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32302] It is appreciated that GAM2316 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2316 target genes. The mRNA of each one of this plurality of GAM2316 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2316 RNA, herein designated GAM RNA, and which when bound by GAM2316 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2316 target proteins.

[32303] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2316 gene, herein designated GAM GENE, on one or more GAM2316 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32304] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2316 correlate with, and may be deduced from, the identity of the target genes which GAM2316 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32305] Nucleotide sequences of the GAM2316 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2316 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2316 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2316 are further described hereinbelow with reference to Table 1.

[32306] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2316 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[32307] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2317 (GAM2317) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32308] GAM2317 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2317 was detected is described hereinabove with reference to Figs. 2-8.

[32309] GAM2317 gene, herein designated GAM GENE, and GAM2317 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[32310] GAM2317 gene, herein designated GAM GENE, encodes a GAM2317 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2317 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2317 precursor RNA is designated SEQ ID:2294, and is provided hereinbelow with reference to the sequence listing part.

[32311] GAM2317 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2317 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

- [32312] An enzyme complex designated DICER COMPLEX, dices the GAM2317 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2317 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2317 RNA is designated SEQ ID:4907, and is provided hereinbelow with reference to the sequence listing part.
- [32313] GAM2317 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2317 target RNA, herein designated GAM TARGET RNA. GAM2317 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [32314] GAM2317 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2317 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2317 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2317 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2317 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32315] The complementary binding of GAM2317 RNA, herein designated GAM RNA, to target binding sites on GAM2317 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2317 target RNA, herein designated GAM TARGET RNA, into GAM2317 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32316] It is appreciated that GAM2317 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2317 target genes. The mRNA of each one of this plurality of GAM2317 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2317 RNA, herein designated GAM RNA, and which when bound by GAM2317 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2317 target proteins.

[32317] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2317 gene, herein designated GAM GENE, on one or more GAM2317 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32318] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2317 correlate with, and may be deduced from, the identity of the target genes which GAM2317 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32319] Nucleotide sequences of the GAM2317 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2317 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2317 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2317 are further described hereinbelow with reference to Table 1.

[32320] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2317 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

[32321] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2318 (GAM2318) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32322] GAM2318 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2318 was detected is described hereinabove with reference to Figs. 2-8.

[32323] GAM2318 gene, herein designated GAM GENE, and GAM2318 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[32324] GAM2318 gene, herein designated GAM GENE, encodes a GAM2318 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2318 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2318 precursor RNA is designated SEQ ID:2295, and is provided hereinbelow with reference to the sequence listing part.

[32325] GAM2318 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2318 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA



encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32326] An enzyme complex designated DICER COMPLEX, dices the GAM2318 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2318 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of GAM2318 RNA is designated SEQ ID:4909, and is provided hereinbelow with reference to the sequence listing part.

[32327] GAM2318 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2318 target RNA, herein designated GAM TARGET RNA. GAM2318 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32328] GAM2318 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2318 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2318 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2318 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2318 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32329] The complementary binding of GAM2318 RNA, herein designated GAM RNA, to target binding sites on GAM2318 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2318 target RNA, herein designated GAM TARGET RNA, into GAM2318 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32330] It is appreciated that GAM2318 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2318 target genes. The mRNA of each one of this plurality of GAM2318 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2318 RNA, herein designated GAM RNA, and which when bound by GAM2318 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2318 target proteins.

[32331] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2318 gene, herein designated GAM GENE, on one or more GAM2318 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32332] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2318 correlate with, and may be deduced from, the identity of the target genes which GAM2318 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32333] Nucleotide sequences of the GAM2318 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2318 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2318 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2318 are further described hereinbelow with reference to Table 1.

- [32334] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2318 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.
- [32335] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2319 (GAM2319) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.
- [32336] GAM2319 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2319 was detected is described hereinabove with reference to Figs. 2-8.
- [32337] GAM2319 gene, herein designated GAM GENE, and GAM2319 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.
- [32338] GAM2319 gene, herein designated GAM GENE, encodes a GAM2319 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2319 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2319 precursor RNA is designated SEQ ID:2296, and is provided hereinbelow with reference to the sequence listing part.

[32339] GAM2319 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2319 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32340] An enzyme complex designated DICER COMPLEX, dices the GAM2319 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2319 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2319 RNA is designated SEQ ID:4910, and is provided hereinbelow with reference to the sequence listing part.

[32341] GAM2319 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2319 target RNA, herein designated GAM TARGET RNA. GAM2319 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32342] GAM2319 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2319 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2319 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2319 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2319 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32343] The complementary binding of GAM2319 RNA, herein designated GAM RNA, to target binding sites on GAM2319 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2319 target RNA, herein designated GAM TARGET RNA, into GAM2319 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32344] It is appreciated that GAM2319 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2319 target genes. The

mRNA of each one of this plurality of GAM2319 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2319 RNA, herein designated GAM RNA, and which when bound by GAM2319 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2319 target proteins.

[32345] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2319 gene, herein designated GAM GENE, on one or more GAM2319 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32346] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2319 correlate with, and may be deduced from, the identity of the target genes which GAM2319 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32347] Nucleotide sequences of the GAM2319 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2319 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2319 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2319 are further described hereinbelow with reference to Table 1.

[32348] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2319 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[32349] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2320 (GAM2320) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32350] GAM2320 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2320 was detected is described hereinabove with reference to Figs. 2-8.

[32351] GAM2320 gene, herein designated GAM GENE, and GAM2320 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[32352] GAM2320 gene, herein designated GAM GENE, encodes a GAM2320 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2320 precursor RNA,



herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2320 precursor RNA is designated SEQ ID:2297, and is provided hereinbelow with reference to the sequence listing part.

[32353] GAM2320 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2320 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32354] An enzyme complex designated DICER COMPLEX, dices the GAM2320 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2320 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 86%) nucleotide sequence of GAM2320 RNA is designated SEQ ID:4911, and is provided hereinbelow with reference to the sequence listing part.

[32355] GAM2320 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2320 target RNA, herein designated GAM TARGET RNA. GAM2320 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32356] GAM2320 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2320 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2320 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2320 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2320 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32357] The complementary binding of GAM2320 RNA, herein designated GAM RNA, to target binding sites on GAM2320 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2320 target RNA, herein designated GAM TARGET RNA, into GAM2320 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32358] It is appreciated that GAM2320 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2320 target genes. The mRNA of each one of this plurality of GAM2320 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2320 RNA, herein designated GAM RNA, and which when bound by GAM2320 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2320 target proteins.

[32359] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2320 gene, herein designated GAM GENE, on one or more GAM2320 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32360] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2320 correlate with, and may be deduced from, the identity of the target

genes which GAM2320 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32361] Nucleotide sequences of the GAM2320 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2320 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2320 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2320 are further described hereinbelow with reference to Table 1.

[32362] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2320 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[32363] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2321 (GAM2321) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32364] GAM2321 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2321 was detected is described hereinabove with reference to Figs. 2-8.

[32365] GAM2321 gene, herein designated GAM GENE, and GAM2321 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

[32366] GAM2321 gene, herein designated GAM GENE, encodes a GAM2321 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2321 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2321 precursor RNA is designated SEQ ID:2298, and is provided hereinbelow with reference to the sequence listing part.

[32367] GAM2321 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2321 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32368] An enzyme complex designated DICER COMPLEX, dices the GAM2321 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2321 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 88%) nucleotide sequence of GAM2321 RNA is designated SEQ ID:4912, and is provided

hereinbelow with reference to the sequence listing part.

[32369] GAM2321 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2321 target RNA, herein designated GAM TARGET RNA. GAM2321 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32370] GAM2321 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2321 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2321 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2321 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2321 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32371] The complementary binding of GAM2321 RNA, herein designated GAM RNA, to target binding sites on GAM2321 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2321 target RNA, herein designated GAM TARGET RNA, into GAM2321 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32372] It is appreciated that GAM2321 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2321 target genes. The mRNA of each one of this plurality of GAM2321 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2321 RNA, herein designated GAM RNA, and which when bound by GAM2321 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2321 target proteins.

[32373] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2321 gene, herein designated GAM GENE, on one or more GAM2321 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32374] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2321 correlate with, and may be deduced from, the identity of the target genes which GAM2321 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32375] Nucleotide sequences of the GAM2321 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2321 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2321 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2321 are further described hereinbelow with reference to Table 1.

[32376] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2321 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[32377] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2322 (GAM2322) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32378] GAM2322 is a novel bioinformatically detected regulatory, non protein



coding, micro RNA (miRNA) gene. The method by which GAM2322 was detected is described hereinabove with reference to Figs. 2-8.

[32379] GAM2322 gene, herein designated GAM GENE, and GAM2322 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[32380] GAM2322 gene, herein designated GAM GENE, encodes a GAM2322 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2322 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2322 precursor RNA is designated SEQ ID:2299, and is provided hereinbelow with reference to the sequence listing part.

[32381] GAM2322 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2322 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32382] An enzyme complex designated DICER COMPLEX, dices the GAM2322 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2322 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2322 RNA is designated SEQ ID:4913, and is provided hereinbelow with reference to the sequence listing part.

[32383] GAM2322 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2322 target RNA, herein designated GAM TARGET RNA. GAM2322 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32384] GAM2322 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2322 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2322 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2322 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2322 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32385] The complementary binding of GAM2322 RNA, herein designated GAM RNA, to target binding sites on GAM2322 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2322 target RNA, herein designated GAM TARGET RNA, into GAM2322 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32386] It is appreciated that GAM2322 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2322 target genes. The mRNA of each one of this plurality of GAM2322 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2322 RNA, herein designated GAM RNA, and which when bound by GAM2322 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2322 target proteins.

[32387] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2322 gene, herein designated GAM GENE, on one or more GAM2322 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32388] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2322 correlate with, and may be deduced from, the identity of the target genes which GAM2322 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32389] Nucleotide sequences of the GAM2322 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2322 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2322 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2322 are further described hereinbelow with reference to Table 1.

[32390] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2322 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[32391] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2323 (GAM2323) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32392] GAM2323 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2323 was detected is described hereinabove with reference to Figs. 2-8.

[32393] GAM2323 gene, herein designated GAM GENE, and GAM2323 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[32394] GAM2323 gene, herein designated GAM GENE, encodes a GAM2323 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2323 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2323 precursor RNA is designated SEQ ID:2300, and is provided hereinbelow with reference to the sequence listing part.

[32395] GAM2323 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2323 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

- [32396] An enzyme complex designated DICER COMPLEX, dices the GAM2323 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2323 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 92%) nucleotide sequence of GAM2323 RNA is designated SEQ ID:4914, and is provided hereinbelow with reference to the sequence listing part.
- [32397] GAM2323 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2323 target RNA, herein designated GAM TARGET RNA. GAM2323 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [32398] GAM2323 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2323 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2323 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2323 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2323 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32399] The complementary binding of GAM2323 RNA, herein designated GAM RNA, to target binding sites on GAM2323 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2323 target RNA, herein designated GAM TARGET RNA, into GAM2323 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32400] It is appreciated that GAM2323 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2323 target genes. The mRNA of each one of this plurality of GAM2323 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2323 RNA, herein designated GAM RNA, and which when bound by GAM2323 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2323 target proteins.

[32401] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2323 gene, herein designated GAM GENE, on one or more GAM2323 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32402] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2323 correlate with, and may be deduced from, the identity of the target genes which GAM2323 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32403] Nucleotide sequences of the GAM2323 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2323 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2323 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2323 are further described hereinbelow with reference to Table 1.

[32404] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2323 RNA, herein designated GAM RNA, are described hereinbelow



with reference to Table 2.

- [32405] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2324 (GAM2324) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.
- [32406] GAM2324 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2324 was detected is described hereinabove with reference to Figs. 2-8.
- [32407] GAM2324 gene, herein designated GAM GENE, and GAM2324 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.
- [32408] GAM2324 gene, herein designated GAM GENE, encodes a GAM2324 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2324 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2324 precursor RNA is designated SEQ ID:2301, and is provided hereinbelow with reference to the sequence listing part.
- [32409] GAM2324 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2324 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32410] An enzyme complex designated DICER COMPLEX, dices the GAM2324 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2324 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2324 RNA is designated SEQ ID:4915, and is provided hereinbelow with reference to the sequence listing part.

[32411] GAM2324 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2324 target RNA, herein designated GAM TARGET RNA. GAM2324 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32412] GAM2324 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2324 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2324 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2324 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2324 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32413] The complementary binding of GAM2324 RNA, herein designated GAM RNA, to target binding sites on GAM2324 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2324 target RNA, herein designated GAM TARGET RNA, into GAM2324 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32414] It is appreciated that GAM2324 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2324 target genes. The mRNA of each one of this plurality of GAM2324 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2324 RNA, herein designated GAM RNA, and which when bound by GAM2324 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2324 target proteins.

[32415] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2324 gene, herein designated GAM GENE, on one or more GAM2324 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32416] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2324 correlate with, and may be deduced from, the identity of the target genes which GAM2324 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32417] Nucleotide sequences of the GAM2324 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2324 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2324 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2324 are further described hereinbelow with reference to Table 1.

[32418] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2324 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[32419] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2325 (GAM2325) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32420] GAM2325 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2325 was detected is described hereinabove with reference to Figs. 2-8.

[32421] GAM2325 gene, herein designated GAM GENE, and GAM2325 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[32422] GAM2325 gene, herein designated GAM GENE, encodes a GAM2325 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2325 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2325 precursor RNA is designated SEQ ID:2302, and is provided hereinbelow with reference to the sequence listing part.

[32423] GAM2325 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2325 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32424] An enzyme complex designated DICER COMPLEX, dices the GAM2325 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2325 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 92%) nucleotide sequence of GAM2325 RNA is designated SEQ ID:4916, and is provided hereinbelow with reference to the sequence listing part.

[32425] GAM2325 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2325 target RNA, herein designated GAM TARGET RNA. GAM2325 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32426] GAM2325 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2325 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2325 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2325 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2325 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32427] The complementary binding of GAM2325 RNA, herein designated GAM RNA, to target binding sites on GAM2325 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2325 target RNA, herein designated GAM TARGET RNA, into GAM2325 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32428] It is appreciated that GAM2325 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2325 target genes. The

mRNA of each one of this plurality of GAM2325 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2325 RNA, herein designated GAM RNA, and which when bound by GAM2325 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2325 target proteins.

[32429] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2325 gene, herein designated GAM GENE, on one or more GAM2325 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32430] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2325 correlate with, and may be deduced from, the identity of the target genes which GAM2325 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32431] Nucleotide sequences of the GAM2325 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2325 RNA, herein



designated GAM RNA, and a schematic representation of the secondary folding of GAM2325 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2325 are further described hereinbelow with reference to Table 1.

[32432] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2325 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[32433] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2326 (GAM2326) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32434] GAM2326 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2326 was detected is described hereinabove with reference to Figs. 2-8.

[32435] GAM2326 gene, herein designated GAM GENE, and GAM2326 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[32436] GAM2326 gene, herein designated GAM GENE, encodes a GAM2326 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2326 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2326 precursor RNA is designated SEQ ID:2303, and is provided hereinbelow with reference to the sequence listing part.

[32437] GAM2326 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2326 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32438] An enzyme complex designated DICER COMPLEX, dices the GAM2326 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2326 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 84%) nucleotide sequence of GAM2326 RNA is designated SEQ ID:4917, and is provided hereinbelow with reference to the sequence listing part.

[32439] GAM2326 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2326 target RNA, herein designated GAM TARGET RNA. GAM2326 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32440] GAM2326 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2326 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2326 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2326 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2326 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32441] The complementary binding of GAM2326 RNA, herein designated GAM RNA, to target binding sites on GAM2326 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2326 target RNA, herein designated GAM TARGET RNA, into GAM2326 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32442] It is appreciated that GAM2326 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2326 target genes. The mRNA of each one of this plurality of GAM2326 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2326 RNA, herein designated GAM RNA, and which when bound by GAM2326 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2326 target proteins.

[32443] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2326 gene, herein designated GAM GENE, on one or more GAM2326 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32444] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2326 correlate with, and may be deduced from, the identity of the target

genes which GAM2326 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32445] Nucleotide sequences of the GAM2326 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2326 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2326 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2326 are further described hereinbelow with reference to Table 1.

[32446] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2326 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[32447] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2327 (GAM2327) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32448] GAM2327 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2327 was detected is described hereinabove with reference to Figs. 2-8.

[32449] GAM2327 gene, herein designated GAM GENE, and GAM2327 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

[32450] GAM2327 gene, herein designated GAM GENE, encodes a GAM2327 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2327 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2327 precursor RNA is designated SEQ ID:2304, and is provided hereinbelow with reference to the sequence listing part.

[32451] GAM2327 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2327 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32452] An enzyme complex designated DICER COMPLEX, dices the GAM2327 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2327 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 83%) nucleotide sequence of GAM2327 RNA is designated SEQ ID:4919, and is provided

hereinbelow with reference to the sequence listing part.

[32453] GAM2327 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2327 target RNA, herein designated GAM TARGET RNA. GAM2327 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32454] GAM2327 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2327 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2327 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2327 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2327 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32455] The complementary binding of GAM2327 RNA, herein designated GAM RNA, to target binding sites on GAM2327 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2327 target RNA, herein designated GAM TARGET RNA, into GAM2327 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32456] It is appreciated that GAM2327 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2327 target genes. The mRNA of each one of this plurality of GAM2327 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2327 RNA, herein designated GAM RNA, and which when bound by GAM2327 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2327 target proteins.

[32457] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2327 gene, herein designated GAM GENE, on one or more GAM2327 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding



sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32458] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2327 correlate with, and may be deduced from, the identity of the target genes which GAM2327 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32459] Nucleotide sequences of the GAM2327 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2327 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2327 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2327 are further described hereinbelow with reference to Table 1.

[32460] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2327 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[32461] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2328 (GAM2328) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32462] GAM2328 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2328 was detected is described hereinabove with reference to Figs. 2-8.

[32463] GAM2328 gene, herein designated GAM GENE, and GAM2328 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[32464] GAM2328 gene, herein designated GAM GENE, encodes a GAM2328 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2328 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2328 precursor RNA is designated SEQ ID:2305, and is provided hereinbelow with reference to the sequence listing part.

[32465] GAM2328 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2328 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32466] An enzyme complex designated DICER COMPLEX, dices the GAM2328 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2328 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of GAM2328 RNA is designated SEQ ID:4918, and is provided hereinbelow with reference to the sequence listing part.

[32467] GAM2328 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2328 target RNA, herein designated GAM TARGET RNA. GAM2328 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32468] GAM2328 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2328 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2328 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2328 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2328 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32469] The complementary binding of GAM2328 RNA, herein designated GAM RNA, to target binding sites on GAM2328 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2328 target RNA, herein designated GAM TARGET RNA, into GAM2328 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32470] It is appreciated that GAM2328 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2328 target genes. The mRNA of each one of this plurality of GAM2328 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2328 RNA, herein designated GAM RNA, and which when bound by GAM2328 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2328 target proteins.

[32471] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2328 gene, herein designated GAM GENE, on one or more GAM2328 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32472] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2328 correlate with, and may be deduced from, the identity of the target genes which GAM2328 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32473] Nucleotide sequences of the GAM2328 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2328 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2328 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2328 are further described hereinbelow with reference to Table 1.

[32474] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2328 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[32475] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2329 (GAM2329) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32476] GAM2329 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2329 was detected is described hereinabove with reference to Figs. 2-8.

[32477] GAM2329 gene, herein designated GAM GENE, and GAM2329 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[32478] GAM2329 gene, herein designated GAM GENE, encodes a GAM2329 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2329 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2329 precursor RNA is designated SEQ ID:2306, and is provided hereinbelow with reference to the sequence listing part.

[32479] GAM2329 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2329 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32480] An enzyme complex designated DICER COMPLEX, dices the GAM2329 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2329 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 83%) nucleotide sequence of GAM2329 RNA is designated SEQ ID:4920, and is provided hereinbelow with reference to the sequence listing part.

[32481] GAM2329 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2329 target RNA, herein designated GAM TARGET RNA. GAM2329 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32482] GAM2329 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2329 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2329 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2329 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2329 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32483] The complementary binding of GAM2329 RNA, herein designated GAM RNA, to target binding sites on GAM2329 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2329 target RNA, herein designated GAM TARGET RNA, into GAM2329 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32484] It is appreciated that GAM2329 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2329 target genes. The mRNA of each one of this plurality of GAM2329 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2329 RNA, herein designated GAM RNA, and which when bound by GAM2329 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2329 target proteins.

[32485] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition



exerted by GAM2329 gene, herein designated GAM GENE, on one or more GAM2329 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32486] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2329 correlate with, and may be deduced from, the identity of the target genes which GAM2329 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32487] Nucleotide sequences of the GAM2329 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2329 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2329 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2329 are further described hereinbelow with reference to Table 1.

[32488] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2329 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

[32489] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2330 (GAM2330) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32490] GAM2330 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2330 was detected is described hereinabove with reference to Figs. 2-8.

[32491] GAM2330 gene, herein designated GAM GENE, and GAM2330 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[32492] GAM2330 gene, herein designated GAM GENE, encodes a GAM2330 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2330 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2330 precursor RNA is designated SEQ ID:2307, and is provided hereinbelow with reference to the sequence listing part.

[32493] GAM2330 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2330 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32494] An enzyme complex designated DICER COMPLEX, dices the GAM2330 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2330 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 84%) nucleotide sequence of GAM2330 RNA is designated SEQ ID:4921, and is provided hereinbelow with reference to the sequence listing part.

[32495] GAM2330 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2330 target RNA, herein designated GAM TARGET RNA. GAM2330 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32496] GAM2330 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2330 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2330 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2330 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2330 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32497] The complementary binding of GAM2330 RNA, herein designated GAM RNA, to target binding sites on GAM2330 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2330 target RNA, herein designated GAM TARGET RNA, into GAM2330 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32498] It is appreciated that GAM2330 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2330 target genes. The mRNA of each one of this plurality of GAM2330 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2330 RNA, herein designated GAM RNA, and which when bound by GAM2330 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2330 target proteins.

[32499] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2330 gene, herein designated GAM GENE, on one or more GAM2330 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32500] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2330 correlate with, and may be deduced from, the identity of the target genes which GAM2330 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32501] Nucleotide sequences of the GAM2330 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2330 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2330 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2330 are further described hereinbelow with reference to Table 1.

[32502] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2330 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[32503] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2331 (GAM2331) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32504] GAM2331 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2331 was detected is described hereinabove with reference to Figs. 2-8.

[32505] GAM2331 gene, herein designated GAM GENE, and GAM2331 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[32506] GAM2331 gene, herein designated GAM GENE, encodes a GAM2331 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2331 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2331 precursor RNA is designated SEQ ID:2308, and is provided hereinbelow with reference to the sequence listing part.

[32507] GAM2331 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2331 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32508] An enzyme complex designated DICER COMPLEX, dices the GAM2331 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2331 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 83%) nucleotide sequence of GAM2331 RNA is designated SEQ ID:4922, and is provided hereinbelow with reference to the sequence listing part.

[32509] GAM2331 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2331 target RNA, herein designated GAM TARGET RNA. GAM2331 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32510] GAM2331 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2331 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2331 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2331 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2331 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32511] The complementary binding of GAM2331 RNA, herein designated GAM RNA, to target binding sites on GAM2331 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2331 target RNA, herein designated GAM TARGET RNA, into GAM2331 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32512] It is appreciated that GAM2331 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2331 target genes. The



mRNA of each one of this plurality of GAM2331 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2331 RNA, herein designated GAM RNA, and which when bound by GAM2331 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2331 target proteins.

[32513] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2331 gene, herein designated GAM GENE, on one or more GAM2331 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32514] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2331 correlate with, and may be deduced from, the identity of the target genes which GAM2331 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32515] Nucleotide sequences of the GAM2331 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2331 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2331 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2331 are further described hereinbelow with reference to Table 1.

[32516] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2331 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[32517] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2332 (GAM2332) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32518] GAM2332 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2332 was detected is described hereinabove with reference to Figs. 2-8.

[32519] GAM2332 gene, herein designated GAM GENE, and GAM2332 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[32520] GAM2332 gene, herein designated GAM GENE, encodes a GAM2332 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2332 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2332 precursor RNA is designated SEQ ID:2309, and is provided hereinbelow with reference to the sequence listing part.

[32521] GAM2332 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2332 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32522] An enzyme complex designated DICER COMPLEX, dices the GAM2332 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2332 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 76%) nucleotide sequence of GAM2332 RNA is designated SEQ ID:4923, and is provided hereinbelow with reference to the sequence listing part.

[32523] GAM2332 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2332 target RNA, herein designated GAM TARGET RNA. GAM2332 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32524] GAM2332 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2332 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2332 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2332 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2332 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32525] The complementary binding of GAM2332 RNA, herein designated GAM RNA, to target binding sites on GAM2332 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2332 target RNA, herein designated GAM TARGET RNA, into GAM2332 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32526] It is appreciated that GAM2332 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2332 target genes. The mRNA of each one of this plurality of GAM2332 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2332 RNA, herein designated GAM RNA, and which when bound by GAM2332 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2332 target proteins.

[32527] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2332 gene, herein designated GAM GENE, on one or more GAM2332 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32528] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2332 correlate with, and may be deduced from, the identity of the target

genes which GAM2332 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32529] Nucleotide sequences of the GAM2332 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2332 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2332 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2332 are further described hereinbelow with reference to Table 1.

[32530] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2332 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[32531] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2333 (GAM2333) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32532] GAM2333 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2333 was detected is described hereinabove with reference to Figs. 2-8.

[32533] GAM2333 gene, herein designated GAM GENE, and GAM2333 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

[32534] GAM2333 gene, herein designated GAM GENE, encodes a GAM2333 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2333 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2333 precursor RNA is designated SEQ ID:2310, and is provided hereinbelow with reference to the sequence listing part.

[32535] GAM2333 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2333 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32536] An enzyme complex designated DICER COMPLEX, dices the GAM2333 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2333 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 76%) nucleotide sequence of GAM2333 RNA is designated SEQ ID:4924, and is provided

hereinbelow with reference to the sequence listing part.

[32537] GAM2333 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2333 target RNA, herein designated GAM TARGET RNA. GAM2333 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32538] GAM2333 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2333 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2333 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2333 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2333 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.



[32539] The complementary binding of GAM2333 RNA, herein designated GAM RNA, to target binding sites on GAM2333 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2333 target RNA, herein designated GAM TARGET RNA, into GAM2333 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32540] It is appreciated that GAM2333 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2333 target genes. The mRNA of each one of this plurality of GAM2333 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2333 RNA, herein designated GAM RNA, and which when bound by GAM2333 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2333 target proteins.

[32541] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2333 gene, herein designated GAM GENE, on one or more GAM2333 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32542] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2333 correlate with, and may be deduced from, the identity of the target genes which GAM2333 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32543] Nucleotide sequences of the GAM2333 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2333 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2333 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2333 are further described hereinbelow with reference to Table 1.

[32544] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2333 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[32545] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2334 (GAM2334) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32546] GAM2334 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2334 was detected is described hereinabove with reference to Figs. 2-8.

[32547] GAM2334 gene, herein designated GAM GENE, and GAM2334 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[32548] GAM2334 gene, herein designated GAM GENE, encodes a GAM2334 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2334 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2334 precursor RNA is designated SEQ ID:2311, and is provided hereinbelow with reference to the sequence listing part.

[32549] GAM2334 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2334 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32550] An enzyme complex designated DICER COMPLEX, dices the GAM2334 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2334 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of GAM2334 RNA is designated SEQ ID:4925, and is provided hereinbelow with reference to the sequence listing part.

[32551] GAM2334 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2334 target RNA, herein designated GAM TARGET RNA. GAM2334 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32552] GAM2334 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2334 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2334 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2334 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2334 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32553] The complementary binding of GAM2334 RNA, herein designated GAM RNA, to target binding sites on GAM2334 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2334 target RNA, herein designated GAM TARGET RNA, into GAM2334 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32554] It is appreciated that GAM2334 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2334 target genes. The mRNA of each one of this plurality of GAM2334 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2334 RNA, herein designated GAM RNA, and which when bound by GAM2334 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2334 target proteins.

[32555] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2334 gene, herein designated GAM GENE, on one or more GAM2334 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32556] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2334 correlate with, and may be deduced from, the identity of the target genes which GAM2334 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32557] Nucleotide sequences of the GAM2334 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2334 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2334 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2334 are further described hereinbelow with reference to Table 1.

[32558] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2334 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[32559] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2335 (GAM2335) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32560] GAM2335 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2335 was detected is described hereinabove with reference to Figs. 2-8.

[32561] GAM2335 gene, herein designated GAM GENE, and GAM2335 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[32562] GAM2335 gene, herein designated GAM GENE, encodes a GAM2335 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2335 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2335 precursor RNA is designated SEQ ID:2312, and is provided hereinbelow with reference to the sequence listing part.

[32563] GAM2335 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2335 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

- [32564] An enzyme complex designated DICER COMPLEX, dices the GAM2335 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2335 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 84%) nucleotide sequence of GAM2335 RNA is designated SEQ ID:4926, and is provided hereinbelow with reference to the sequence listing part.
- [32565] GAM2335 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2335 target RNA, herein designated GAM TARGET RNA. GAM2335 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [32566] GAM2335 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2335 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2335 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an



illustration only, and is not meant to be limiting GAM2335 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2335 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32567] The complementary binding of GAM2335 RNA, herein designated GAM RNA, to target binding sites on GAM2335 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2335 target RNA, herein designated GAM TARGET RNA, into GAM2335 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32568] It is appreciated that GAM2335 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2335 target genes. The mRNA of each one of this plurality of GAM2335 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2335 RNA, herein designated GAM RNA, and which when bound by GAM2335 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2335 target proteins.

[32569] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2335 gene, herein designated GAM GENE, on one or more GAM2335 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32570] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2335 correlate with, and may be deduced from, the identity of the target genes which GAM2335 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32571] Nucleotide sequences of the GAM2335 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2335 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2335 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2335 are further described hereinbelow with reference to Table 1.

[32572] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2335 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

[32573] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2336 (GAM2336) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32574] GAM2336 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2336 was detected is described hereinabove with reference to Figs. 2-8.

[32575] GAM2336 gene, herein designated GAM GENE, and GAM2336 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[32576] GAM2336 gene, herein designated GAM GENE, encodes a GAM2336 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2336 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2336 precursor RNA is designated SEQ ID:2313, and is provided hereinbelow with reference to the sequence listing part.

[32577] GAM2336 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2336 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32578] An enzyme complex designated DICER COMPLEX, dices the GAM2336 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2336 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of GAM2336 RNA is designated SEQ ID:4927, and is provided hereinbelow with reference to the sequence listing part.

[32579] GAM2336 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2336 target RNA, herein designated GAM TARGET RNA. GAM2336 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32580] GAM2336 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2336 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2336 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2336 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2336 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32581] The complementary binding of GAM2336 RNA, herein designated GAM RNA, to target binding sites on GAM2336 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2336 target RNA, herein designated GAM TARGET RNA, into GAM2336 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32582] It is appreciated that GAM2336 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2336 target genes. The mRNA of each one of this plurality of GAM2336 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2336 RNA, herein designated GAM RNA, and which when bound by GAM2336 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2336 target proteins.

[32583] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2336 gene, herein designated GAM GENE, on one or more GAM2336 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32584] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2336 correlate with, and may be deduced from, the identity of the target genes which GAM2336 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32585] Nucleotide sequences of the GAM2336 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2336 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2336 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2336 are further described hereinbelow with reference to Table 1.

[32586] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2336 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[32587] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2337 (GAM2337) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32588] GAM2337 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2337 was detected is described hereinabove with reference to Figs. 2-8.

[32589] GAM2337 gene, herein designated GAM GENE, and GAM2337 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[32590] GAM2337 gene, herein designated GAM GENE, encodes a GAM2337 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2337 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2337 precursor RNA is designated SEQ ID:2314, and is provided hereinbelow with reference to the sequence listing part.

[32591] GAM2337 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2337 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32592] An enzyme complex designated DICER COMPLEX, dices the GAM2337 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2337 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 84%) nucleotide sequence of GAM2337 RNA is designated SEQ ID:4928, and is provided hereinbelow with reference to the sequence listing part.

[32593] GAM2337 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2337 target RNA, herein designated GAM TARGET RNA. GAM2337 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.



[32594] GAM2337 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2337 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2337 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2337 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2337 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32595] The complementary binding of GAM2337 RNA, herein designated GAM RNA, to target binding sites on GAM2337 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2337 target RNA, herein designated GAM TARGET RNA, into GAM2337 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32596] It is appreciated that GAM2337 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2337 target genes. The

mRNA of each one of this plurality of GAM2337 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2337 RNA, herein designated GAM RNA, and which when bound by GAM2337 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2337 target proteins.

[32597] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2337 gene, herein designated GAM GENE, on one or more GAM2337 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32598] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2337 correlate with, and may be deduced from, the identity of the target genes which GAM2337 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32599] Nucleotide sequences of the GAM2337 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2337 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2337 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2337 are further described hereinbelow with reference to Table 1.

[32600] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2337 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[32601] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2338 (GAM2338) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32602] GAM2338 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2338 was detected is described hereinabove with reference to Figs. 2-8.

[32603] GAM2338 gene, herein designated GAM GENE, and GAM2338 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[32604] GAM2338 gene, herein designated GAM GENE, encodes a GAM2338 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2338 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2338 precursor RNA is designated SEQ ID:2315, and is provided hereinbelow with reference to the sequence listing part.

[32605] GAM2338 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2338 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32606] An enzyme complex designated DICER COMPLEX, dices the GAM2338 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2338 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of GAM2338 RNA is designated SEQ ID:4929, and is provided hereinbelow with reference to the sequence listing part.

[32607] GAM2338 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2338 target RNA, herein designated GAM TARGET RNA. GAM2338 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32608] GAM2338 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2338 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2338 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2338 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2338 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32609] The complementary binding of GAM2338 RNA, herein designated GAM RNA, to target binding sites on GAM2338 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2338 target RNA, herein designated GAM TARGET RNA, into GAM2338 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32610] It is appreciated that GAM2338 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2338 target genes. The mRNA of each one of this plurality of GAM2338 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2338 RNA, herein designated GAM RNA, and which when bound by GAM2338 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2338 target proteins.

[32611] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2338 gene, herein designated GAM GENE, on one or more GAM2338 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32612] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2338 correlate with, and may be deduced from, the identity of the target

genes which GAM2338 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32613] Nucleotide sequences of the GAM2338 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2338 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2338 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2338 are further described hereinbelow with reference to Table 1.

[32614] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2338 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[32615] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2339 (GAM2339) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32616] GAM2339 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2339 was detected is described hereinabove with reference to Figs. 2-8.

[32617] GAM2339 gene, herein designated GAM GENE, and GAM2339 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

[32618] GAM2339 gene, herein designated GAM GENE, encodes a GAM2339 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2339 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2339 precursor RNA is designated SEQ ID:2316, and is provided hereinbelow with reference to the sequence listing part.

[32619] GAM2339 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2339 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32620] An enzyme complex designated DICER COMPLEX, dices the GAM2339 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2339 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2339 RNA is designated SEQ ID:4930, and is provided



hereinbelow with reference to the sequence listing part.

[32621] GAM2339 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2339 target RNA, herein designated GAM TARGET RNA. GAM2339 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32622] GAM2339 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2339 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2339 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2339 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2339 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32623] The complementary binding of GAM2339 RNA, herein designated GAM RNA, to target binding sites on GAM2339 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2339 target RNA, herein designated GAM TARGET RNA, into GAM2339 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32624] It is appreciated that GAM2339 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2339 target genes. The mRNA of each one of this plurality of GAM2339 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2339 RNA, herein designated GAM RNA, and which when bound by GAM2339 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2339 target proteins.

[32625] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2339 gene, herein designated GAM GENE, on one or more GAM2339 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32626] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2339 correlate with, and may be deduced from, the identity of the target genes which GAM2339 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32627] Nucleotide sequences of the GAM2339 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2339 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2339 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2339 are further described hereinbelow with reference to Table 1.

[32628] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2339 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[32629] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2340 (GAM2340) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32630] GAM2340 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2340 was detected is described hereinabove with reference to Figs. 2-8.

[32631] GAM2340 gene, herein designated GAM GENE, and GAM2340 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[32632] GAM2340 gene, herein designated GAM GENE, encodes a GAM2340 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2340 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2340 precursor RNA is designated SEQ ID:2317, and is provided hereinbelow with reference to the sequence listing part.

[32633] GAM2340 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2340 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

- [32634] An enzyme complex designated DICER COMPLEX, dices the GAM2340 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2340 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of GAM2340 RNA is designated SEQ ID:4931, and is provided hereinbelow with reference to the sequence listing part.
- [32635] GAM2340 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2340 target RNA, herein designated GAM TARGET RNA. GAM2340 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [32636] GAM2340 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2340 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2340 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2340 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2340 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32637] The complementary binding of GAM2340 RNA, herein designated GAM RNA, to target binding sites on GAM2340 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2340 target RNA, herein designated GAM TARGET RNA, into GAM2340 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32638] It is appreciated that GAM2340 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2340 target genes. The mRNA of each one of this plurality of GAM2340 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2340 RNA, herein designated GAM RNA, and which when bound by GAM2340 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2340 target proteins.

[32639] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2340 gene, herein designated GAM GENE, on one or more GAM2340 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32640] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2340 correlate with, and may be deduced from, the identity of the target genes which GAM2340 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32641] Nucleotide sequences of the GAM2340 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2340 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2340 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2340 are further described hereinbelow with reference to Table 1.

[32642] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2340 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

[32643] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2341 (GAM2341) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32644] GAM2341 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2341 was detected is described hereinabove with reference to Figs. 2-8.

[32645] GAM2341 gene, herein designated GAM GENE, and GAM2341 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[32646] GAM2341 gene, herein designated GAM GENE, encodes a GAM2341 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2341 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2341 precursor RNA is designated SEQ ID:2318, and is provided hereinbelow with reference to the sequence listing part.

[32647] GAM2341 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2341 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA



encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32648] An enzyme complex designated DICER COMPLEX, dices the GAM2341 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2341 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2341 RNA is designated SEQ ID:4932, and is provided hereinbelow with reference to the sequence listing part.

[32649] GAM2341 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2341 target RNA, herein designated GAM TARGET RNA. GAM2341 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32650] GAM2341 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2341 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2341 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2341 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2341 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32651] The complementary binding of GAM2341 RNA, herein designated GAM RNA, to target binding sites on GAM2341 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2341 target RNA, herein designated GAM TARGET RNA, into GAM2341 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32652] It is appreciated that GAM2341 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2341 target genes. The mRNA of each one of this plurality of GAM2341 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2341 RNA, herein designated GAM RNA, and which when bound by GAM2341 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2341 target proteins.

[32653] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2341 gene, herein designated GAM GENE, on one or more GAM2341 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32654] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2341 correlate with, and may be deduced from, the identity of the target genes which GAM2341 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32655] Nucleotide sequences of the GAM2341 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2341 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2341 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2341 are further described hereinbelow with reference to Table 1.

[32656] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2341 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[32657] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2342 (GAM2342) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32658] GAM2342 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2342 was detected is described hereinabove with reference to Figs. 2-8.

[32659] GAM2342 gene, herein designated GAM GENE, and GAM2342 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[32660] GAM2342 gene, herein designated GAM GENE, encodes a GAM2342 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2342 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2342 precursor RNA is designated SEQ ID:2319, and is provided hereinbelow with reference to the sequence listing part.

[32661] GAM2342 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2342 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32662] An enzyme complex designated DICER COMPLEX, dices the GAM2342 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2342 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of GAM2342 RNA is designated SEQ ID:4933, and is provided hereinbelow with reference to the sequence listing part.

[32663] GAM2342 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2342 target RNA, herein designated GAM TARGET RNA. GAM2342 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32664] GAM2342 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2342 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2342 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2342 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2342 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32665] The complementary binding of GAM2342 RNA, herein designated GAM RNA, to target binding sites on GAM2342 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2342 target RNA, herein designated GAM TARGET RNA, into GAM2342 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32666] It is appreciated that GAM2342 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2342 target genes. The

mRNA of each one of this plurality of GAM2342 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2342 RNA, herein designated GAM RNA, and which when bound by GAM2342 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2342 target proteins.

[32667] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2342 gene, herein designated GAM GENE, on one or more GAM2342 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32668] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2342 correlate with, and may be deduced from, the identity of the target genes which GAM2342 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32669] Nucleotide sequences of the GAM2342 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2342 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2342 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2342 are further described hereinbelow with reference to Table 1.

[32670] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2342 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[32671] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2343 (GAM2343) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32672] GAM2343 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2343 was detected is described hereinabove with reference to Figs. 2-8.

[32673] GAM2343 gene, herein designated GAM GENE, and GAM2343 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[32674] GAM2343 gene, herein designated GAM GENE, encodes a GAM2343 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2343 precursor RNA,



herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2343 precursor RNA is designated SEQ ID:2320, and is provided hereinbelow with reference to the sequence listing part.

[32675] GAM2343 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2343 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32676] An enzyme complex designated DICER COMPLEX, dices the GAM2343 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2343 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 92%) nucleotide sequence of GAM2343 RNA is designated SEQ ID:4934, and is provided hereinbelow with reference to the sequence listing part.

[32677] GAM2343 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2343 target RNA, herein designated GAM TARGET RNA. GAM2343 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32678] GAM2343 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2343 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2343 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2343 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2343 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32679] The complementary binding of GAM2343 RNA, herein designated GAM RNA, to target binding sites on GAM2343 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2343 target RNA, herein designated GAM TARGET RNA, into GAM2343 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32680] It is appreciated that GAM2343 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2343 target genes. The mRNA of each one of this plurality of GAM2343 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2343 RNA, herein designated GAM RNA, and which when bound by GAM2343 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2343 target proteins.

[32681] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2343 gene, herein designated GAM GENE, on one or more GAM2343 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32682] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2343 correlate with, and may be deduced from, the identity of the target

genes which GAM2343 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32683] Nucleotide sequences of the GAM2343 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2343 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2343 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2343 are further described hereinbelow with reference to Table 1.

[32684] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2343 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[32685] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2344 (GAM2344) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32686] GAM2344 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2344 was detected is described hereinabove with reference to Figs. 2-8.

[32687] GAM2344 gene, herein designated GAM GENE, and GAM2344 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

[32688] GAM2344 gene, herein designated GAM GENE, encodes a GAM2344 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2344 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2344 precursor RNA is designated SEQ ID:2321, and is provided hereinbelow with reference to the sequence listing part.

[32689] GAM2344 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2344 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32690] An enzyme complex designated DICER COMPLEX, dices the GAM2344 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2344 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2344 RNA is designated SEQ ID:4935, and is provided

hereinbelow with reference to the sequence listing part.

[32691] GAM2344 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2344 target RNA, herein designated GAM TARGET RNA. GAM2344 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32692] GAM2344 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2344 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2344 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2344 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2344 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32693] The complementary binding of GAM2344 RNA, herein designated GAM RNA, to target binding sites on GAM2344 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2344 target RNA, herein designated GAM TARGET RNA, into GAM2344 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32694] It is appreciated that GAM2344 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2344 target genes. The mRNA of each one of this plurality of GAM2344 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2344 RNA, herein designated GAM RNA, and which when bound by GAM2344 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2344 target proteins.

[32695] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2344 gene, herein designated GAM GENE, on one or more GAM2344 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32696] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2344 correlate with, and may be deduced from, the identity of the target genes which GAM2344 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32697] Nucleotide sequences of the GAM2344 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2344 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2344 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2344 are further described hereinbelow with reference to Table 1.

[32698] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2344 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[32699] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2345 (GAM2345) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32700] GAM2345 is a novel bioinformatically detected regulatory, non protein



coding, micro RNA (miRNA) gene. The method by which GAM2345 was detected is described hereinabove with reference to Figs. 2-8.

[32701] GAM2345 gene, herein designated GAM GENE, and GAM2345 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[32702] GAM2345 gene, herein designated GAM GENE, encodes a GAM2345 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2345 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2345 precursor RNA is designated SEQ ID:2322, and is provided hereinbelow with reference to the sequence listing part.

[32703] GAM2345 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2345 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32704] An enzyme complex designated DICER COMPLEX, dices the GAM2345 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2345 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of GAM2345 RNA is designated SEQ ID:4936, and is provided hereinbelow with reference to the sequence listing part.

[32705] GAM2345 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2345 target RNA, herein designated GAM TARGET RNA. GAM2345 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32706] GAM2345 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2345 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2345 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2345 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2345 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32707] The complementary binding of GAM2345 RNA, herein designated GAM RNA, to target binding sites on GAM2345 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2345 target RNA, herein designated GAM TARGET RNA, into GAM2345 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32708] It is appreciated that GAM2345 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2345 target genes. The mRNA of each one of this plurality of GAM2345 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2345 RNA, herein designated GAM RNA, and which when bound by GAM2345 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2345 target proteins.

[32709] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2345 gene, herein designated GAM GENE, on one or more GAM2345 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32710] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2345 correlate with, and may be deduced from, the identity of the target genes which GAM2345 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32711] Nucleotide sequences of the GAM2345 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2345 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2345 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2345 are further described hereinbelow with reference to Table 1.

[32712] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2345 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[32713] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2346 (GAM2346) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32714] GAM2346 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2346 was detected is described hereinabove with reference to Figs. 2-8.

[32715] GAM2346 gene, herein designated GAM GENE, and GAM2346 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[32716] GAM2346 gene, herein designated GAM GENE, encodes a GAM2346 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2346 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2346 precursor RNA is designated SEQ ID:2323, and is provided hereinbelow with reference to the sequence listing part.

[32717] GAM2346 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2346 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32718] An enzyme complex designated DICER COMPLEX, dices the GAM2346 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2346 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 92%) nucleotide sequence of GAM2346 RNA is designated SEQ ID:4937, and is provided hereinbelow with reference to the sequence listing part.

[32719] GAM2346 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2346 target RNA, herein designated GAM TARGET RNA. GAM2346 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32720] GAM2346 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2346 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2346 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2346 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2346 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32721] The complementary binding of GAM2346 RNA, herein designated GAM RNA, to target binding sites on GAM2346 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2346 target RNA, herein designated GAM TARGET RNA, into GAM2346 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32722] It is appreciated that GAM2346 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2346 target genes. The mRNA of each one of this plurality of GAM2346 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2346 RNA, herein designated GAM RNA, and which when bound by GAM2346 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2346 target proteins.

[32723] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2346 gene, herein designated GAM GENE, on one or more GAM2346 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32724] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2346 correlate with, and may be deduced from, the identity of the target genes which GAM2346 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32725] Nucleotide sequences of the GAM2346 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2346 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2346 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2346 are further described hereinbelow with reference to Table 1.

[32726] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2346 RNA, herein designated GAM RNA, are described hereinbelow



with reference to Table 2.

[32727] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2347 (GAM2347) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32728] GAM2347 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2347 was detected is described hereinabove with reference to Figs. 2-8.

[32729] GAM2347 gene, herein designated GAM GENE, and GAM2347 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[32730] GAM2347 gene, herein designated GAM GENE, encodes a GAM2347 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2347 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2347 precursor RNA is designated SEQ ID:2324, and is provided hereinbelow with reference to the sequence listing part.

[32731] GAM2347 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2347 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32732] An enzyme complex designated DICER COMPLEX, dices the GAM2347 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2347 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 25%) nucleotide sequence of GAM2347 RNA is designated SEQ ID:4938, and is provided hereinbelow with reference to the sequence listing part.

[32733] GAM2347 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2347 target RNA, herein designated GAM TARGET RNA. GAM2347 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32734] GAM2347 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2347 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2347 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2347 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2347 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32735] The complementary binding of GAM2347 RNA, herein designated GAM RNA, to target binding sites on GAM2347 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2347 target RNA, herein designated GAM TARGET RNA, into GAM2347 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32736] It is appreciated that GAM2347 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2347 target genes. The mRNA of each one of this plurality of GAM2347 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2347 RNA, herein designated GAM RNA, and which when bound by GAM2347 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2347 target proteins.

[32737] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2347 gene, herein designated GAM GENE, on one or more GAM2347 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32738] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2347 correlate with, and may be deduced from, the identity of the target genes which GAM2347 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32739] Nucleotide sequences of the GAM2347 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2347 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2347 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2347 are further described hereinbelow with reference to Table 1.

[32740] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2347 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[32741] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2348 (GAM2348) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32742] GAM2348 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2348 was detected is described hereinabove with reference to Figs. 2-8.

[32743] GAM2348 gene, herein designated GAM GENE, and GAM2348 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[32744] GAM2348 gene, herein designated GAM GENE, encodes a GAM2348 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2348 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2348 precursor RNA is designated SEQ ID:2325, and is provided hereinbelow with reference to the sequence listing part.

[32745] GAM2348 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2348 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32746] An enzyme complex designated DICER COMPLEX, dices the GAM2348 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2348 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 88%) nucleotide sequence of GAM2348 RNA is designated SEQ ID:4939, and is provided hereinbelow with reference to the sequence listing part.

[32747] GAM2348 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2348 target RNA, herein designated GAM TARGET RNA. GAM2348 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32748] GAM2348 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2348 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2348 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2348 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2348 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32749] The complementary binding of GAM2348 RNA, herein designated GAM RNA, to target binding sites on GAM2348 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2348 target RNA, herein designated GAM TARGET RNA, into GAM2348 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32750] It is appreciated that GAM2348 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2348 target genes. The

mRNA of each one of this plurality of GAM2348 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2348 RNA, herein designated GAM RNA, and which when bound by GAM2348 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2348 target proteins.

[32751] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2348 gene, herein designated GAM GENE, on one or more GAM2348 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32752] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2348 correlate with, and may be deduced from, the identity of the target genes which GAM2348 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32753] Nucleotide sequences of the GAM2348 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2348 RNA, herein



designated GAM RNA, and a schematic representation of the secondary folding of GAM2348 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2348 are further described hereinbelow with reference to Table 1.

[32754] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2348 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[32755] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2349 (GAM2349) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32756] GAM2349 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2349 was detected is described hereinabove with reference to Figs. 2-8.

[32757] GAM2349 gene, herein designated GAM GENE, and GAM2349 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[32758] GAM2349 gene, herein designated GAM GENE, encodes a GAM2349 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2349 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2349 precursor RNA is designated SEQ ID:2326, and is provided hereinbelow with reference to the sequence listing part.

[32759] GAM2349 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2349 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32760] An enzyme complex designated DICER COMPLEX, dices the GAM2349 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2349 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of GAM2349 RNA is designated SEQ ID:4940, and is provided hereinbelow with reference to the sequence listing part.

[32761] GAM2349 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2349 target RNA, herein designated GAM TARGET RNA. GAM2349 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32762] GAM2349 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2349 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2349 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2349 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2349 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32763] The complementary binding of GAM2349 RNA, herein designated GAM RNA, to target binding sites on GAM2349 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2349 target RNA, herein designated GAM TARGET RNA, into GAM2349 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32764] It is appreciated that GAM2349 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2349 target genes. The mRNA of each one of this plurality of GAM2349 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2349 RNA, herein designated GAM RNA, and which when bound by GAM2349 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2349 target proteins.

[32765] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2349 gene, herein designated GAM GENE, on one or more GAM2349 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32766] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2349 correlate with, and may be deduced from, the identity of the target

genes which GAM2349 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32767] Nucleotide sequences of the GAM2349 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2349 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2349 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2349 are further described hereinbelow with reference to Table 1.

[32768] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2349 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[32769] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2350 (GAM2350) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32770] GAM2350 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2350 was detected is described hereinabove with reference to Figs. 2-8.

[32771] GAM2350 gene, herein designated GAM GENE, and GAM2350 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

[32772] GAM2350 gene, herein designated GAM GENE, encodes a GAM2350 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2350 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2350 precursor RNA is designated SEQ ID:2327, and is provided hereinbelow with reference to the sequence listing part.

[32773] GAM2350 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2350 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32774] An enzyme complex designated DICER COMPLEX, dices the GAM2350 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2350 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of GAM2350 RNA is designated SEQ ID:4941, and is provided

hereinbelow with reference to the sequence listing part.

[32775] GAM2350 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2350 target RNA, herein designated GAM TARGET RNA. GAM2350 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32776] GAM2350 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2350 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2350 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2350 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2350 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32777] The complementary binding of GAM2350 RNA, herein designated GAM RNA, to target binding sites on GAM2350 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2350 target RNA, herein designated GAM TARGET RNA, into GAM2350 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32778] It is appreciated that GAM2350 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2350 target genes. The mRNA of each one of this plurality of GAM2350 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2350 RNA, herein designated GAM RNA, and which when bound by GAM2350 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2350 target proteins.

[32779] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2350 gene, herein designated GAM GENE, on one or more GAM2350 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding



sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32780] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2350 correlate with, and may be deduced from, the identity of the target genes which GAM2350 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32781] Nucleotide sequences of the GAM2350 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2350 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2350 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2350 are further described hereinbelow with reference to Table 1.

[32782] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2350 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[32783] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2351 (GAM2351) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32784] GAM2351 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2351 was detected is described hereinabove with reference to Figs. 2-8.

[32785] GAM2351 gene, herein designated GAM GENE, and GAM2351 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[32786] GAM2351 gene, herein designated GAM GENE, encodes a GAM2351 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2351 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2351 precursor RNA is designated SEQ ID:2328, and is provided hereinbelow with reference to the sequence listing part.

[32787] GAM2351 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2351 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32788] An enzyme complex designated DICER COMPLEX, dices the GAM2351 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2351 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 85%) nucleotide sequence of GAM2351 RNA is designated SEQ ID:4942, and is provided hereinbelow with reference to the sequence listing part.

[32789] GAM2351 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2351 target RNA, herein designated GAM TARGET RNA. GAM2351 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32790] GAM2351 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2351 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2351 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2351 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2351 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32791] The complementary binding of GAM2351 RNA, herein designated GAM RNA, to target binding sites on GAM2351 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2351 target RNA, herein designated GAM TARGET RNA, into GAM2351 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32792] It is appreciated that GAM2351 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2351 target genes. The mRNA of each one of this plurality of GAM2351 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2351 RNA, herein designated GAM RNA, and which when bound by GAM2351 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2351 target proteins.

[32793] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2351 gene, herein designated GAM GENE, on one or more GAM2351 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32794] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2351 correlate with, and may be deduced from, the identity of the target genes which GAM2351 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32795] Nucleotide sequences of the GAM2351 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2351 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2351 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2351 are further described hereinbelow with reference to Table 1.

[32796] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2351 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[32797] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2352 (GAM2352) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32798] GAM2352 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2352 was detected is described hereinabove with reference to Figs. 2-8.

[32799] GAM2352 gene, herein designated GAM GENE, and GAM2352 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[32800] GAM2352 gene, herein designated GAM GENE, encodes a GAM2352 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2352 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2352 precursor RNA is designated SEQ ID:2329, and is provided hereinbelow with reference to the sequence listing part.

[32801] GAM2352 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2352 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32802] An enzyme complex designated DICER COMPLEX, dices the GAM2352 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2352 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of GAM2352 RNA is designated SEQ ID:4943, and is provided hereinbelow with reference to the sequence listing part.

[32803] GAM2352 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2352 target RNA, herein designated GAM TARGET RNA. GAM2352 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32804] GAM2352 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2352 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2352 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2352 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2352 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32805] The complementary binding of GAM2352 RNA, herein designated GAM RNA, to target binding sites on GAM2352 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2352 target RNA, herein designated GAM TARGET RNA, into GAM2352 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32806] It is appreciated that GAM2352 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2352 target genes. The mRNA of each one of this plurality of GAM2352 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2352 RNA, herein designated GAM RNA, and which when bound by GAM2352 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2352 target proteins.

[32807] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition



exerted by GAM2352 gene, herein designated GAM GENE, on one or more GAM2352 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32808] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2352 correlate with, and may be deduced from, the identity of the target genes which GAM2352 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32809] Nucleotide sequences of the GAM2352 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2352 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2352 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2352 are further described hereinbelow with reference to Table 1.

[32810] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2352 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

- [32811] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2353 (GAM2353) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.
- [32812] GAM2353 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2353 was detected is described hereinabove with reference to Figs. 2-8.
- [32813] GAM2353 gene, herein designated GAM GENE, and GAM2353 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.
- [32814] GAM2353 gene, herein designated GAM GENE, encodes a GAM2353 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2353 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2353 precursor RNA is designated SEQ ID:2330, and is provided hereinbelow with reference to the sequence listing part.
- [32815] GAM2353 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2353 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32816] An enzyme complex designated DICER COMPLEX, dices the GAM2353 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2353 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 84%) nucleotide sequence of GAM2353 RNA is designated SEQ ID:4944, and is provided hereinbelow with reference to the sequence listing part.

[32817] GAM2353 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2353 target RNA, herein designated GAM TARGET RNA. GAM2353 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32818] GAM2353 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2353 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2353 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2353 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2353 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32819] The complementary binding of GAM2353 RNA, herein designated GAM RNA, to target binding sites on GAM2353 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2353 target RNA, herein designated GAM TARGET RNA, into GAM2353 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32820] It is appreciated that GAM2353 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2353 target genes. The mRNA of each one of this plurality of GAM2353 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2353 RNA, herein designated GAM RNA, and which when bound by GAM2353 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2353 target proteins.

[32821] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2353 gene, herein designated GAM GENE, on one or more GAM2353 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32822] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2353 correlate with, and may be deduced from, the identity of the target genes which GAM2353 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32823] Nucleotide sequences of the GAM2353 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2353 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2353 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2353 are further described hereinbelow with reference to Table 1.

[32824] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2353 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[32825] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2354 (GAM2354) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32826] GAM2354 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2354 was detected is described hereinabove with reference to Figs. 2-8.

[32827] GAM2354 gene, herein designated GAM GENE, and GAM2354 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[32828] GAM2354 gene, herein designated GAM GENE, encodes a GAM2354 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2354 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2354 precursor RNA is designated SEQ ID:2331, and is provided hereinbelow with reference to the sequence listing part.

[32829] GAM2354 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2354 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32830] An enzyme complex designated DICER COMPLEX, dices the GAM2354 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2354 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 90%) nucleotide sequence of GAM2354 RNA is designated SEQ ID:4945, and is provided hereinbelow with reference to the sequence listing part.

[32831] GAM2354 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2354 target RNA, herein designated GAM TARGET RNA. GAM2354 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32832] GAM2354 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2354 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2354 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2354 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2354 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32833] The complementary binding of GAM2354 RNA, herein designated GAM RNA, to target binding sites on GAM2354 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2354 target RNA, herein designated GAM TARGET RNA, into GAM2354 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32834] It is appreciated that GAM2354 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2354 target genes. The



mRNA of each one of this plurality of GAM2354 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2354 RNA, herein designated GAM RNA, and which when bound by GAM2354 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2354 target proteins.

[32835] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2354 gene, herein designated GAM GENE, on one or more GAM2354 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32836] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2354 correlate with, and may be deduced from, the identity of the target genes which GAM2354 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32837] Nucleotide sequences of the GAM2354 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2354 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2354 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2354 are further described hereinbelow with reference to Table 1.

[32838] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2354 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[32839] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2355 (GAM2355) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32840] GAM2355 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2355 was detected is described hereinabove with reference to Figs. 2-8.

[32841] GAM2355 gene, herein designated GAM GENE, and GAM2355 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[32842] GAM2355 gene, herein designated GAM GENE, encodes a GAM2355 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2355 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2355 precursor RNA is designated SEQ ID:2332, and is provided hereinbelow with reference to the sequence listing part.

[32843] GAM2355 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2355 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32844] An enzyme complex designated DICER COMPLEX, dices the GAM2355 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2355 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of GAM2355 RNA is designated SEQ ID:4946, and is provided hereinbelow with reference to the sequence listing part.

[32845] GAM2355 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2355 target RNA, herein designated GAM TARGET RNA. GAM2355 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32846] GAM2355 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2355 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2355 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2355 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2355 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32847] The complementary binding of GAM2355 RNA, herein designated GAM RNA, to target binding sites on GAM2355 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2355 target RNA, herein designated GAM TARGET RNA, into GAM2355 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32848] It is appreciated that GAM2355 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2355 target genes. The mRNA of each one of this plurality of GAM2355 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2355 RNA, herein designated GAM RNA, and which when bound by GAM2355 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2355 target proteins.

[32849] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2355 gene, herein designated GAM GENE, on one or more GAM2355 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32850] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2355 correlate with, and may be deduced from, the identity of the target

genes which GAM2355 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32851] Nucleotide sequences of the GAM2355 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2355 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2355 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2355 are further described hereinbelow with reference to Table 1.

[32852] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2355 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[32853] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2356 (GAM2356) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32854] GAM2356 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2356 was detected is described hereinabove with reference to Figs. 2-8.

[32855] GAM2356 gene, herein designated GAM GENE, and GAM2356 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

[32856] GAM2356 gene, herein designated GAM GENE, encodes a GAM2356 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2356 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2356 precursor RNA is designated SEQ ID:2333, and is provided hereinbelow with reference to the sequence listing part.

[32857] GAM2356 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2356 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32858] An enzyme complex designated DICER COMPLEX, dices the GAM2356 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2356 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of GAM2356 RNA is designated SEQ ID:4947, and is provided

hereinbelow with reference to the sequence listing part.

[32859] GAM2356 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2356 target RNA, herein designated GAM TARGET RNA. GAM2356 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32860] GAM2356 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2356 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2356 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2356 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2356 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.



[32861] The complementary binding of GAM2356 RNA, herein designated GAM RNA, to target binding sites on GAM2356 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2356 target RNA, herein designated GAM TARGET RNA, into GAM2356 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32862] It is appreciated that GAM2356 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2356 target genes. The mRNA of each one of this plurality of GAM2356 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2356 RNA, herein designated GAM RNA, and which when bound by GAM2356 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2356 target proteins.

[32863] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2356 gene, herein designated GAM GENE, on one or more GAM2356 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32864] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2356 correlate with, and may be deduced from, the identity of the target genes which GAM2356 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32865] Nucleotide sequences of the GAM2356 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2356 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2356 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2356 are further described hereinbelow with reference to Table 1.

[32866] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2356 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[32867] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2357 (GAM2357) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32868] GAM2357 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2357 was detected is described hereinabove with reference to Figs. 2-8.

[32869] GAM2357 gene, herein designated GAM GENE, and GAM2357 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[32870] GAM2357 gene, herein designated GAM GENE, encodes a GAM2357 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2357 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2357 precursor RNA is designated SEQ ID:2334, and is provided hereinbelow with reference to the sequence listing part.

[32871] GAM2357 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2357 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32872] An enzyme complex designated DICER COMPLEX, dices the GAM2357 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2357 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 84%) nucleotide sequence of GAM2357 RNA is designated SEQ ID:4948, and is provided hereinbelow with reference to the sequence listing part.

[32873] GAM2357 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2357 target RNA, herein designated GAM TARGET RNA. GAM2357 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32874] GAM2357 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2357 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2357 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2357 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2357 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32875] The complementary binding of GAM2357 RNA, herein designated GAM RNA, to target binding sites on GAM2357 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2357 target RNA, herein designated GAM TARGET RNA, into GAM2357 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32876] It is appreciated that GAM2357 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2357 target genes. The mRNA of each one of this plurality of GAM2357 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2357 RNA, herein designated GAM RNA, and which when bound by GAM2357 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2357 target proteins.

[32877] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2357 gene, herein designated GAM GENE, on one or more GAM2357 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32878] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2357 correlate with, and may be deduced from, the identity of the target genes which GAM2357 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32879] Nucleotide sequences of the GAM2357 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2357 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2357 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2357 are further described hereinbelow with reference to Table 1.

[32880] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2357 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[32881] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2358 (GAM2358) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32882] GAM2358 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2358 was detected is described hereinabove with reference to Figs. 2-8.

[32883] GAM2358 gene, herein designated GAM GENE, and GAM2358 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[32884] GAM2358 gene, herein designated GAM GENE, encodes a GAM2358 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2358 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2358 precursor RNA is designated SEQ ID:2335, and is provided hereinbelow with reference to the sequence listing part.

[32885] GAM2358 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2358 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

- [32886] An enzyme complex designated DICER COMPLEX, dices the GAM2358 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2358 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of GAM2358 RNA is designated SEQ ID:4949, and is provided hereinbelow with reference to the sequence listing part.
- [32887] GAM2358 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2358 target RNA, herein designated GAM TARGET RNA. GAM2358 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [32888] GAM2358 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2358 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2358 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an



illustration only, and is not meant to be limiting GAM2358 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2358 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32889] The complementary binding of GAM2358 RNA, herein designated GAM RNA, to target binding sites on GAM2358 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2358 target RNA, herein designated GAM TARGET RNA, into GAM2358 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32890] It is appreciated that GAM2358 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2358 target genes. The mRNA of each one of this plurality of GAM2358 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2358 RNA, herein designated GAM RNA, and which when bound by GAM2358 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2358 target proteins.

[32891] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2358 gene, herein designated GAM GENE, on one or more GAM2358 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32892] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2358 correlate with, and may be deduced from, the identity of the target genes which GAM2358 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32893] Nucleotide sequences of the GAM2358 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2358 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2358 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2358 are further described hereinbelow with reference to Table 1.

[32894] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2358 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

[32895] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2359 (GAM2359) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32896] GAM2359 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2359 was detected is described hereinabove with reference to Figs. 2-8.

[32897] GAM2359 gene, herein designated GAM GENE, and GAM2359 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[32898] GAM2359 gene, herein designated GAM GENE, encodes a GAM2359 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2359 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2359 precursor RNA is designated SEQ ID:2336, and is provided hereinbelow with reference to the sequence listing part.

[32899] GAM2359 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2359 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32900] An enzyme complex designated DICER COMPLEX, dices the GAM2359 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2359 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2359 RNA is designated SEQ ID:4950, and is provided hereinbelow with reference to the sequence listing part.

[32901] GAM2359 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2359 target RNA, herein designated GAM TARGET RNA. GAM2359 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32902] GAM2359 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2359 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2359 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2359 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2359 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32903] The complementary binding of GAM2359 RNA, herein designated GAM RNA, to target binding sites on GAM2359 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2359 target RNA, herein designated GAM TARGET RNA, into GAM2359 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32904] It is appreciated that GAM2359 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2359 target genes. The mRNA of each one of this plurality of GAM2359 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2359 RNA, herein designated GAM RNA, and which when bound by GAM2359 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2359 target proteins.

[32905] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2359 gene, herein designated GAM GENE, on one or more GAM2359 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32906] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2359 correlate with, and may be deduced from, the identity of the target genes which GAM2359 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32907] Nucleotide sequences of the GAM2359 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2359 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2359 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2359 are further described hereinbelow with reference to Table 1.

[32908] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2359 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[32909] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2360 (GAM2360) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32910] GAM2360 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2360 was detected is described hereinabove with reference to Figs. 2-8.

[32911] GAM2360 gene, herein designated GAM GENE, and GAM2360 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[32912] GAM2360 gene, herein designated GAM GENE, encodes a GAM2360 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2360 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2360 precursor RNA is designated SEQ ID:2337, and is provided hereinbelow with reference to the sequence listing part.

[32913] GAM2360 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2360 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32914] An enzyme complex designated DICER COMPLEX, dices the GAM2360 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2360 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 84%) nucleotide sequence of GAM2360 RNA is designated SEQ ID:4951, and is provided hereinbelow with reference to the sequence listing part.

[32915] GAM2360 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2360 target RNA, herein designated GAM TARGET RNA. GAM2360 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.



[32916] GAM2360 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2360 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2360 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2360 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2360 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32917] The complementary binding of GAM2360 RNA, herein designated GAM RNA, to target binding sites on GAM2360 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2360 target RNA, herein designated GAM TARGET RNA, into GAM2360 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32918] It is appreciated that GAM2360 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2360 target genes. The

mRNA of each one of this plurality of GAM2360 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2360 RNA, herein designated GAM RNA, and which when bound by GAM2360 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2360 target proteins.

[32919] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2360 gene, herein designated GAM GENE, on one or more GAM2360 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32920] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2360 correlate with, and may be deduced from, the identity of the target genes which GAM2360 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32921] Nucleotide sequences of the GAM2360 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2360 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2360 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2360 are further described hereinbelow with reference to Table 1.

[32922] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2360 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[32923] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2361 (GAM2361) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32924] GAM2361 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2361 was detected is described hereinabove with reference to Figs. 2-8.

[32925] GAM2361 gene, herein designated GAM GENE, and GAM2361 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[32926] GAM2361 gene, herein designated GAM GENE, encodes a GAM2361 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2361 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2361 precursor RNA is designated SEQ ID:2338, and is provided hereinbelow with reference to the sequence listing part.

[32927] GAM2361 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2361 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32928] An enzyme complex designated DICER COMPLEX, dices the GAM2361 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2361 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2361 RNA is designated SEQ ID:4952, and is provided hereinbelow with reference to the sequence listing part.

[32929] GAM2361 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2361 target RNA, herein designated GAM TARGET RNA. GAM2361 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32930] GAM2361 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2361 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2361 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2361 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2361 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32931] The complementary binding of GAM2361 RNA, herein designated GAM RNA, to target binding sites on GAM2361 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2361 target RNA, herein designated GAM TARGET RNA, into GAM2361 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32932] It is appreciated that GAM2361 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2361 target genes. The mRNA of each one of this plurality of GAM2361 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2361 RNA, herein designated GAM RNA, and which when bound by GAM2361 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2361 target proteins.

[32933] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2361 gene, herein designated GAM GENE, on one or more GAM2361 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32934] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2361 correlate with, and may be deduced from, the identity of the target

genes which GAM2361 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32935] Nucleotide sequences of the GAM2361 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2361 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2361 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2361 are further described hereinbelow with reference to Table 1.

[32936] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2361 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[32937] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2362 (GAM2362) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32938] GAM2362 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2362 was detected is described hereinabove with reference to Figs. 2-8.

[32939] GAM2362 gene, herein designated GAM GENE, and GAM2362 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

[32940] GAM2362 gene, herein designated GAM GENE, encodes a GAM2362 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2362 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2362 precursor RNA is designated SEQ ID:2339, and is provided hereinbelow with reference to the sequence listing part.

[32941] GAM2362 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2362 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32942] An enzyme complex designated DICER COMPLEX, dices the GAM2362 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2362 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of GAM2362 RNA is designated SEQ ID:4953, and is provided



hereinbelow with reference to the sequence listing part.

[32943] GAM2362 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2362 target RNA, herein designated GAM TARGET RNA. GAM2362 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32944] GAM2362 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2362 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2362 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2362 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2362 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32945] The complementary binding of GAM2362 RNA, herein designated GAM RNA, to target binding sites on GAM2362 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2362 target RNA, herein designated GAM TARGET RNA, into GAM2362 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32946] It is appreciated that GAM2362 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2362 target genes. The mRNA of each one of this plurality of GAM2362 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2362 RNA, herein designated GAM RNA, and which when bound by GAM2362 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2362 target proteins.

[32947] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2362 gene, herein designated GAM GENE, on one or more GAM2362 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32948] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2362 correlate with, and may be deduced from, the identity of the target genes which GAM2362 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32949] Nucleotide sequences of the GAM2362 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2362 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2362 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2362 are further described hereinbelow with reference to Table 1.

[32950] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2362 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[32951] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2363 (GAM2363) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32952] GAM2363 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2363 was detected is described hereinabove with reference to Figs. 2-8.

[32953] GAM2363 gene, herein designated GAM GENE, and GAM2363 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[32954] GAM2363 gene, herein designated GAM GENE, encodes a GAM2363 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2363 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2363 precursor RNA is designated SEQ ID:2340, and is provided hereinbelow with reference to the sequence listing part.

[32955] GAM2363 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2363 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32956] An enzyme complex designated DICER COMPLEX, dices the GAM2363 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2363 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of GAM2363 RNA is designated SEQ ID:4954, and is provided hereinbelow with reference to the sequence listing part.

[32957] GAM2363 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2363 target RNA, herein designated GAM TARGET RNA. GAM2363 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32958] GAM2363 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2363 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2363 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2363 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2363 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32959] The complementary binding of GAM2363 RNA, herein designated GAM RNA, to target binding sites on GAM2363 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2363 target RNA, herein designated GAM TARGET RNA, into GAM2363 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32960] It is appreciated that GAM2363 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2363 target genes. The mRNA of each one of this plurality of GAM2363 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2363 RNA, herein designated GAM RNA, and which when bound by GAM2363 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2363 target proteins.

[32961] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2363 gene, herein designated GAM GENE, on one or more GAM2363 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32962] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2363 correlate with, and may be deduced from, the identity of the target genes which GAM2363 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32963] Nucleotide sequences of the GAM2363 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2363 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2363 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2363 are further described hereinbelow with reference to Table 1.

[32964] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2363 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[32965] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2364 (GAM2364) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32966] GAM2364 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2364 was detected is described hereinabove with reference to Figs. 2-8.

[32967] GAM2364 gene, herein designated GAM GENE, and GAM2364 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[32968] GAM2364 gene, herein designated GAM GENE, encodes a GAM2364 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2364 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2364 precursor RNA is designated SEQ ID:2341, and is provided hereinbelow with reference to the sequence listing part.

[32969] GAM2364 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2364 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.



- [32970] An enzyme complex designated DICER COMPLEX, dices the GAM2364 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2364 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of GAM2364 RNA is designated SEQ ID:4955, and is provided hereinbelow with reference to the sequence listing part.
- [32971] GAM2364 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2364 target RNA, herein designated GAM TARGET RNA. GAM2364 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [32972] GAM2364 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2364 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2364 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2364 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2364 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32973] The complementary binding of GAM2364 RNA, herein designated GAM RNA, to target binding sites on GAM2364 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2364 target RNA, herein designated GAM TARGET RNA, into GAM2364 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32974] It is appreciated that GAM2364 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2364 target genes. The mRNA of each one of this plurality of GAM2364 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2364 RNA, herein designated GAM RNA, and which when bound by GAM2364 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2364 target proteins.

[32975] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2364 gene, herein designated GAM GENE, on one or more GAM2364 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32976] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2364 correlate with, and may be deduced from, the identity of the target genes which GAM2364 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32977] Nucleotide sequences of the GAM2364 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2364 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2364 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2364 are further described hereinbelow with reference to Table 1.

[32978] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2364 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

[32979] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2365 (GAM2365) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32980] GAM2365 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2365 was detected is described hereinabove with reference to Figs. 2-8.

[32981] GAM2365 gene, herein designated GAM GENE, and GAM2365 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[32982] GAM2365 gene, herein designated GAM GENE, encodes a GAM2365 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2365 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2365 precursor RNA is designated SEQ ID:2342, and is provided hereinbelow with reference to the sequence listing part.

[32983] GAM2365 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2365 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32984] An enzyme complex designated DICER COMPLEX, dices the GAM2365 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2365 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of GAM2365 RNA is designated SEQ ID:4956, and is provided hereinbelow with reference to the sequence listing part.

[32985] GAM2365 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2365 target RNA, herein designated GAM TARGET RNA. GAM2365 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[32986] GAM2365 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2365 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2365 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2365 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2365 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[32987] The complementary binding of GAM2365 RNA, herein designated GAM RNA, to target binding sites on GAM2365 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2365 target RNA, herein designated GAM TARGET RNA, into GAM2365 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32988] It is appreciated that GAM2365 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2365 target genes. The mRNA of each one of this plurality of GAM2365 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2365 RNA, herein designated GAM RNA, and which when bound by GAM2365 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2365 target proteins.

[32989] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2365 gene, herein designated GAM GENE, on one or more GAM2365 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32990] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2365 correlate with, and may be deduced from, the identity of the target genes which GAM2365 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32991] Nucleotide sequences of the GAM2365 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2365 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2365 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2365 are further described hereinbelow with reference to Table 1.

[32992] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2365 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[32993] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2366 (GAM2366) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32994] GAM2366 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2366 was detected is described hereinabove with reference to Figs. 2-8.

[32995] GAM2366 gene, herein designated GAM GENE, and GAM2366 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[32996] GAM2366 gene, herein designated GAM GENE, encodes a GAM2366 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2366 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2366 precursor RNA is designated SEQ ID:2343, and is provided hereinbelow with reference to the sequence listing part.



[32997] GAM2366 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2366 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32998] An enzyme complex designated DICER COMPLEX, dices the GAM2366 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2366 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of GAM2366 RNA is designated SEQ ID:4957, and is provided hereinbelow with reference to the sequence listing part.

[32999] GAM2366 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2366 target RNA, herein designated GAM TARGET RNA. GAM2366 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33000] GAM2366 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2366 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2366 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2366 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2366 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33001] The complementary binding of GAM2366 RNA, herein designated GAM RNA, to target binding sites on GAM2366 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2366 target RNA, herein designated GAM TARGET RNA, into GAM2366 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33002] It is appreciated that GAM2366 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2366 target genes. The

mRNA of each one of this plurality of GAM2366 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2366 RNA, herein designated GAM RNA, and which when bound by GAM2366 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2366 target proteins.

[33003] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2366 gene, herein designated GAM GENE, on one or more GAM2366 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33004] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2366 correlate with, and may be deduced from, the identity of the target genes which GAM2366 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33005] Nucleotide sequences of the GAM2366 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2366 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2366 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2366 are further described hereinbelow with reference to Table 1.

[33006] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2366 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[33007] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2367 (GAM2367) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[33008] GAM2367 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2367 was detected is described hereinabove with reference to Figs. 2-8.

[33009] GAM2367 gene, herein designated GAM GENE, and GAM2367 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[33010] GAM2367 gene, herein designated GAM GENE, encodes a GAM2367 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2367 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2367 precursor RNA is designated SEQ ID:2344, and is provided hereinbelow with reference to the sequence listing part.

[33011] GAM2367 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2367 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33012] An enzyme complex designated DICER COMPLEX, dices the GAM2367 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2367 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of GAM2367 RNA is designated SEQ ID:4958, and is provided hereinbelow with reference to the sequence listing part.

[33013] GAM2367 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2367 target RNA, herein designated GAM TARGET RNA. GAM2367 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33014] GAM2367 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2367 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2367 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2367 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2367 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33015] The complementary binding of GAM2367 RNA, herein designated GAM RNA, to target binding sites on GAM2367 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2367 target RNA, herein designated GAM TARGET RNA, into GAM2367 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33016] It is appreciated that GAM2367 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2367 target genes. The mRNA of each one of this plurality of GAM2367 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2367 RNA, herein designated GAM RNA, and which when bound by GAM2367 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2367 target proteins.

[33017] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2367 gene, herein designated GAM GENE, on one or more GAM2367 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33018] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2367 correlate with, and may be deduced from, the identity of the target

genes which GAM2367 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33019] Nucleotide sequences of the GAM2367 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2367 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2367 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2367 are further described hereinbelow with reference to Table 1.

[33020] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2367 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[33021] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2368 (GAM2368) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[33022] GAM2368 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2368 was detected is described hereinabove with reference to Figs. 2-8.

[33023] GAM2368 gene, herein designated GAM GENE, and GAM2368 target gene, herein designated GAM TARGET GENE, are human genes contained in the



human genome.

- [33024] GAM2368 gene, herein designated GAM GENE, encodes a GAM2368 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2368 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2368 precursor RNA is designated SEQ ID:2345, and is provided hereinbelow with reference to the sequence listing part.
- [33025] GAM2368 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2368 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.
- [33026] An enzyme complex designated DICER COMPLEX, dices the GAM2368 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2368 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2368 RNA is designated SEQ ID:4959, and is provided

hereinbelow with reference to the sequence listing part.

[33027] GAM2368 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2368 target RNA, herein designated GAM TARGET RNA. GAM2368 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33028] GAM2368 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2368 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2368 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2368 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2368 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33029] The complementary binding of GAM2368 RNA, herein designated GAM RNA, to target binding sites on GAM2368 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2368 target RNA, herein designated GAM TARGET RNA, into GAM2368 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33030] It is appreciated that GAM2368 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2368 target genes. The mRNA of each one of this plurality of GAM2368 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2368 RNA, herein designated GAM RNA, and which when bound by GAM2368 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2368 target proteins.

[33031] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2368 gene, herein designated GAM GENE, on one or more GAM2368 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33032] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2368 correlate with, and may be deduced from, the identity of the target genes which GAM2368 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33033] Nucleotide sequences of the GAM2368 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2368 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2368 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2368 are further described hereinbelow with reference to Table 1.

[33034] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2368 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[33035] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2369 (GAM2369) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[33036] GAM2369 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2369 was detected is described hereinabove with reference to Figs. 2-8.

[33037] GAM2369 gene, herein designated GAM GENE, and GAM2369 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[33038] GAM2369 gene, herein designated GAM GENE, encodes a GAM2369 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2369 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2369 precursor RNA is designated SEQ ID:2346, and is provided hereinbelow with reference to the sequence listing part.

[33039] GAM2369 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2369 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33040] An enzyme complex designated DICER COMPLEX, dices the GAM2369 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2369 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2369 RNA is designated SEQ ID:4960, and is provided hereinbelow with reference to the sequence listing part.

[33041] GAM2369 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2369 target RNA, herein designated GAM TARGET RNA. GAM2369 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33042] GAM2369 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2369 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2369 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2369 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2369 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33043] The complementary binding of GAM2369 RNA, herein designated GAM RNA, to target binding sites on GAM2369 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2369 target RNA, herein designated GAM TARGET RNA, into GAM2369 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33044] It is appreciated that GAM2369 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2369 target genes. The mRNA of each one of this plurality of GAM2369 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2369 RNA, herein designated GAM RNA, and which when bound by GAM2369 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2369 target proteins.

[33045] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2369 gene, herein designated GAM GENE, on one or more GAM2369 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33046] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2369 correlate with, and may be deduced from, the identity of the target genes which GAM2369 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33047] Nucleotide sequences of the GAM2369 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2369 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2369 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2369 are further described hereinbelow with reference to Table 1.

[33048] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2369 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[33049] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2370 (GAM2370) gene, which modulates



expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[33050] GAM2370 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2370 was detected is described hereinabove with reference to Figs. 2-8.

[33051] GAM2370 gene, herein designated GAM GENE, and GAM2370 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[33052] GAM2370 gene, herein designated GAM GENE, encodes a GAM2370 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2370 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2370 precursor RNA is designated SEQ ID:2347, and is provided hereinbelow with reference to the sequence listing part.

[33053] GAM2370 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2370 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

- [33054] An enzyme complex designated DICER COMPLEX, dices the GAM2370 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2370 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 90%) nucleotide sequence of GAM2370 RNA is designated SEQ ID:4961, and is provided hereinbelow with reference to the sequence listing part.
- [33055] GAM2370 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2370 target RNA, herein designated GAM TARGET RNA. GAM2370 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [33056] GAM2370 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2370 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2370 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2370 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2370 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33057] The complementary binding of GAM2370 RNA, herein designated GAM RNA, to target binding sites on GAM2370 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2370 target RNA, herein designated GAM TARGET RNA, into GAM2370 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33058] It is appreciated that GAM2370 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2370 target genes. The mRNA of each one of this plurality of GAM2370 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2370 RNA, herein designated GAM RNA, and which when bound by GAM2370 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2370 target proteins.

[33059] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2370 gene, herein designated GAM GENE, on one or more GAM2370 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33060] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2370 correlate with, and may be deduced from, the identity of the target genes which GAM2370 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33061] Nucleotide sequences of the GAM2370 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2370 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2370 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2370 are further described hereinbelow with reference to Table 1.

[33062] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2370 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

- [33063] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2371 (GAM2371) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.
- [33064] GAM2371 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2371 was detected is described hereinabove with reference to Figs. 2-8.
- [33065] GAM2371 gene, herein designated GAM GENE, and GAM2371 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.
- [33066] GAM2371 gene, herein designated GAM GENE, encodes a GAM2371 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2371 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2371 precursor RNA is designated SEQ ID:2348, and is provided hereinbelow with reference to the sequence listing part.
- [33067] GAM2371 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2371 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33068] An enzyme complex designated DICER COMPLEX, dices the GAM2371 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2371 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2371 RNA is designated SEQ ID:4963, and is provided hereinbelow with reference to the sequence listing part.

[33069] GAM2371 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2371 target RNA, herein designated GAM TARGET RNA. GAM2371 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33070] GAM2371 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2371 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2371 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2371 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2371 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33071] The complementary binding of GAM2371 RNA, herein designated GAM RNA, to target binding sites on GAM2371 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2371 target RNA, herein designated GAM TARGET RNA, into GAM2371 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33072] It is appreciated that GAM2371 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2371 target genes. The mRNA of each one of this plurality of GAM2371 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2371 RNA, herein designated GAM RNA, and which when bound by GAM2371 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2371 target proteins.

[33073] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2371 gene, herein designated GAM GENE, on one or more GAM2371 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33074] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2371 correlate with, and may be deduced from, the identity of the target genes which GAM2371 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33075] Nucleotide sequences of the GAM2371 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2371 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2371 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2371 are further described hereinbelow with reference to Table 1.



[33076] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2371 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[33077] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2372 (GAM2372) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[33078] GAM2372 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2372 was detected is described hereinabove with reference to Figs. 2-8.

[33079] GAM2372 gene, herein designated GAM GENE, and GAM2372 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[33080] GAM2372 gene, herein designated GAM GENE, encodes a GAM2372 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2372 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2372 precursor RNA is designated SEQ ID:2349, and is provided hereinbelow with reference to the sequence listing part.

[33081] GAM2372 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2372 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33082] An enzyme complex designated DICER COMPLEX, dices the GAM2372 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2372 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of GAM2372 RNA is designated SEQ ID:4962, and is provided hereinbelow with reference to the sequence listing part.

[33083] GAM2372 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2372 target RNA, herein designated GAM TARGET RNA. GAM2372 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33084] GAM2372 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2372 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2372 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2372 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2372 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33085] The complementary binding of GAM2372 RNA, herein designated GAM RNA, to target binding sites on GAM2372 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2372 target RNA, herein designated GAM TARGET RNA, into GAM2372 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33086] It is appreciated that GAM2372 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2372 target genes. The

mRNA of each one of this plurality of GAM2372 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2372 RNA, herein designated GAM RNA, and which when bound by GAM2372 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2372 target proteins.

[33087] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2372 gene, herein designated GAM GENE, on one or more GAM2372 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33088] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2372 correlate with, and may be deduced from, the identity of the target genes which GAM2372 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33089] Nucleotide sequences of the GAM2372 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2372 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2372 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2372 are further described hereinbelow with reference to Table 1.

[33090] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2372 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[33091] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2373 (GAM2373) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[33092] GAM2373 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2373 was detected is described hereinabove with reference to Figs. 2-8.

[33093] GAM2373 gene, herein designated GAM GENE, and GAM2373 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[33094] GAM2373 gene, herein designated GAM GENE, encodes a GAM2373 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2373 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2373 precursor RNA is designated SEQ ID:2350, and is provided hereinbelow with reference to the sequence listing part.

[33095] GAM2373 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2373 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33096] An enzyme complex designated DICER COMPLEX, dices the GAM2373 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2373 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2373 RNA is designated SEQ ID:4964, and is provided hereinbelow with reference to the sequence listing part.

[33097] GAM2373 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2373 target RNA, herein designated GAM TARGET RNA. GAM2373 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33098] GAM2373 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2373 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2373 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2373 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2373 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33099] The complementary binding of GAM2373 RNA, herein designated GAM RNA, to target binding sites on GAM2373 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2373 target RNA, herein designated GAM TARGET RNA, into GAM2373 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33100] It is appreciated that GAM2373 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2373 target genes. The mRNA of each one of this plurality of GAM2373 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2373 RNA, herein designated GAM RNA, and which when bound by GAM2373 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2373 target proteins.

[33101] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2373 gene, herein designated GAM GENE, on one or more GAM2373 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33102] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2373 correlate with, and may be deduced from, the identity of the target



genes which GAM2373 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33103] Nucleotide sequences of the GAM2373 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2373 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2373 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2373 are further described hereinbelow with reference to Table 1.

[33104] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2373 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[33105] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2374 (GAM2374) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[33106] GAM2374 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2374 was detected is described hereinabove with reference to Figs. 2-8.

[33107] GAM2374 gene, herein designated GAM GENE, and GAM2374 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

- [33108] GAM2374 gene, herein designated GAM GENE, encodes a GAM2374 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2374 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2374 precursor RNA is designated SEQ ID:2351, and is provided hereinbelow with reference to the sequence listing part.
- [33109] GAM2374 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2374 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.
- [33110] An enzyme complex designated DICER COMPLEX, dices the GAM2374 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2374 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of GAM2374 RNA is designated SEQ ID:4965, and is provided

hereinbelow with reference to the sequence listing part.

[33111] GAM2374 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2374 target RNA, herein designated GAM TARGET RNA. GAM2374 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33112] GAM2374 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2374 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2374 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2374 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2374 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33113] The complementary binding of GAM2374 RNA, herein designated GAM RNA, to target binding sites on GAM2374 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2374 target RNA, herein designated GAM TARGET RNA, into GAM2374 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33114] It is appreciated that GAM2374 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2374 target genes. The mRNA of each one of this plurality of GAM2374 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2374 RNA, herein designated GAM RNA, and which when bound by GAM2374 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2374 target proteins.

[33115] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2374 gene, herein designated GAM GENE, on one or more GAM2374 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33116] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2374 correlate with, and may be deduced from, the identity of the target genes which GAM2374 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33117] Nucleotide sequences of the GAM2374 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2374 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2374 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2374 are further described hereinbelow with reference to Table 1.

[33118] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2374 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[33119] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2375 (GAM2375) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[33120] GAM2375 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2375 was detected is described hereinabove with reference to Figs. 2-8.

[33121] GAM2375 gene, herein designated GAM GENE, and GAM2375 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[33122] GAM2375 gene, herein designated GAM GENE, encodes a GAM2375 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2375 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2375 precursor RNA is designated SEQ ID:2352, and is provided hereinbelow with reference to the sequence listing part.

[33123] GAM2375 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2375 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33124] An enzyme complex designated DICER COMPLEX, dices the GAM2375 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2375 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of GAM2375 RNA is designated SEQ ID:4966, and is provided hereinbelow with reference to the sequence listing part.

[33125] GAM2375 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2375 target RNA, herein designated GAM TARGET RNA. GAM2375 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33126] GAM2375 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2375 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2375 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2375 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2375 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33127] The complementary binding of GAM2375 RNA, herein designated GAM RNA, to target binding sites on GAM2375 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2375 target RNA, herein designated GAM TARGET RNA, into GAM2375 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33128] It is appreciated that GAM2375 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2375 target genes. The mRNA of each one of this plurality of GAM2375 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2375 RNA, herein designated GAM RNA, and which when bound by GAM2375 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2375 target proteins.

[33129] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2375 gene, herein designated GAM GENE, on one or more GAM2375 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary



binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33130] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2375 correlate with, and may be deduced from, the identity of the target genes which GAM2375 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33131] Nucleotide sequences of the GAM2375 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2375 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2375 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2375 are further described hereinbelow with reference to Table 1.

[33132] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2375 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[33133] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2376 (GAM2376) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

- [33134] GAM2376 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2376 was detected is described hereinabove with reference to Figs. 2-8.
- [33135] GAM2376 gene, herein designated GAM GENE, and GAM2376 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.
- [33136] GAM2376 gene, herein designated GAM GENE, encodes a GAM2376 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2376 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2376 precursor RNA is designated SEQ ID:2353, and is provided hereinbelow with reference to the sequence listing part.
- [33137] GAM2376 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2376 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

- [33138] An enzyme complex designated DICER COMPLEX, dices the GAM2376 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2376 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of GAM2376 RNA is designated SEQ ID:4967, and is provided hereinbelow with reference to the sequence listing part.
- [33139] GAM2376 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2376 target RNA, herein designated GAM TARGET RNA. GAM2376 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [33140] GAM2376 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2376 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2376 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2376 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2376 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33141] The complementary binding of GAM2376 RNA, herein designated GAM RNA, to target binding sites on GAM2376 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2376 target RNA, herein designated GAM TARGET RNA, into GAM2376 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33142] It is appreciated that GAM2376 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2376 target genes. The mRNA of each one of this plurality of GAM2376 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2376 RNA, herein designated GAM RNA, and which when bound by GAM2376 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2376 target proteins.

[33143] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2376 gene, herein designated GAM GENE, on one or more GAM2376 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33144] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2376 correlate with, and may be deduced from, the identity of the target genes which GAM2376 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33145] Nucleotide sequences of the GAM2376 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2376 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2376 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2376 are further described hereinbelow with reference to Table 1.

[33146] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2376 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

- [33147] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2377 (GAM2377) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.
- [33148] GAM2377 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2377 was detected is described hereinabove with reference to Figs. 2-8.
- [33149] GAM2377 gene, herein designated GAM GENE, and GAM2377 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.
- [33150] GAM2377 gene, herein designated GAM GENE, encodes a GAM2377 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2377 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2377 precursor RNA is designated SEQ ID:2354, and is provided hereinbelow with reference to the sequence listing part.
- [33151] GAM2377 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2377 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33152] An enzyme complex designated DICER COMPLEX, dices the GAM2377 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2377 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 85%) nucleotide sequence of GAM2377 RNA is designated SEQ ID:4968, and is provided hereinbelow with reference to the sequence listing part.

[33153] GAM2377 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2377 target RNA, herein designated GAM TARGET RNA. GAM2377 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33154] GAM2377 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2377 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2377 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2377 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2377 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33155] The complementary binding of GAM2377 RNA, herein designated GAM RNA, to target binding sites on GAM2377 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2377 target RNA, herein designated GAM TARGET RNA, into GAM2377 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33156] It is appreciated that GAM2377 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2377 target genes. The mRNA of each one of this plurality of GAM2377 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2377 RNA, herein designated GAM RNA, and which when bound by GAM2377 RNA, herein designated GAM RNA,



causes inhibition of translation of respective one or more GAM2377 target proteins.

[33157] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2377 gene, herein designated GAM GENE, on one or more GAM2377 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33158] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2377 correlate with, and may be deduced from, the identity of the target genes which GAM2377 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33159] Nucleotide sequences of the GAM2377 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2377 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2377 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2377 are further described hereinbelow with reference to Table 1.

[33160] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2377 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[33161] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2378 (GAM2378) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[33162] GAM2378 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2378 was detected is described hereinabove with reference to Figs. 2-8.

[33163] GAM2378 gene, herein designated GAM GENE, and GAM2378 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[33164] GAM2378 gene, herein designated GAM GENE, encodes a GAM2378 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2378 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2378 precursor RNA is designated SEQ ID:2355, and is provided hereinbelow with reference to the sequence listing part.

[33165] GAM2378 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2378 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33166] An enzyme complex designated DICER COMPLEX, dices the GAM2378 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2378 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2378 RNA is designated SEQ ID:4969, and is provided hereinbelow with reference to the sequence listing part.

[33167] GAM2378 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2378 target RNA, herein designated GAM TARGET RNA. GAM2378 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33168] GAM2378 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2378 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2378 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2378 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2378 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33169] The complementary binding of GAM2378 RNA, herein designated GAM RNA, to target binding sites on GAM2378 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2378 target RNA, herein designated GAM TARGET RNA, into GAM2378 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33170] It is appreciated that GAM2378 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2378 target genes. The

mRNA of each one of this plurality of GAM2378 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2378 RNA, herein designated GAM RNA, and which when bound by GAM2378 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2378 target proteins.

[33171] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2378 gene, herein designated GAM GENE, on one or more GAM2378 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33172] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2378 correlate with, and may be deduced from, the identity of the target genes which GAM2378 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33173] Nucleotide sequences of the GAM2378 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2378 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2378 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2378 are further described hereinbelow with reference to Table 1.

[33174] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2378 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[33175] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2379 (GAM2379) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[33176] GAM2379 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2379 was detected is described hereinabove with reference to Figs. 2-8.

[33177] GAM2379 gene, herein designated GAM GENE, and GAM2379 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[33178] GAM2379 gene, herein designated GAM GENE, encodes a GAM2379 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2379 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2379 precursor RNA is designated SEQ ID:2356, and is provided hereinbelow with reference to the sequence listing part.

[33179] GAM2379 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2379 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33180] An enzyme complex designated DICER COMPLEX, dices the GAM2379 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2379 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 84%) nucleotide sequence of GAM2379 RNA is designated SEQ ID:4970, and is provided hereinbelow with reference to the sequence listing part.

[33181] GAM2379 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2379 target RNA, herein designated GAM TARGET RNA. GAM2379 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33182] GAM2379 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2379 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2379 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2379 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2379 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33183] The complementary binding of GAM2379 RNA, herein designated GAM RNA, to target binding sites on GAM2379 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2379 target RNA, herein designated GAM TARGET RNA, into GAM2379 target protein, herein



designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33184] It is appreciated that GAM2379 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2379 target genes. The mRNA of each one of this plurality of GAM2379 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2379 RNA, herein designated GAM RNA, and which when bound by GAM2379 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2379 target proteins.

[33185] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2379 gene, herein designated GAM GENE, on one or more GAM2379 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33186] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2379 correlate with, and may be deduced from, the identity of the target

genes which GAM2379 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33187] Nucleotide sequences of the GAM2379 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2379 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2379 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2379 are further described hereinbelow with reference to Table 1.

[33188] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2379 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[33189] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2380 (GAM2380) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[33190] GAM2380 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2380 was detected is described hereinabove with reference to Figs. 2-8.

[33191] GAM2380 gene, herein designated GAM GENE, and GAM2380 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

- [33192] GAM2380 gene, herein designated GAM GENE, encodes a GAM2380 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2380 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2380 precursor RNA is designated SEQ ID:2357, and is provided hereinbelow with reference to the sequence listing part.
- [33193] GAM2380 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2380 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.
- [33194] An enzyme complex designated DICER COMPLEX, dices the GAM2380 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2380 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 83%) nucleotide sequence of GAM2380 RNA is designated SEQ ID:4971, and is provided

hereinbelow with reference to the sequence listing part.

[33195] GAM2380 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2380 target RNA, herein designated GAM TARGET RNA. GAM2380 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33196] GAM2380 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2380 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2380 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2380 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2380 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33197] The complementary binding of GAM2380 RNA, herein designated GAM RNA, to target binding sites on GAM2380 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2380 target RNA, herein designated GAM TARGET RNA, into GAM2380 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33198] It is appreciated that GAM2380 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2380 target genes. The mRNA of each one of this plurality of GAM2380 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2380 RNA, herein designated GAM RNA, and which when bound by GAM2380 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2380 target proteins.

[33199] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2380 gene, herein designated GAM GENE, on one or more GAM2380 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33200] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2380 correlate with, and may be deduced from, the identity of the target genes which GAM2380 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33201] Nucleotide sequences of the GAM2380 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2380 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2380 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2380 are further described hereinbelow with reference to Table 1.

[33202] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2380 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[33203] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2381 (GAM2381) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[33204] GAM2381 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2381 was detected is described hereinabove with reference to Figs. 2-8.

[33205] GAM2381 gene, herein designated GAM GENE, and GAM2381 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[33206] GAM2381 gene, herein designated GAM GENE, encodes a GAM2381 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2381 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2381 precursor RNA is designated SEQ ID:2358, and is provided hereinbelow with reference to the sequence listing part.

[33207] GAM2381 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2381 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33208] An enzyme complex designated DICER COMPLEX, dices the GAM2381 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2381 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2381 RNA is designated SEQ ID:4972, and is provided hereinbelow with reference to the sequence listing part.

[33209] GAM2381 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2381 target RNA, herein designated GAM TARGET RNA. GAM2381 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33210] GAM2381 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2381 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2381 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2381 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2381 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target



binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33211] The complementary binding of GAM2381 RNA, herein designated GAM RNA, to target binding sites on GAM2381 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2381 target RNA, herein designated GAM TARGET RNA, into GAM2381 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33212] It is appreciated that GAM2381 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2381 target genes. The mRNA of each one of this plurality of GAM2381 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2381 RNA, herein designated GAM RNA, and which when bound by GAM2381 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2381 target proteins.

[33213] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2381 gene, herein designated GAM GENE, on one or more GAM2381 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33214] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2381 correlate with, and may be deduced from, the identity of the target genes which GAM2381 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33215] Nucleotide sequences of the GAM2381 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2381 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2381 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2381 are further described hereinbelow with reference to Table 1.

[33216] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2381 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[33217] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2382 (GAM2382) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

- [33218] GAM2382 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2382 was detected is described hereinabove with reference to Figs. 2-8.
- [33219] GAM2382 gene, herein designated GAM GENE, and GAM2382 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.
- [33220] GAM2382 gene, herein designated GAM GENE, encodes a GAM2382 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2382 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2382 precursor RNA is designated SEQ ID:2359, and is provided hereinbelow with reference to the sequence listing part.
- [33221] GAM2382 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2382 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

- [33222] An enzyme complex designated DICER COMPLEX, dices the GAM2382 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2382 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2382 RNA is designated SEQ ID:4973, and is provided hereinbelow with reference to the sequence listing part.
- [33223] GAM2382 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2382 target RNA, herein designated GAM TARGET RNA. GAM2382 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [33224] GAM2382 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2382 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2382 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2382 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2382 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33225] The complementary binding of GAM2382 RNA, herein designated GAM RNA, to target binding sites on GAM2382 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2382 target RNA, herein designated GAM TARGET RNA, into GAM2382 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33226] It is appreciated that GAM2382 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2382 target genes. The mRNA of each one of this plurality of GAM2382 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2382 RNA, herein designated GAM RNA, and which when bound by GAM2382 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2382 target proteins.

[33227] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2382 gene, herein designated GAM GENE, on one or more GAM2382 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33228] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2382 correlate with, and may be deduced from, the identity of the target genes which GAM2382 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33229] Nucleotide sequences of the GAM2382 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2382 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2382 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2382 are further described hereinbelow with reference to Table 1.

[33230] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2382 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

[33231] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2383 (GAM2383) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[33232] GAM2383 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2383 was detected is described hereinabove with reference to Figs. 2-8.

[33233] GAM2383 gene, herein designated GAM GENE, and GAM2383 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[33234] GAM2383 gene, herein designated GAM GENE, encodes a GAM2383 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2383 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2383 precursor RNA is designated SEQ ID:2360, and is provided hereinbelow with reference to the sequence listing part.

[33235] GAM2383 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2383 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33236] An enzyme complex designated DICER COMPLEX, dices the GAM2383 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2383 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 85%) nucleotide sequence of GAM2383 RNA is designated SEQ ID:4974, and is provided hereinbelow with reference to the sequence listing part.

[33237] GAM2383 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2383 target RNA, herein designated GAM TARGET RNA. GAM2383 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33238] GAM2383 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2383 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2383 RNA,



herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2383 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2383 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33239] The complementary binding of GAM2383 RNA, herein designated GAM RNA, to target binding sites on GAM2383 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2383 target RNA, herein designated GAM TARGET RNA, into GAM2383 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33240] It is appreciated that GAM2383 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2383 target genes. The mRNA of each one of this plurality of GAM2383 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2383 RNA, herein designated GAM RNA, and which when bound by GAM2383 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2383 target proteins.

[33241] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2383 gene, herein designated GAM GENE, on one or more GAM2383 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33242] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2383 correlate with, and may be deduced from, the identity of the target genes which GAM2383 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33243] Nucleotide sequences of the GAM2383 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2383 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2383 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2383 are further described hereinbelow with reference to Table 1.

[33244] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2383 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[33245] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2384 (GAM2384) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[33246] GAM2384 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2384 was detected is described hereinabove with reference to Figs. 2-8.

[33247] GAM2384 gene, herein designated GAM GENE, and GAM2384 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[33248] GAM2384 gene, herein designated GAM GENE, encodes a GAM2384 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2384 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2384 precursor RNA is designated SEQ ID:2361, and is provided hereinbelow with reference to the sequence listing part.

[33249] GAM2384 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2384 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33250] An enzyme complex designated DICER COMPLEX, dices the GAM2384 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2384 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2384 RNA is designated SEQ ID:4975, and is provided hereinbelow with reference to the sequence listing part.

[33251] GAM2384 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2384 target RNA, herein designated GAM TARGET RNA. GAM2384 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33252] GAM2384 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2384 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2384 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2384 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2384 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33253] The complementary binding of GAM2384 RNA, herein designated GAM RNA, to target binding sites on GAM2384 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2384 target RNA, herein designated GAM TARGET RNA, into GAM2384 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33254] It is appreciated that GAM2384 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2384 target genes. The

mRNA of each one of this plurality of GAM2384 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2384 RNA, herein designated GAM RNA, and which when bound by GAM2384 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2384 target proteins.

[33255] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2384 gene, herein designated GAM GENE, on one or more GAM2384 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33256] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2384 correlate with, and may be deduced from, the identity of the target genes which GAM2384 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33257] Nucleotide sequences of the GAM2384 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2384 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2384 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2384 are further described hereinbelow with reference to Table 1.

[33258] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2384 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[33259] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2385 (GAM2385) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[33260] GAM2385 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2385 was detected is described hereinabove with reference to Figs. 2-8.

[33261] GAM2385 gene, herein designated GAM GENE, and GAM2385 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[33262] GAM2385 gene, herein designated GAM GENE, encodes a GAM2385 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2385 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2385 precursor RNA is designated SEQ ID:2362, and is provided hereinbelow with reference to the sequence listing part.

[33263] GAM2385 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2385 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33264] An enzyme complex designated DICER COMPLEX, dices the GAM2385 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2385 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 83%) nucleotide sequence of GAM2385 RNA is designated SEQ ID:4976, and is provided hereinbelow with reference to the sequence listing part.

[33265] GAM2385 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2385 target RNA, herein designated GAM TARGET RNA. GAM2385 target RNA, herein designated GAM



TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33266] GAM2385 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2385 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2385 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2385 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2385 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33267] The complementary binding of GAM2385 RNA, herein designated GAM RNA, to target binding sites on GAM2385 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2385 target RNA, herein designated GAM TARGET RNA, into GAM2385 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33268] It is appreciated that GAM2385 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2385 target genes. The mRNA of each one of this plurality of GAM2385 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2385 RNA, herein designated GAM RNA, and which when bound by GAM2385 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2385 target proteins.

[33269] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2385 gene, herein designated GAM GENE, on one or more GAM2385 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33270] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2385 correlate with, and may be deduced from, the identity of the target

genes which GAM2385 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33271] Nucleotide sequences of the GAM2385 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2385 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2385 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2385 are further described hereinbelow with reference to Table 1.

[33272] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2385 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[33273] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2386 (GAM2386) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[33274] GAM2386 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2386 was detected is described hereinabove with reference to Figs. 2-8.

[33275] GAM2386 gene, herein designated GAM GENE, and GAM2386 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

[33276] GAM2386 gene, herein designated GAM GENE, encodes a GAM2386 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2386 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2386 precursor RNA is designated SEQ ID:2363, and is provided hereinbelow with reference to the sequence listing part.

[33277] GAM2386 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2386 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33278] An enzyme complex designated DICER COMPLEX, dices the GAM2386 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2386 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 84%) nucleotide sequence of GAM2386 RNA is designated SEQ ID:4977, and is provided

hereinbelow with reference to the sequence listing part.

[33279] GAM2386 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2386 target RNA, herein designated GAM TARGET RNA. GAM2386 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33280] GAM2386 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2386 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2386 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2386 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2386 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33281] The complementary binding of GAM2386 RNA, herein designated GAM RNA, to target binding sites on GAM2386 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2386 target RNA, herein designated GAM TARGET RNA, into GAM2386 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33282] It is appreciated that GAM2386 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2386 target genes. The mRNA of each one of this plurality of GAM2386 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2386 RNA, herein designated GAM RNA, and which when bound by GAM2386 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2386 target proteins.

[33283] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2386 gene, herein designated GAM GENE, on one or more GAM2386 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33284] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2386 correlate with, and may be deduced from, the identity of the target genes which GAM2386 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33285] Nucleotide sequences of the GAM2386 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2386 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2386 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2386 are further described hereinbelow with reference to Table 1.

[33286] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2386 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[33287] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2387 (GAM2387) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[33288] GAM2387 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2387 was detected is described hereinabove with reference to Figs. 2-8.

[33289] GAM2387 gene, herein designated GAM GENE, and GAM2387 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[33290] GAM2387 gene, herein designated GAM GENE, encodes a GAM2387 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2387 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2387 precursor RNA is designated SEQ ID:2364, and is provided hereinbelow with reference to the sequence listing part.

[33291] GAM2387 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2387 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33292] An enzyme complex designated DICER COMPLEX, dices the GAM2387 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2387 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin



structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of GAM2387 RNA is designated SEQ ID:4978, and is provided hereinbelow with reference to the sequence listing part.

[33293] GAM2387 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2387 target RNA, herein designated GAM TARGET RNA. GAM2387 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33294] GAM2387 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2387 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2387 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2387 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2387 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33295] The complementary binding of GAM2387 RNA, herein designated GAM RNA, to target binding sites on GAM2387 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2387 target RNA, herein designated GAM TARGET RNA, into GAM2387 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33296] It is appreciated that GAM2387 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2387 target genes. The mRNA of each one of this plurality of GAM2387 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2387 RNA, herein designated GAM RNA, and which when bound by GAM2387 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2387 target proteins.

[33297] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2387 gene, herein designated GAM GENE, on one or more GAM2387 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33298] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2387 correlate with, and may be deduced from, the identity of the target genes which GAM2387 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33299] Nucleotide sequences of the GAM2387 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2387 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2387 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2387 are further described hereinbelow with reference to Table 1.

[33300] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2387 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[33301] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2388 (GAM2388) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

- [33302] GAM2388 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2388 was detected is described hereinabove with reference to Figs. 2-8.
- [33303] GAM2388 gene, herein designated GAM GENE, and GAM2388 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.
- [33304] GAM2388 gene, herein designated GAM GENE, encodes a GAM2388 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2388 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2388 precursor RNA is designated SEQ ID:2365, and is provided hereinbelow with reference to the sequence listing part.
- [33305] GAM2388 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2388 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

- [33306] An enzyme complex designated DICER COMPLEX, dices the GAM2388 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2388 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of GAM2388 RNA is designated SEQ ID:4979, and is provided hereinbelow with reference to the sequence listing part.
- [33307] GAM2388 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2388 target RNA, herein designated GAM TARGET RNA. GAM2388 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [33308] GAM2388 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2388 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2388 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2388 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2388 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33309] The complementary binding of GAM2388 RNA, herein designated GAM RNA, to target binding sites on GAM2388 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2388 target RNA, herein designated GAM TARGET RNA, into GAM2388 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33310] It is appreciated that GAM2388 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2388 target genes. The mRNA of each one of this plurality of GAM2388 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2388 RNA, herein designated GAM RNA, and which when bound by GAM2388 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2388 target proteins.

[33311] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2388 gene, herein designated GAM GENE, on one or more GAM2388 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33312] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2388 correlate with, and may be deduced from, the identity of the target genes which GAM2388 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33313] Nucleotide sequences of the GAM2388 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2388 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2388 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2388 are further described hereinbelow with reference to Table 1.

[33314] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2388 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

- [33315] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2389 (GAM2389) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.
- [33316] GAM2389 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2389 was detected is described hereinabove with reference to Figs. 2-8.
- [33317] GAM2389 gene, herein designated GAM GENE, and GAM2389 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.
- [33318] GAM2389 gene, herein designated GAM GENE, encodes a GAM2389 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2389 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2389 precursor RNA is designated SEQ ID:2366, and is provided hereinbelow with reference to the sequence listing part.
- [33319] GAM2389 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2389 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA



encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33320] An enzyme complex designated DICER COMPLEX, dices the GAM2389 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2389 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of GAM2389 RNA is designated SEQ ID:4980, and is provided hereinbelow with reference to the sequence listing part.

[33321] GAM2389 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2389 target RNA, herein designated GAM TARGET RNA. GAM2389 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33322] GAM2389 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2389 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2389 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2389 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2389 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33323] The complementary binding of GAM2389 RNA, herein designated GAM RNA, to target binding sites on GAM2389 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2389 target RNA, herein designated GAM TARGET RNA, into GAM2389 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33324] It is appreciated that GAM2389 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2389 target genes. The mRNA of each one of this plurality of GAM2389 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2389 RNA, herein designated GAM RNA, and which when bound by GAM2389 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2389 target proteins.

[33325] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2389 gene, herein designated GAM GENE, on one or more GAM2389 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33326] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2389 correlate with, and may be deduced from, the identity of the target genes which GAM2389 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33327] Nucleotide sequences of the GAM2389 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2389 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2389 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2389 are further described hereinbelow with reference to Table 1.

[33328] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2389 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[33329] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2390 (GAM2390) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[33330] GAM2390 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2390 was detected is described hereinabove with reference to Figs. 2-8.

[33331] GAM2390 gene, herein designated GAM GENE, and GAM2390 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[33332] GAM2390 gene, herein designated GAM GENE, encodes a GAM2390 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2390 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2390 precursor RNA is designated SEQ ID:2367, and is provided hereinbelow with reference to the sequence listing part.

[33333] GAM2390 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2390 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33334] An enzyme complex designated DICER COMPLEX, dices the GAM2390 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2390 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM2390 RNA is designated SEQ ID:4981, and is provided hereinbelow with reference to the sequence listing part.

[33335] GAM2390 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2390 target RNA, herein designated GAM TARGET RNA. GAM2390 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33336] GAM2390 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2390 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2390 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2390 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2390 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33337] The complementary binding of GAM2390 RNA, herein designated GAM RNA, to target binding sites on GAM2390 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2390 target RNA, herein designated GAM TARGET RNA, into GAM2390 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33338] It is appreciated that GAM2390 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2390 target genes. The

mRNA of each one of this plurality of GAM2390 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2390 RNA, herein designated GAM RNA, and which when bound by GAM2390 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2390 target proteins.

[33339] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2390 gene, herein designated GAM GENE, on one or more GAM2390 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33340] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2390 correlate with, and may be deduced from, the identity of the target genes which GAM2390 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33341] Nucleotide sequences of the GAM2390 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2390 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2390 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2390 are further described hereinbelow with reference to Table 1.

[33342] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2390 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[33343] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2391 (GAM2391) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[33344] GAM2391 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2391 was detected is described hereinabove with reference to Figs. 2-8.

[33345] GAM2391 gene, herein designated GAM GENE, and GAM2391 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[33346] GAM2391 gene, herein designated GAM GENE, encodes a GAM2391 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2391 precursor RNA,



herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2391 precursor RNA is designated SEQ ID:2368, and is provided hereinbelow with reference to the sequence listing part.

[33347] GAM2391 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2391 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33348] An enzyme complex designated DICER COMPLEX, dices the GAM2391 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2391 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2391 RNA is designated SEQ ID:4982, and is provided hereinbelow with reference to the sequence listing part.

[33349] GAM2391 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2391 target RNA, herein designated GAM TARGET RNA. GAM2391 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33350] GAM2391 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2391 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2391 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2391 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2391 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33351] The complementary binding of GAM2391 RNA, herein designated GAM RNA, to target binding sites on GAM2391 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2391 target RNA, herein designated GAM TARGET RNA, into GAM2391 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33352] It is appreciated that GAM2391 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2391 target genes. The mRNA of each one of this plurality of GAM2391 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2391 RNA, herein designated GAM RNA, and which when bound by GAM2391 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2391 target proteins.

[33353] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2391 gene, herein designated GAM GENE, on one or more GAM2391 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33354] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2391 correlate with, and may be deduced from, the identity of the target

genes which GAM2391 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33355] Nucleotide sequences of the GAM2391 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2391 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2391 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2391 are further described hereinbelow with reference to Table 1.

[33356] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2391 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[33357] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2392 (GAM2392) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[33358] GAM2392 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2392 was detected is described hereinabove with reference to Figs. 2-8.

[33359] GAM2392 gene, herein designated GAM GENE, and GAM2392 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

[33360] GAM2392 gene, herein designated GAM GENE, encodes a GAM2392 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2392 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2392 precursor RNA is designated SEQ ID:2369, and is provided hereinbelow with reference to the sequence listing part.

[33361] GAM2392 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2392 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33362] An enzyme complex designated DICER COMPLEX, dices the GAM2392 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2392 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of GAM2392 RNA is designated SEQ ID:4983, and is provided

hereinbelow with reference to the sequence listing part.

[33363] GAM2392 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2392 target RNA, herein designated GAM TARGET RNA. GAM2392 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33364] GAM2392 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2392 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2392 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2392 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2392 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33365] The complementary binding of GAM2392 RNA, herein designated GAM RNA, to target binding sites on GAM2392 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2392 target RNA, herein designated GAM TARGET RNA, into GAM2392 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33366] It is appreciated that GAM2392 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2392 target genes. The mRNA of each one of this plurality of GAM2392 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2392 RNA, herein designated GAM RNA, and which when bound by GAM2392 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2392 target proteins.

[33367] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2392 gene, herein designated GAM GENE, on one or more GAM2392 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33368] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2392 correlate with, and may be deduced from, the identity of the target genes which GAM2392 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33369] Nucleotide sequences of the GAM2392 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2392 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2392 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2392 are further described hereinbelow with reference to Table 1.

[33370] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2392 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[33371] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2393 (GAM2393) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[33372] GAM2393 is a novel bioinformatically detected regulatory, non protein



coding, micro RNA (miRNA) gene. The method by which GAM2393 was detected is described hereinabove with reference to Figs. 2-8.

[33373] GAM2393 gene, herein designated GAM GENE, and GAM2393 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[33374] GAM2393 gene, herein designated GAM GENE, encodes a GAM2393 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2393 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2393 precursor RNA is designated SEQ ID:2370, and is provided hereinbelow with reference to the sequence listing part.

[33375] GAM2393 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2393 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33376] An enzyme complex designated DICER COMPLEX, dices the GAM2393 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2393 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 88%) nucleotide sequence of GAM2393 RNA is designated SEQ ID:4985, and is provided hereinbelow with reference to the sequence listing part.

[33377] GAM2393 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2393 target RNA, herein designated GAM TARGET RNA. GAM2393 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33378] GAM2393 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2393 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2393 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2393 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2393 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33379] The complementary binding of GAM2393 RNA, herein designated GAM RNA, to target binding sites on GAM2393 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2393 target RNA, herein designated GAM TARGET RNA, into GAM2393 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33380] It is appreciated that GAM2393 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2393 target genes. The mRNA of each one of this plurality of GAM2393 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2393 RNA, herein designated GAM RNA, and which when bound by GAM2393 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2393 target proteins.

[33381] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2393 gene, herein designated GAM GENE, on one or more GAM2393 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33382] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2393 correlate with, and may be deduced from, the identity of the target genes which GAM2393 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33383] Nucleotide sequences of the GAM2393 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2393 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2393 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2393 are further described hereinbelow with reference to Table 1.

[33384] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2393 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[33385] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2394 (GAM2394) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[33386] GAM2394 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2394 was detected is described hereinabove with reference to Figs. 2-8.

[33387] GAM2394 gene, herein designated GAM GENE, and GAM2394 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[33388] GAM2394 gene, herein designated GAM GENE, encodes a GAM2394 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2394 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2394 precursor RNA is designated SEQ ID:2371, and is provided hereinbelow with reference to the sequence listing part.

[33389] GAM2394 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2394 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33390] An enzyme complex designated DICER COMPLEX, dices the GAM2394 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2394 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2394 RNA is designated SEQ ID:4984, and is provided hereinbelow with reference to the sequence listing part.

[33391] GAM2394 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2394 target RNA, herein designated GAM TARGET RNA. GAM2394 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33392] GAM2394 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2394 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2394 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2394 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2394 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33393] The complementary binding of GAM2394 RNA, herein designated GAM RNA, to target binding sites on GAM2394 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2394 target RNA, herein designated GAM TARGET RNA, into GAM2394 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33394] It is appreciated that GAM2394 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2394 target genes. The mRNA of each one of this plurality of GAM2394 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2394 RNA, herein designated GAM RNA, and which when bound by GAM2394 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2394 target proteins.

[33395] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2394 gene, herein designated GAM GENE, on one or more GAM2394 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33396] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2394 correlate with, and may be deduced from, the identity of the target genes which GAM2394 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33397] Nucleotide sequences of the GAM2394 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2394 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2394 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2394 are further described hereinbelow with reference to Table 1.

[33398] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2394 RNA, herein designated GAM RNA, are described hereinbelow



with reference to Table 2.

[33399] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2395 (GAM2395) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[33400] GAM2395 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2395 was detected is described hereinabove with reference to Figs. 2-8.

[33401] GAM2395 gene, herein designated GAM GENE, and GAM2395 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[33402] GAM2395 gene, herein designated GAM GENE, encodes a GAM2395 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2395 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2395 precursor RNA is designated SEQ ID:2372, and is provided hereinbelow with reference to the sequence listing part.

[33403] GAM2395 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2395 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33404] An enzyme complex designated DICER COMPLEX, dices the GAM2395 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2395 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 88%) nucleotide sequence of GAM2395 RNA is designated SEQ ID:4986, and is provided hereinbelow with reference to the sequence listing part.

[33405] GAM2395 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2395 target RNA, herein designated GAM TARGET RNA. GAM2395 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33406] GAM2395 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2395 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2395 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2395 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2395 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33407] The complementary binding of GAM2395 RNA, herein designated GAM RNA, to target binding sites on GAM2395 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2395 target RNA, herein designated GAM TARGET RNA, into GAM2395 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33408] It is appreciated that GAM2395 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2395 target genes. The mRNA of each one of this plurality of GAM2395 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2395 RNA, herein designated GAM RNA, and which when bound by GAM2395 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2395 target proteins.

[33409] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2395 gene, herein designated GAM GENE, on one or more GAM2395 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33410] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2395 correlate with, and may be deduced from, the identity of the target genes which GAM2395 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33411] Nucleotide sequences of the GAM2395 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2395 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2395 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2395 are further described hereinbelow with reference to Table 1.

[33412] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2395 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[33413] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2396 (GAM2396) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[33414] GAM2396 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2396 was detected is described hereinabove with reference to Figs. 2-8.

[33415] GAM2396 gene, herein designated GAM GENE, and GAM2396 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[33416] GAM2396 gene, herein designated GAM GENE, encodes a GAM2396 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2396 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2396 precursor RNA is designated SEQ ID:2373, and is provided hereinbelow with reference to the sequence listing part.

[33417] GAM2396 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2396 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33418] An enzyme complex designated DICER COMPLEX, dices the GAM2396 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2396 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of GAM2396 RNA is designated SEQ ID:4987, and is provided hereinbelow with reference to the sequence listing part.

[33419] GAM2396 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2396 target RNA, herein designated GAM TARGET RNA. GAM2396 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33420] GAM2396 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2396 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2396 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2396 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2396 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33421] The complementary binding of GAM2396 RNA, herein designated GAM RNA, to target binding sites on GAM2396 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2396 target RNA, herein designated GAM TARGET RNA, into GAM2396 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33422] It is appreciated that GAM2396 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2396 target genes. The

mRNA of each one of this plurality of GAM2396 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2396 RNA, herein designated GAM RNA, and which when bound by GAM2396 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2396 target proteins.

[33423] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2396 gene, herein designated GAM GENE, on one or more GAM2396 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33424] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2396 correlate with, and may be deduced from, the identity of the target genes which GAM2396 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33425] Nucleotide sequences of the GAM2396 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2396 RNA, herein



designated GAM RNA, and a schematic representation of the secondary folding of GAM2396 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2396 are further described hereinbelow with reference to Table 1.

[33426] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2396 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[33427] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2397 (GAM2397) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[33428] GAM2397 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2397 was detected is described hereinabove with reference to Figs. 2-8.

[33429] GAM2397 gene, herein designated GAM GENE, and GAM2397 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[33430] GAM2397 gene, herein designated GAM GENE, encodes a GAM2397 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2397 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2397 precursor RNA is designated SEQ ID:2374, and is provided hereinbelow with reference to the sequence listing part.

[33431] GAM2397 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2397 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33432] An enzyme complex designated DICER COMPLEX, dices the GAM2397 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2397 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of GAM2397 RNA is designated SEQ ID:4988, and is provided hereinbelow with reference to the sequence listing part.

[33433] GAM2397 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2397 target RNA, herein designated GAM TARGET RNA. GAM2397 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33434] GAM2397 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2397 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2397 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2397 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2397 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33435] The complementary binding of GAM2397 RNA, herein designated GAM RNA, to target binding sites on GAM2397 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2397 target RNA, herein designated GAM TARGET RNA, into GAM2397 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33436] It is appreciated that GAM2397 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2397 target genes. The mRNA of each one of this plurality of GAM2397 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2397 RNA, herein designated GAM RNA, and which when bound by GAM2397 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2397 target proteins.

[33437] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2397 gene, herein designated GAM GENE, on one or more GAM2397 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33438] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2397 correlate with, and may be deduced from, the identity of the target

genes which GAM2397 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33439] Nucleotide sequences of the GAM2397 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2397 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2397 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2397 are further described hereinbelow with reference to Table 1.

[33440] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2397 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[33441] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2398 (GAM2398) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[33442] GAM2398 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2398 was detected is described hereinabove with reference to Figs. 2-8.

[33443] GAM2398 gene, herein designated GAM GENE, and GAM2398 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

[33444] GAM2398 gene, herein designated GAM GENE, encodes a GAM2398 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2398 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2398 precursor RNA is designated SEQ ID:2375, and is provided hereinbelow with reference to the sequence listing part.

[33445] GAM2398 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2398 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33446] An enzyme complex designated DICER COMPLEX, dices the GAM2398 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2398 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of GAM2398 RNA is designated SEQ ID:4989, and is provided

hereinbelow with reference to the sequence listing part.

[33447] GAM2398 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2398 target RNA, herein designated GAM TARGET RNA. GAM2398 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33448] GAM2398 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2398 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2398 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2398 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2398 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33449] The complementary binding of GAM2398 RNA, herein designated GAM RNA, to target binding sites on GAM2398 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2398 target RNA, herein designated GAM TARGET RNA, into GAM2398 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33450] It is appreciated that GAM2398 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2398 target genes. The mRNA of each one of this plurality of GAM2398 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2398 RNA, herein designated GAM RNA, and which when bound by GAM2398 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2398 target proteins.

[33451] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2398 gene, herein designated GAM GENE, on one or more GAM2398 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding



sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33452] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2398 correlate with, and may be deduced from, the identity of the target genes which GAM2398 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33453] Nucleotide sequences of the GAM2398 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2398 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2398 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2398 are further described hereinbelow with reference to Table 1.

[33454] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2398 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[33455] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2399 (GAM2399) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[33456] GAM2399 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2399 was detected is described hereinabove with reference to Figs. 2-8.

[33457] GAM2399 gene, herein designated GAM GENE, and GAM2399 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[33458] GAM2399 gene, herein designated GAM GENE, encodes a GAM2399 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2399 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2399 precursor RNA is designated SEQ ID:2376, and is provided hereinbelow with reference to the sequence listing part.

[33459] GAM2399 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2399 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33460] An enzyme complex designated DICER COMPLEX, dices the GAM2399 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2399 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of GAM2399 RNA is designated SEQ ID:4990, and is provided hereinbelow with reference to the sequence listing part.

[33461] GAM2399 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2399 target RNA, herein designated GAM TARGET RNA. GAM2399 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33462] GAM2399 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2399 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2399 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2399 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2399 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33463] The complementary binding of GAM2399 RNA, herein designated GAM RNA, to target binding sites on GAM2399 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2399 target RNA, herein designated GAM TARGET RNA, into GAM2399 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33464] It is appreciated that GAM2399 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2399 target genes. The mRNA of each one of this plurality of GAM2399 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2399 RNA, herein designated GAM RNA, and which when bound by GAM2399 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2399 target proteins.

[33465] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2399 gene, herein designated GAM GENE, on one or more GAM2399 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33466] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2399 correlate with, and may be deduced from, the identity of the target genes which GAM2399 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33467] Nucleotide sequences of the GAM2399 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2399 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2399 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2399 are further described hereinbelow with reference to Table 1.

[33468] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2399 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[33469] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2400 (GAM2400) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[33470] GAM2400 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2400 was detected is described hereinabove with reference to Figs. 2-8.

[33471] GAM2400 gene, herein designated GAM GENE, and GAM2400 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[33472] GAM2400 gene, herein designated GAM GENE, encodes a GAM2400 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2400 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2400 precursor RNA is designated SEQ ID:2377, and is provided hereinbelow with reference to the sequence listing part.

[33473] GAM2400 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2400 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

- [33474] An enzyme complex designated DICER COMPLEX, dices the GAM2400 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2400 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2400 RNA is designated SEQ ID:4991, and is provided hereinbelow with reference to the sequence listing part.
- [33475] GAM2400 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2400 target RNA, herein designated GAM TARGET RNA. GAM2400 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [33476] GAM2400 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2400 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2400 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2400 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2400 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33477] The complementary binding of GAM2400 RNA, herein designated GAM RNA, to target binding sites on GAM2400 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2400 target RNA, herein designated GAM TARGET RNA, into GAM2400 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33478] It is appreciated that GAM2400 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2400 target genes. The mRNA of each one of this plurality of GAM2400 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2400 RNA, herein designated GAM RNA, and which when bound by GAM2400 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2400 target proteins.

[33479] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition



exerted by GAM2400 gene, herein designated GAM GENE, on one or more GAM2400 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33480] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2400 correlate with, and may be deduced from, the identity of the target genes which GAM2400 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33481] Nucleotide sequences of the GAM2400 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2400 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2400 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2400 are further described hereinbelow with reference to Table 1.

[33482] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2400 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

[33483] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2401 (GAM2401) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[33484] GAM2401 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2401 was detected is described hereinabove with reference to Figs. 2-8.

[33485] GAM2401 gene, herein designated GAM GENE, and GAM2401 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[33486] GAM2401 gene, herein designated GAM GENE, encodes a GAM2401 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2401 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2401 precursor RNA is designated SEQ ID:2378, and is provided hereinbelow with reference to the sequence listing part.

[33487] GAM2401 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2401 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33488] An enzyme complex designated DICER COMPLEX, dices the GAM2401 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2401 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 91%) nucleotide sequence of GAM2401 RNA is designated SEQ ID:4992, and is provided hereinbelow with reference to the sequence listing part.

[33489] GAM2401 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2401 target RNA, herein designated GAM TARGET RNA. GAM2401 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33490] GAM2401 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2401 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2401 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2401 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2401 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33491] The complementary binding of GAM2401 RNA, herein designated GAM RNA, to target binding sites on GAM2401 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2401 target RNA, herein designated GAM TARGET RNA, into GAM2401 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33492] It is appreciated that GAM2401 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2401 target genes. The mRNA of each one of this plurality of GAM2401 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2401 RNA, herein designated GAM RNA, and which when bound by GAM2401 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2401 target proteins.

[33493] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2401 gene, herein designated GAM GENE, on one or more GAM2401 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33494] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2401 correlate with, and may be deduced from, the identity of the target genes which GAM2401 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33495] Nucleotide sequences of the GAM2401 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2401 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2401 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2401 are further described hereinbelow with reference to Table 1.

[33496] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2401 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[33497] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2402 (GAM2402) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[33498] GAM2402 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2402 was detected is described hereinabove with reference to Figs. 2-8.

[33499] GAM2402 gene, herein designated GAM GENE, and GAM2402 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[33500] GAM2402 gene, herein designated GAM GENE, encodes a GAM2402 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2402 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2402 precursor RNA is designated SEQ ID:2379, and is provided hereinbelow with reference to the sequence listing part.

[33501] GAM2402 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2402 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33502] An enzyme complex designated DICER COMPLEX, dices the GAM2402 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2402 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2402 RNA is designated SEQ ID:4993, and is provided hereinbelow with reference to the sequence listing part.

[33503] GAM2402 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2402 target RNA, herein designated GAM TARGET RNA. GAM2402 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33504] GAM2402 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2402 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2402 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2402 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2402 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33505] The complementary binding of GAM2402 RNA, herein designated GAM RNA, to target binding sites on GAM2402 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2402 target RNA, herein designated GAM TARGET RNA, into GAM2402 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33506] It is appreciated that GAM2402 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2402 target genes. The



mRNA of each one of this plurality of GAM2402 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2402 RNA, herein designated GAM RNA, and which when bound by GAM2402 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2402 target proteins.

[33507] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2402 gene, herein designated GAM GENE, on one or more GAM2402 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33508] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2402 correlate with, and may be deduced from, the identity of the target genes which GAM2402 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33509] Nucleotide sequences of the GAM2402 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2402 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2402 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2402 are further described hereinbelow with reference to Table 1.

[33510] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2402 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[33511] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2403 (GAM2403) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[33512] GAM2403 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2403 was detected is described hereinabove with reference to Figs. 2-8.

[33513] GAM2403 gene, herein designated GAM GENE, and GAM2403 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[33514] GAM2403 gene, herein designated GAM GENE, encodes a GAM2403 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2403 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2403 precursor RNA is designated SEQ ID:2380, and is provided hereinbelow with reference to the sequence listing part.

[33515] GAM2403 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2403 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33516] An enzyme complex designated DICER COMPLEX, dices the GAM2403 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2403 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 88%) nucleotide sequence of GAM2403 RNA is designated SEQ ID:4994, and is provided hereinbelow with reference to the sequence listing part.

[33517] GAM2403 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2403 target RNA, herein designated GAM TARGET RNA. GAM2403 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33518] GAM2403 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2403 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2403 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2403 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2403 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33519] The complementary binding of GAM2403 RNA, herein designated GAM RNA, to target binding sites on GAM2403 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2403 target RNA, herein designated GAM TARGET RNA, into GAM2403 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33520] It is appreciated that GAM2403 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2403 target genes. The mRNA of each one of this plurality of GAM2403 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2403 RNA, herein designated GAM RNA, and which when bound by GAM2403 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2403 target proteins.

[33521] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2403 gene, herein designated GAM GENE, on one or more GAM2403 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33522] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2403 correlate with, and may be deduced from, the identity of the target

genes which GAM2403 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33523] Nucleotide sequences of the GAM2403 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2403 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2403 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2403 are further described hereinbelow with reference to Table 1.

[33524] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2403 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[33525] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2404 (GAM2404) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[33526] GAM2404 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2404 was detected is described hereinabove with reference to Figs. 2-8.

[33527] GAM2404 gene, herein designated GAM GENE, and GAM2404 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

[33528] GAM2404 gene, herein designated GAM GENE, encodes a GAM2404 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2404 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2404 precursor RNA is designated SEQ ID:2381, and is provided hereinbelow with reference to the sequence listing part.

[33529] GAM2404 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2404 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33530] An enzyme complex designated DICER COMPLEX, dices the GAM2404 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2404 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2404 RNA is designated SEQ ID:4995, and is provided

hereinbelow with reference to the sequence listing part.

[33531] GAM2404 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2404 target RNA, herein designated GAM TARGET RNA. GAM2404 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33532] GAM2404 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2404 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2404 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2404 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2404 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.



[33533] The complementary binding of GAM2404 RNA, herein designated GAM RNA, to target binding sites on GAM2404 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2404 target RNA, herein designated GAM TARGET RNA, into GAM2404 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33534] It is appreciated that GAM2404 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2404 target genes. The mRNA of each one of this plurality of GAM2404 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2404 RNA, herein designated GAM RNA, and which when bound by GAM2404 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2404 target proteins.

[33535] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2404 gene, herein designated GAM GENE, on one or more GAM2404 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33536] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2404 correlate with, and may be deduced from, the identity of the target genes which GAM2404 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33537] Nucleotide sequences of the GAM2404 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2404 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2404 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2404 are further described hereinbelow with reference to Table 1.

[33538] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2404 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[33539] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2405 (GAM2405) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[33540] GAM2405 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2405 was detected is described hereinabove with reference to Figs. 2-8.

[33541] GAM2405 gene, herein designated GAM GENE, and GAM2405 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[33542] GAM2405 gene, herein designated GAM GENE, encodes a GAM2405 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2405 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2405 precursor RNA is designated SEQ ID:2382, and is provided hereinbelow with reference to the sequence listing part.

[33543] GAM2405 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2405 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33544] An enzyme complex designated DICER COMPLEX, dices the GAM2405 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2405 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 87%) nucleotide sequence of GAM2405 RNA is designated SEQ ID:4996, and is provided hereinbelow with reference to the sequence listing part.

[33545] GAM2405 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2405 target RNA, herein designated GAM TARGET RNA. GAM2405 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33546] GAM2405 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2405 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2405 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2405 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2405 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33547] The complementary binding of GAM2405 RNA, herein designated GAM RNA, to target binding sites on GAM2405 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2405 target RNA, herein designated GAM TARGET RNA, into GAM2405 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33548] It is appreciated that GAM2405 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2405 target genes. The mRNA of each one of this plurality of GAM2405 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2405 RNA, herein designated GAM RNA, and which when bound by GAM2405 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2405 target proteins.

[33549] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2405 gene, herein designated GAM GENE, on one or more GAM2405 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33550] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2405 correlate with, and may be deduced from, the identity of the target genes which GAM2405 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33551] Nucleotide sequences of the GAM2405 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2405 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2405 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2405 are further described hereinbelow with reference to Table 1.

[33552] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2405 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[33553] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2406 (GAM2406) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[33554] GAM2406 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2406 was detected is described hereinabove with reference to Figs. 2-8.

[33555] GAM2406 gene, herein designated GAM GENE, and GAM2406 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[33556] GAM2406 gene, herein designated GAM GENE, encodes a GAM2406 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2406 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2406 precursor RNA is designated SEQ ID:2383, and is provided hereinbelow with reference to the sequence listing part.

[33557] GAM2406 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2406 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

- [33558] An enzyme complex designated DICER COMPLEX, dices the GAM2406 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2406 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 88%) nucleotide sequence of GAM2406 RNA is designated SEQ ID:4997, and is provided hereinbelow with reference to the sequence listing part.
- [33559] GAM2406 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2406 target RNA, herein designated GAM TARGET RNA. GAM2406 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [33560] GAM2406 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2406 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2406 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an



illustration only, and is not meant to be limiting GAM2406 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2406 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33561] The complementary binding of GAM2406 RNA, herein designated GAM RNA, to target binding sites on GAM2406 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2406 target RNA, herein designated GAM TARGET RNA, into GAM2406 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33562] It is appreciated that GAM2406 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2406 target genes. The mRNA of each one of this plurality of GAM2406 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2406 RNA, herein designated GAM RNA, and which when bound by GAM2406 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2406 target proteins.

[33563] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2406 gene, herein designated GAM GENE, on one or more GAM2406 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33564] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2406 correlate with, and may be deduced from, the identity of the target genes which GAM2406 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33565] Nucleotide sequences of the GAM2406 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2406 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2406 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2406 are further described hereinbelow with reference to Table 1.

[33566] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2406 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

- [33567] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2407 (GAM2407) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.
- [33568] GAM2407 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2407 was detected is described hereinabove with reference to Figs. 2-8.
- [33569] GAM2407 gene, herein designated GAM GENE, and GAM2407 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.
- [33570] GAM2407 gene, herein designated GAM GENE, encodes a GAM2407 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2407 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2407 precursor RNA is designated SEQ ID:2384, and is provided hereinbelow with reference to the sequence listing part.
- [33571] GAM2407 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2407 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33572] An enzyme complex designated DICER COMPLEX, dices the GAM2407 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2407 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of GAM2407 RNA is designated SEQ ID:4998, and is provided hereinbelow with reference to the sequence listing part.

[33573] GAM2407 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2407 target RNA, herein designated GAM TARGET RNA. GAM2407 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33574] GAM2407 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2407 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2407 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2407 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2407 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33575] The complementary binding of GAM2407 RNA, herein designated GAM RNA, to target binding sites on GAM2407 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2407 target RNA, herein designated GAM TARGET RNA, into GAM2407 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33576] It is appreciated that GAM2407 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2407 target genes. The mRNA of each one of this plurality of GAM2407 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2407 RNA, herein designated GAM RNA, and which when bound by GAM2407 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2407 target proteins.

[33577] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2407 gene, herein designated GAM GENE, on one or more GAM2407 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33578] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2407 correlate with, and may be deduced from, the identity of the target genes which GAM2407 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33579] Nucleotide sequences of the GAM2407 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2407 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2407 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2407 are further described hereinbelow with reference to Table 1.

[33580] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2407 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[33581] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2408 (GAM2408) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[33582] GAM2408 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2408 was detected is described hereinabove with reference to Figs. 2-8.

[33583] GAM2408 gene, herein designated GAM GENE, and GAM2408 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[33584] GAM2408 gene, herein designated GAM GENE, encodes a GAM2408 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2408 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2408 precursor RNA is designated SEQ ID:2385, and is provided hereinbelow with reference to the sequence listing part.

[33585] GAM2408 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2408 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33586] An enzyme complex designated DICER COMPLEX, dices the GAM2408 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2408 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 76%) nucleotide sequence of GAM2408 RNA is designated SEQ ID:4999, and is provided hereinbelow with reference to the sequence listing part.

[33587] GAM2408 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2408 target RNA, herein designated GAM TARGET RNA. GAM2408 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.



[33588] GAM2408 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2408 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2408 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2408 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2408 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33589] The complementary binding of GAM2408 RNA, herein designated GAM RNA, to target binding sites on GAM2408 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2408 target RNA, herein designated GAM TARGET RNA, into GAM2408 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33590] It is appreciated that GAM2408 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2408 target genes. The

mRNA of each one of this plurality of GAM2408 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2408 RNA, herein designated GAM RNA, and which when bound by GAM2408 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2408 target proteins.

[33591] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2408 gene, herein designated GAM GENE, on one or more GAM2408 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33592] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2408 correlate with, and may be deduced from, the identity of the target genes which GAM2408 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33593] Nucleotide sequences of the GAM2408 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2408 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2408 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2408 are further described hereinbelow with reference to Table 1.

[33594] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2408 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[33595] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2409 (GAM2409) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[33596] GAM2409 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2409 was detected is described hereinabove with reference to Figs. 2-8.

[33597] GAM2409 gene, herein designated GAM GENE, and GAM2409 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[33598] GAM2409 gene, herein designated GAM GENE, encodes a GAM2409 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2409 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2409 precursor RNA is designated SEQ ID:2386, and is provided hereinbelow with reference to the sequence listing part.

[33599] GAM2409 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2409 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33600] An enzyme complex designated DICER COMPLEX, dices the GAM2409 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2409 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 84%) nucleotide sequence of GAM2409 RNA is designated SEQ ID:5000, and is provided hereinbelow with reference to the sequence listing part.

[33601] GAM2409 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2409 target RNA, herein designated GAM TARGET RNA. GAM2409 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33602] GAM2409 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2409 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2409 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2409 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2409 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33603] The complementary binding of GAM2409 RNA, herein designated GAM RNA, to target binding sites on GAM2409 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2409 target RNA, herein designated GAM TARGET RNA, into GAM2409 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33604] It is appreciated that GAM2409 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2409 target genes. The mRNA of each one of this plurality of GAM2409 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2409 RNA, herein designated GAM RNA, and which when bound by GAM2409 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2409 target proteins.

[33605] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2409 gene, herein designated GAM GENE, on one or more GAM2409 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33606] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2409 correlate with, and may be deduced from, the identity of the target

genes which GAM2409 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33607] Nucleotide sequences of the GAM2409 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2409 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2409 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2409 are further described hereinbelow with reference to Table 1.

[33608] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2409 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[33609] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2410 (GAM2410) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[33610] GAM2410 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2410 was detected is described hereinabove with reference to Figs. 2-8.

[33611] GAM2410 gene, herein designated GAM GENE, and GAM2410 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

- [33612] GAM2410 gene, herein designated GAM GENE, encodes a GAM2410 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2410 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2410 precursor RNA is designated SEQ ID:2387, and is provided hereinbelow with reference to the sequence listing part.
- [33613] GAM2410 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2410 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.
- [33614] An enzyme complex designated DICER COMPLEX, dices the GAM2410 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2410 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 84%) nucleotide sequence of GAM2410 RNA is designated SEQ ID:5001, and is provided



hereinbelow with reference to the sequence listing part.

[33615] GAM2410 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2410 target RNA, herein designated GAM TARGET RNA. GAM2410 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33616] GAM2410 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2410 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2410 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2410 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2410 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33617] The complementary binding of GAM2410 RNA, herein designated GAM RNA, to target binding sites on GAM2410 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2410 target RNA, herein designated GAM TARGET RNA, into GAM2410 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33618] It is appreciated that GAM2410 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2410 target genes. The mRNA of each one of this plurality of GAM2410 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2410 RNA, herein designated GAM RNA, and which when bound by GAM2410 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2410 target proteins.

[33619] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2410 gene, herein designated GAM GENE, on one or more GAM2410 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33620] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2410 correlate with, and may be deduced from, the identity of the target genes which GAM2410 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33621] Nucleotide sequences of the GAM2410 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2410 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2410 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2410 are further described hereinbelow with reference to Table 1.

[33622] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2410 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[33623] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2411 (GAM2411) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[33624] GAM2411 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2411 was detected is described hereinabove with reference to Figs. 2-8.

[33625] GAM2411 gene, herein designated GAM GENE, and GAM2411 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[33626] GAM2411 gene, herein designated GAM GENE, encodes a GAM2411 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2411 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2411 precursor RNA is designated SEQ ID:2388, and is provided hereinbelow with reference to the sequence listing part.

[33627] GAM2411 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2411 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33628] An enzyme complex designated DICER COMPLEX, dices the GAM2411 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2411 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of GAM2411 RNA is designated SEQ ID:5002, and is provided hereinbelow with reference to the sequence listing part.

[33629] GAM2411 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2411 target RNA, herein designated GAM TARGET RNA. GAM2411 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33630] GAM2411 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2411 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2411 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2411 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2411 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33631] The complementary binding of GAM2411 RNA, herein designated GAM RNA, to target binding sites on GAM2411 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2411 target RNA, herein designated GAM TARGET RNA, into GAM2411 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33632] It is appreciated that GAM2411 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2411 target genes. The mRNA of each one of this plurality of GAM2411 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2411 RNA, herein designated GAM RNA, and which when bound by GAM2411 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2411 target proteins.

[33633] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2411 gene, herein designated GAM GENE, on one or more GAM2411 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33634] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2411 correlate with, and may be deduced from, the identity of the target genes which GAM2411 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33635] Nucleotide sequences of the GAM2411 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2411 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2411 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2411 are further described hereinbelow with reference to Table 1.

[33636] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2411 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[33637] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2412 (GAM2412) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[33638] GAM2412 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2412 was detected is described hereinabove with reference to Figs. 2-8.

[33639] GAM2412 gene, herein designated GAM GENE, and GAM2412 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[33640] GAM2412 gene, herein designated GAM GENE, encodes a GAM2412 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2412 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2412 precursor RNA is designated SEQ ID:2389, and is provided hereinbelow with reference to the sequence listing part.

[33641] GAM2412 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2412 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.



- [33642] An enzyme complex designated DICER COMPLEX, dices the GAM2412 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2412 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of GAM2412 RNA is designated SEQ ID:5003, and is provided hereinbelow with reference to the sequence listing part.
- [33643] GAM2412 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2412 target RNA, herein designated GAM TARGET RNA. GAM2412 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [33644] GAM2412 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2412 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2412 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2412 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2412 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33645] The complementary binding of GAM2412 RNA, herein designated GAM RNA, to target binding sites on GAM2412 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2412 target RNA, herein designated GAM TARGET RNA, into GAM2412 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33646] It is appreciated that GAM2412 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2412 target genes. The mRNA of each one of this plurality of GAM2412 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2412 RNA, herein designated GAM RNA, and which when bound by GAM2412 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2412 target proteins.

[33647] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2412 gene, herein designated GAM GENE, on one or more GAM2412 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33648] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2412 correlate with, and may be deduced from, the identity of the target genes which GAM2412 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33649] Nucleotide sequences of the GAM2412 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2412 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2412 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2412 are further described hereinbelow with reference to Table 1.

[33650] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2412 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

[33651] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2413 (GAM2413) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[33652] GAM2413 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2413 was detected is described hereinabove with reference to Figs. 2-8.

[33653] GAM2413 gene, herein designated GAM GENE, and GAM2413 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[33654] GAM2413 gene, herein designated GAM GENE, encodes a GAM2413 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2413 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2413 precursor RNA is designated SEQ ID:2390, and is provided hereinbelow with reference to the sequence listing part.

[33655] GAM2413 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2413 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33656] An enzyme complex designated DICER COMPLEX, dices the GAM2413 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2413 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer

together with other necessary proteins. A probable (over 78%) nucleotide sequence of GAM2413 RNA is designated SEQ ID:5005, and is provided hereinbelow with reference to the sequence listing part.

[33657] GAM2413 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2413 target RNA, herein designated GAM TARGET RNA. GAM2413 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33658] GAM2413 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2413 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2413 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2413 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2413 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or

in both 3UTR and 5UTR regions.

[33659] The complementary binding of GAM2413 RNA, herein designated GAM RNA, to target binding sites on GAM2413 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2413 target RNA, herein designated GAM TARGET RNA, into GAM2413 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33660] It is appreciated that GAM2413 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2413 target genes. The mRNA of each one of this plurality of GAM2413 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2413 RNA, herein designated GAM RNA, and which when bound by GAM2413 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2413 target proteins.

[33661] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2413 gene, herein designated GAM GENE, on one or more GAM2413 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes

are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33662] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2413 correlate with, and may be deduced from, the identity of the target genes which GAM2413 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33663] Nucleotide sequences of the GAM2413 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2413 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2413 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2413 are further described hereinbelow with reference to Table 1.

[33664] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2413 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[33665] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2414 (GAM2414) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.



- [33666] GAM2414 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2414 was detected is described hereinabove with reference to Figs. 2-8.
- [33667] GAM2414 gene, herein designated GAM GENE, and GAM2414 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.
- [33668] GAM2414 gene, herein designated GAM GENE, encodes a GAM2414 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2414 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2414 precursor RNA is designated SEQ ID:2391, and is provided hereinbelow with reference to the sequence listing part.
- [33669] GAM2414 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2414 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.
- [33670] An enzyme complex designated DICER COMPLEX, dices the GAM2414 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2414 RNA, herein designated GAM RNA, a single stranded

~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2414 RNA is designated SEQ ID:5004, and is provided hereinbelow with reference to the sequence listing part.

[33671] GAM2414 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2414 target RNA, herein designated GAM TARGET RNA. GAM2414 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33672] GAM2414 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2414 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2414 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2414 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2414 target RNA, herein designated GAM

TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33673] The complementary binding of GAM2414 RNA, herein designated GAM RNA, to target binding sites on GAM2414 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2414 target RNA, herein designated GAM TARGET RNA, into GAM2414 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33674] It is appreciated that GAM2414 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2414 target genes. The mRNA of each one of this plurality of GAM2414 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2414 RNA, herein designated GAM RNA, and which when bound by GAM2414 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2414 target proteins.

[33675] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2414 gene, herein designated GAM GENE, on one or more GAM2414 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with

reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33676] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2414 correlate with, and may be deduced from, the identity of the target genes which GAM2414 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33677] Nucleotide sequences of the GAM2414 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2414 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2414 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2414 are further described hereinbelow with reference to Table 1.

[33678] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2414 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[33679] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as

Genomic Address Messenger 2415 (GAM2415) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

- [33680] GAM2415 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2415 was detected is described hereinabove with reference to Figs. 2-8.
- [33681] GAM2415 gene, herein designated GAM GENE, and GAM2415 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.
- [33682] GAM2415 gene, herein designated GAM GENE, encodes a GAM2415 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2415 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2415 precursor RNA is designated SEQ ID:2392, and is provided hereinbelow with reference to the sequence listing part.
- [33683] GAM2415 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2415 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

- [33684] An enzyme complex designated DICER COMPLEX, dices the GAM2415 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2415 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 87%) nucleotide sequence of GAM2415 RNA is designated SEQ ID:5006, and is provided hereinbelow with reference to the sequence listing part.
- [33685] GAM2415 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2415 target RNA, herein designated GAM TARGET RNA. GAM2415 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [33686] GAM2415 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2415 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2415 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2415 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2415 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33687] The complementary binding of GAM2415 RNA, herein designated GAM RNA, to target binding sites on GAM2415 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2415 target RNA, herein designated GAM TARGET RNA, into GAM2415 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33688] It is appreciated that GAM2415 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2415 target genes. The mRNA of each one of this plurality of GAM2415 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2415 RNA, herein designated GAM RNA, and which when bound by GAM2415 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2415 target proteins.

[33689] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2415 gene, herein designated GAM GENE, on one or more GAM2415 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33690] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2415 correlate with, and may be deduced from, the identity of the target genes which GAM2415 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33691] Nucleotide sequences of the GAM2415 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2415 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2415 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2415 are further described hereinbelow with reference to Table 1.

[33692] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2415 RNA, herein designated GAM RNA, are described hereinbelow



with reference to Table 2.

[33693] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2416 (GAM2416) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[33694] GAM2416 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2416 was detected is described hereinabove with reference to Figs. 2-8.

[33695] GAM2416 gene, herein designated GAM GENE, and GAM2416 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[33696] GAM2416 gene, herein designated GAM GENE, encodes a GAM2416 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2416 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2416 precursor RNA is designated SEQ ID:2393, and is provided hereinbelow with reference to the sequence listing part.

[33697] GAM2416 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2416 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33698] An enzyme complex designated DICER COMPLEX, dices the GAM2416 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2416 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 86%) nucleotide sequence of GAM2416 RNA is designated SEQ ID:5007, and is provided hereinbelow with reference to the sequence listing part.

[33699] GAM2416 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2416 target RNA, herein designated GAM TARGET RNA. GAM2416 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33700] GAM2416 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2416 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2416 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2416 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2416 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33701] The complementary binding of GAM2416 RNA, herein designated GAM RNA, to target binding sites on GAM2416 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2416 target RNA, herein designated GAM TARGET RNA, into GAM2416 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33702] It is appreciated that GAM2416 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2416 target genes. The mRNA of each one of this plurality of GAM2416 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2416 RNA, herein designated GAM RNA, and which when bound by GAM2416 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2416 target proteins.

[33703] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2416 gene, herein designated GAM GENE, on one or more GAM2416 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33704] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2416 correlate with, and may be deduced from, the identity of the target genes which GAM2416 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33705] Nucleotide sequences of the GAM2416 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2416 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2416 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2416 are further described hereinbelow with reference to Table 1.

[33706] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2416 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[33707] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2417 (GAM2417) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[33708] GAM2417 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2417 was detected is described hereinabove with reference to Figs. 2-8.

[33709] GAM2417 gene, herein designated GAM GENE, and GAM2417 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[33710] GAM2417 gene, herein designated GAM GENE, encodes a GAM2417 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2417 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2417 precursor RNA is designated SEQ ID:2394, and is provided hereinbelow with reference to the sequence listing part.

[33711] GAM2417 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2417 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33712] An enzyme complex designated DICER COMPLEX, dices the GAM2417 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2417 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2417 RNA is designated SEQ ID:5008, and is provided hereinbelow with reference to the sequence listing part.

[33713] GAM2417 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2417 target RNA, herein designated GAM TARGET RNA. GAM2417 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33714] GAM2417 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2417 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2417 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2417 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2417 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33715] The complementary binding of GAM2417 RNA, herein designated GAM RNA, to target binding sites on GAM2417 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2417 target RNA, herein designated GAM TARGET RNA, into GAM2417 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33716] It is appreciated that GAM2417 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2417 target genes. The

mRNA of each one of this plurality of GAM2417 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2417 RNA, herein designated GAM RNA, and which when bound by GAM2417 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2417 target proteins.

[33717] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2417 gene, herein designated GAM GENE, on one or more GAM2417 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33718] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2417 correlate with, and may be deduced from, the identity of the target genes which GAM2417 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33719] Nucleotide sequences of the GAM2417 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2417 RNA, herein



designated GAM RNA, and a schematic representation of the secondary folding of GAM2417 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2417 are further described hereinbelow with reference to Table 1.

[33720] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2417 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[33721] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2418 (GAM2418) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[33722] GAM2418 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2418 was detected is described hereinabove with reference to Figs. 2-8.

[33723] GAM2418 gene, herein designated GAM GENE, and GAM2418 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[33724] GAM2418 gene, herein designated GAM GENE, encodes a GAM2418 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2418 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2418 precursor RNA is designated SEQ ID:2395, and is provided hereinbelow with reference to the sequence listing part.

[33725] GAM2418 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2418 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33726] An enzyme complex designated DICER COMPLEX, dices the GAM2418 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2418 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of GAM2418 RNA is designated SEQ ID:5009, and is provided hereinbelow with reference to the sequence listing part.

[33727] GAM2418 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2418 target RNA, herein designated GAM TARGET RNA. GAM2418 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33728] GAM2418 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2418 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2418 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2418 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2418 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33729] The complementary binding of GAM2418 RNA, herein designated GAM RNA, to target binding sites on GAM2418 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2418 target RNA, herein designated GAM TARGET RNA, into GAM2418 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33730] It is appreciated that GAM2418 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2418 target genes. The mRNA of each one of this plurality of GAM2418 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2418 RNA, herein designated GAM RNA, and which when bound by GAM2418 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2418 target proteins.

[33731] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2418 gene, herein designated GAM GENE, on one or more GAM2418 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33732] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2418 correlate with, and may be deduced from, the identity of the target

genes which GAM2418 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33733] Nucleotide sequences of the GAM2418 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2418 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2418 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2418 are further described hereinbelow with reference to Table 1.

[33734] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2418 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[33735] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2419 (GAM2419) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[33736] GAM2419 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2419 was detected is described hereinabove with reference to Figs. 2-8.

[33737] GAM2419 gene, herein designated GAM GENE, and GAM2419 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

[33738] GAM2419 gene, herein designated GAM GENE, encodes a GAM2419 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2419 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2419 precursor RNA is designated SEQ ID:2396, and is provided hereinbelow with reference to the sequence listing part.

[33739] GAM2419 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2419 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33740] An enzyme complex designated DICER COMPLEX, dices the GAM2419 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2419 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2419 RNA is designated SEQ ID:5010, and is provided

hereinbelow with reference to the sequence listing part.

[33741] GAM2419 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2419 target RNA, herein designated GAM TARGET RNA. GAM2419 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33742] GAM2419 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2419 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2419 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2419 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2419 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33743] The complementary binding of GAM2419 RNA, herein designated GAM RNA, to target binding sites on GAM2419 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2419 target RNA, herein designated GAM TARGET RNA, into GAM2419 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33744] It is appreciated that GAM2419 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2419 target genes. The mRNA of each one of this plurality of GAM2419 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2419 RNA, herein designated GAM RNA, and which when bound by GAM2419 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2419 target proteins.

[33745] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2419 gene, herein designated GAM GENE, on one or more GAM2419 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding



sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33746] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2419 correlate with, and may be deduced from, the identity of the target genes which GAM2419 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33747] Nucleotide sequences of the GAM2419 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2419 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2419 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2419 are further described hereinbelow with reference to Table 1.

[33748] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2419 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[33749] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2420 (GAM2420) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[33750] GAM2420 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2420 was detected is described hereinabove with reference to Figs. 2-8.

[33751] GAM2420 gene, herein designated GAM GENE, and GAM2420 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[33752] GAM2420 gene, herein designated GAM GENE, encodes a GAM2420 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2420 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2420 precursor RNA is designated SEQ ID:2397, and is provided hereinbelow with reference to the sequence listing part.

[33753] GAM2420 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2420 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33754] An enzyme complex designated DICER COMPLEX, dices the GAM2420 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2420 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 25%) nucleotide sequence of GAM2420 RNA is designated SEQ ID:5011, and is provided hereinbelow with reference to the sequence listing part.

[33755] GAM2420 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2420 target RNA, herein designated GAM TARGET RNA. GAM2420 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33756] GAM2420 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2420 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2420 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2420 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2420 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33757] The complementary binding of GAM2420 RNA, herein designated GAM RNA, to target binding sites on GAM2420 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2420 target RNA, herein designated GAM TARGET RNA, into GAM2420 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33758] It is appreciated that GAM2420 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2420 target genes. The mRNA of each one of this plurality of GAM2420 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2420 RNA, herein designated GAM RNA, and which when bound by GAM2420 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2420 target proteins.

[33759] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2420 gene, herein designated GAM GENE, on one or more GAM2420 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33760] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2420 correlate with, and may be deduced from, the identity of the target genes which GAM2420 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33761] Nucleotide sequences of the GAM2420 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2420 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2420 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2420 are further described hereinbelow with reference to Table 1.

[33762] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2420 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[33763] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2421 (GAM2421) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[33764] GAM2421 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2421 was detected is described hereinabove with reference to Figs. 2-8.

[33765] GAM2421 gene, herein designated GAM GENE, and GAM2421 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[33766] GAM2421 gene, herein designated GAM GENE, encodes a GAM2421 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2421 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2421 precursor RNA is designated SEQ ID:2398, and is provided hereinbelow with reference to the sequence listing part.

[33767] GAM2421 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2421 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

- [33768] An enzyme complex designated DICER COMPLEX, dices the GAM2421 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2421 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM2421 RNA is designated SEQ ID:5012, and is provided hereinbelow with reference to the sequence listing part.
- [33769] GAM2421 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2421 target RNA, herein designated GAM TARGET RNA. GAM2421 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [33770] GAM2421 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2421 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2421 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2421 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2421 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33771] The complementary binding of GAM2421 RNA, herein designated GAM RNA, to target binding sites on GAM2421 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2421 target RNA, herein designated GAM TARGET RNA, into GAM2421 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33772] It is appreciated that GAM2421 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2421 target genes. The mRNA of each one of this plurality of GAM2421 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2421 RNA, herein designated GAM RNA, and which when bound by GAM2421 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2421 target proteins.

[33773] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition



exerted by GAM2421 gene, herein designated GAM GENE, on one or more GAM2421 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33774] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2421 correlate with, and may be deduced from, the identity of the target genes which GAM2421 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33775] Nucleotide sequences of the GAM2421 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2421 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2421 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2421 are further described hereinbelow with reference to Table 1.

[33776] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2421 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

[33777] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2422 (GAM2422) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[33778] GAM2422 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2422 was detected is described hereinabove with reference to Figs. 2-8.

[33779] GAM2422 gene, herein designated GAM GENE, and GAM2422 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[33780] GAM2422 gene, herein designated GAM GENE, encodes a GAM2422 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2422 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2422 precursor RNA is designated SEQ ID:2399, and is provided hereinbelow with reference to the sequence listing part.

[33781] GAM2422 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2422 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33782] An enzyme complex designated DICER COMPLEX, dices the GAM2422 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2422 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of GAM2422 RNA is designated SEQ ID:5014, and is provided hereinbelow with reference to the sequence listing part.

[33783] GAM2422 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2422 target RNA, herein designated GAM TARGET RNA. GAM2422 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33784] GAM2422 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2422 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2422 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2422 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2422 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33785] The complementary binding of GAM2422 RNA, herein designated GAM RNA, to target binding sites on GAM2422 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2422 target RNA, herein designated GAM TARGET RNA, into GAM2422 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33786] It is appreciated that GAM2422 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2422 target genes. The mRNA of each one of this plurality of GAM2422 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2422 RNA, herein designated GAM RNA, and which when bound by GAM2422 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2422 target proteins.

[33787] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2422 gene, herein designated GAM GENE, on one or more GAM2422 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33788] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2422 correlate with, and may be deduced from, the identity of the target genes which GAM2422 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33789] Nucleotide sequences of the GAM2422 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2422 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2422 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2422 are further described hereinbelow with reference to Table 1.

[33790] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2422 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[33791] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2423 (GAM2423) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[33792] GAM2423 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2423 was detected is described hereinabove with reference to Figs. 2-8.

[33793] GAM2423 gene, herein designated GAM GENE, and GAM2423 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[33794] GAM2423 gene, herein designated GAM GENE, encodes a GAM2423 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2423 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2423 precursor RNA is designated SEQ ID:2400, and is provided hereinbelow with reference to the sequence listing part.

[33795] GAM2423 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2423 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33796] An enzyme complex designated DICER COMPLEX, dices the GAM2423 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2423 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2423 RNA is designated SEQ ID:5013, and is provided hereinbelow with reference to the sequence listing part.

[33797] GAM2423 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2423 target RNA, herein designated GAM TARGET RNA. GAM2423 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33798] GAM2423 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2423 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2423 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2423 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2423 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33799] The complementary binding of GAM2423 RNA, herein designated GAM RNA, to target binding sites on GAM2423 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2423 target RNA, herein designated GAM TARGET RNA, into GAM2423 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33800] It is appreciated that GAM2423 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2423 target genes. The



mRNA of each one of this plurality of GAM2423 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2423 RNA, herein designated GAM RNA, and which when bound by GAM2423 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2423 target proteins.

[33801] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2423 gene, herein designated GAM GENE, on one or more GAM2423 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33802] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2423 correlate with, and may be deduced from, the identity of the target genes which GAM2423 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33803] Nucleotide sequences of the GAM2423 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2423 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2423 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2423 are further described hereinbelow with reference to Table 1.

[33804] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2423 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[33805]

[33806] Fig. 8 further provides a conceptual description of a novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2424 (GAM2424) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[33807] GAM2424 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2424 was detected is described hereinabove with reference to Figs. 2-8.

[33808] GAM2424 gene, herein designated GAM GENE, and GAM2424 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[33809] GAM2424 gene, herein designated GAM GENE, encodes a GAM2424 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other

miRNA genes, and unlike most ordinary genes, GAM2424 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2424 precursor RNA is designated SEQ ID:2401, and is provided hereinbelow with reference to the sequence listing part.

[33810] GAM2424 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2424 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33811] An enzyme complex designated DICER COMPLEX, dices the GAM2424 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2424 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 91%) nucleotide sequence of GAM2424 RNA is designated SEQ ID:5015, and is provided hereinbelow with reference to the sequence listing part.

[33812] GAM2424 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2424 target RNA, herein designated

GAM TARGET RNA. GAM2424 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33813] GAM2424 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2424 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2424 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2424 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2424 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33814] The complementary binding of GAM2424 RNA, herein designated GAM RNA, to target binding sites on GAM2424 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2424 target RNA, herein

designated GAM TARGET RNA, into GAM2424 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33815] It is appreciated that GAM2424 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2424 target genes. The mRNA of each one of this plurality of GAM2424 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2424 RNA, herein designated GAM RNA, and which when bound by GAM2424 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2424 target proteins.

[33816] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2424 gene, herein designated GAM GENE, on one or more GAM2424 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33817] It is yet further appreciated that specific functions, and accordingly utilities, of

GAM2424 correlate with, and may be deduced from, the identity of the target genes which GAM2424 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33818] Nucleotide sequences of the GAM2424 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2424 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2424 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2424 are further described hereinbelow with reference to Table 1.

[33819] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2424 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[33820] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2425 (GAM2425) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[33821] GAM2425 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2425 was detected is described hereinabove with reference to Figs. 2-8.

[33822] GAM2425 gene, herein designated GAM GENE, and GAM2425 target gene,

herein designated GAM TARGET GENE, are human genes contained in the human genome.

[33823] GAM2425 gene, herein designated GAM GENE, encodes a GAM2425 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2425 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2425 precursor RNA is designated SEQ ID:2402, and is provided hereinbelow with reference to the sequence listing part.

[33824] GAM2425 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2425 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33825] An enzyme complex designated DICER COMPLEX, dices the GAM2425 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2425 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide

sequence of GAM2425 RNA is designated SEQ ID:5016, and is provided hereinbelow with reference to the sequence listing part.

[33826] GAM2425 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2425 target RNA, herein designated GAM TARGET RNA. GAM2425 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33827] GAM2425 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2425 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2425 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2425 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2425 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.



[33828] The complementary binding of GAM2425 RNA, herein designated GAM RNA, to target binding sites on GAM2425 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2425 target RNA, herein designated GAM TARGET RNA, into GAM2425 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33829] It is appreciated that GAM2425 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2425 target genes. The mRNA of each one of this plurality of GAM2425 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2425 RNA, herein designated GAM RNA, and which when bound by GAM2425 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2425 target proteins.

[33830] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2425 gene, herein designated GAM GENE, on one or more GAM2425 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33831] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2425 correlate with, and may be deduced from, the identity of the target genes which GAM2425 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33832] Nucleotide sequences of the GAM2425 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2425 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2425 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2425 are further described hereinbelow with reference to Table 1.

[33833] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2425 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[33834] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2426 (GAM2426) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[33835] GAM2426 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2426 was detected is described hereinabove with reference to Figs. 2-8.

[33836] GAM2426 gene, herein designated GAM GENE, and GAM2426 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[33837] GAM2426 gene, herein designated GAM GENE, encodes a GAM2426 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2426 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2426 precursor RNA is designated SEQ ID:2403, and is provided hereinbelow with reference to the sequence listing part.

[33838] GAM2426 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2426 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33839] An enzyme complex designated DICER COMPLEX, dices the GAM2426 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2426 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 93%) nucleotide sequence of GAM2426 RNA is designated SEQ ID:5017, and is provided hereinbelow with reference to the sequence listing part.

[33840] GAM2426 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2426 target RNA, herein designated GAM TARGET RNA. GAM2426 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33841] GAM2426 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2426 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2426 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2426 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2426 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33842] The complementary binding of GAM2426 RNA, herein designated GAM RNA, to target binding sites on GAM2426 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2426 target RNA, herein designated GAM TARGET RNA, into GAM2426 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33843] It is appreciated that GAM2426 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2426 target genes. The mRNA of each one of this plurality of GAM2426 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2426 RNA, herein designated GAM RNA, and which when bound by GAM2426 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2426 target proteins.

[33844] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2426 gene, herein designated GAM GENE, on one or more GAM2426 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33845] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2426 correlate with, and may be deduced from, the identity of the target genes which GAM2426 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33846] Nucleotide sequences of the GAM2426 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2426 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2426 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2426 are further described hereinbelow with reference to Table 1.

[33847] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2426 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[33848] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2427 (GAM2427) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[33849] GAM2427 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2427 was detected is described hereinabove with reference to Figs. 2-8.

[33850] GAM2427 gene, herein designated GAM GENE, and GAM2427 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[33851] GAM2427 gene, herein designated GAM GENE, encodes a GAM2427 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2427 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2427 precursor RNA is designated SEQ ID:2404, and is provided hereinbelow with reference to the sequence listing part.

[33852] GAM2427 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2427 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

- [33853] An enzyme complex designated DICER COMPLEX, dices the GAM2427 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2427 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of GAM2427 RNA is designated SEQ ID:5018, and is provided hereinbelow with reference to the sequence listing part.
- [33854] GAM2427 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2427 target RNA, herein designated GAM TARGET RNA. GAM2427 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [33855] GAM2427 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2427 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2427 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an



illustration only, and is not meant to be limiting GAM2427 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2427 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33856] The complementary binding of GAM2427 RNA, herein designated GAM RNA, to target binding sites on GAM2427 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2427 target RNA, herein designated GAM TARGET RNA, into GAM2427 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33857] It is appreciated that GAM2427 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2427 target genes. The mRNA of each one of this plurality of GAM2427 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2427 RNA, herein designated GAM RNA, and which when bound by GAM2427 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2427 target proteins.

[33858] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2427 gene, herein designated GAM GENE, on one or more GAM2427 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33859] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2427 correlate with, and may be deduced from, the identity of the target genes which GAM2427 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33860] Nucleotide sequences of the GAM2427 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2427 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2427 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2427 are further described hereinbelow with reference to Table 1.

[33861] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2427 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

[33862] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2428 (GAM2428) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[33863] GAM2428 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2428 was detected is described hereinabove with reference to Figs. 2-8.

[33864] GAM2428 gene, herein designated GAM GENE, and GAM2428 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[33865] GAM2428 gene, herein designated GAM GENE, encodes a GAM2428 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2428 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2428 precursor RNA is designated SEQ ID:2405, and is provided hereinbelow with reference to the sequence listing part.

[33866] GAM2428 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2428 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33867] An enzyme complex designated DICER COMPLEX, dices the GAM2428 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2428 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 88%) nucleotide sequence of GAM2428 RNA is designated SEQ ID:5019, and is provided hereinbelow with reference to the sequence listing part.

[33868] GAM2428 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2428 target RNA, herein designated GAM TARGET RNA. GAM2428 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33869] GAM2428 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2428 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2428 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2428 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2428 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33870] The complementary binding of GAM2428 RNA, herein designated GAM RNA, to target binding sites on GAM2428 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2428 target RNA, herein designated GAM TARGET RNA, into GAM2428 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33871] It is appreciated that GAM2428 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2428 target genes. The mRNA of each one of this plurality of GAM2428 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2428 RNA, herein designated GAM RNA, and which when bound by GAM2428 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2428 target proteins.

[33872] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2428 gene, herein designated GAM GENE, on one or more GAM2428 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33873] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2428 correlate with, and may be deduced from, the identity of the target genes which GAM2428 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33874] Nucleotide sequences of the GAM2428 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2428 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2428 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2428 are further described hereinbelow with reference to Table 1.

[33875] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2428 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[33876] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2429 (GAM2429) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[33877] GAM2429 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2429 was detected is described hereinabove with reference to Figs. 2-8.

[33878] GAM2429 gene, herein designated GAM GENE, and GAM2429 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[33879] GAM2429 gene, herein designated GAM GENE, encodes a GAM2429 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2429 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2429 precursor RNA is designated SEQ ID:2406, and is provided hereinbelow with reference to the sequence listing part.

[33880] GAM2429 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2429 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33881] An enzyme complex designated DICER COMPLEX, dices the GAM2429 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2429 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 86%) nucleotide sequence of GAM2429 RNA is designated SEQ ID:5020, and is provided hereinbelow with reference to the sequence listing part.

[33882] GAM2429 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2429 target RNA, herein designated GAM TARGET RNA. GAM2429 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.



[33883] GAM2429 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2429 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2429 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2429 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2429 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33884] The complementary binding of GAM2429 RNA, herein designated GAM RNA, to target binding sites on GAM2429 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2429 target RNA, herein designated GAM TARGET RNA, into GAM2429 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33885] It is appreciated that GAM2429 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2429 target genes. The

mRNA of each one of this plurality of GAM2429 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2429 RNA, herein designated GAM RNA, and which when bound by GAM2429 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2429 target proteins.

[33886] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2429 gene, herein designated GAM GENE, on one or more GAM2429 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33887] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2429 correlate with, and may be deduced from, the identity of the target genes which GAM2429 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33888] Nucleotide sequences of the GAM2429 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2429 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2429 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2429 are further described hereinbelow with reference to Table 1.

[33889] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2429 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[33890] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2430 (GAM2430) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[33891] GAM2430 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2430 was detected is described hereinabove with reference to Figs. 2-8.

[33892] GAM2430 gene, herein designated GAM GENE, and GAM2430 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[33893] GAM2430 gene, herein designated GAM GENE, encodes a GAM2430 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2430 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2430 precursor RNA is designated SEQ ID:2407, and is provided hereinbelow with reference to the sequence listing part.

[33894] GAM2430 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2430 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33895] An enzyme complex designated DICER COMPLEX, dices the GAM2430 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2430 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2430 RNA is designated SEQ ID:5021, and is provided hereinbelow with reference to the sequence listing part.

[33896] GAM2430 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2430 target RNA, herein designated GAM TARGET RNA. GAM2430 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33897] GAM2430 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2430 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2430 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2430 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2430 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33898] The complementary binding of GAM2430 RNA, herein designated GAM RNA, to target binding sites on GAM2430 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2430 target RNA, herein designated GAM TARGET RNA, into GAM2430 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33899] It is appreciated that GAM2430 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2430 target genes. The mRNA of each one of this plurality of GAM2430 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2430 RNA, herein designated GAM RNA, and which when bound by GAM2430 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2430 target proteins.

[33900] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2430 gene, herein designated GAM GENE, on one or more GAM2430 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33901] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2430 correlate with, and may be deduced from, the identity of the target

genes which GAM2430 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33902] Nucleotide sequences of the GAM2430 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2430 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2430 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2430 are further described hereinbelow with reference to Table 1.

[33903] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2430 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[33904] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2431 (GAM2431) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[33905] GAM2431 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2431 was detected is described hereinabove with reference to Figs. 2-8.

[33906] GAM2431 gene, herein designated GAM GENE, and GAM2431 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

[33907] GAM2431 gene, herein designated GAM GENE, encodes a GAM2431 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2431 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2431 precursor RNA is designated SEQ ID:2408, and is provided hereinbelow with reference to the sequence listing part.

[33908] GAM2431 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2431 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33909] An enzyme complex designated DICER COMPLEX, dices the GAM2431 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2431 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of GAM2431 RNA is designated SEQ ID:5022, and is provided



hereinbelow with reference to the sequence listing part.

[33910] GAM2431 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2431 target RNA, herein designated GAM TARGET RNA. GAM2431 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33911] GAM2431 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2431 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2431 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2431 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2431 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33912] The complementary binding of GAM2431 RNA, herein designated GAM RNA, to target binding sites on GAM2431 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2431 target RNA, herein designated GAM TARGET RNA, into GAM2431 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33913] It is appreciated that GAM2431 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2431 target genes. The mRNA of each one of this plurality of GAM2431 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2431 RNA, herein designated GAM RNA, and which when bound by GAM2431 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2431 target proteins.

[33914] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2431 gene, herein designated GAM GENE, on one or more GAM2431 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33915] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2431 correlate with, and may be deduced from, the identity of the target genes which GAM2431 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33916] Nucleotide sequences of the GAM2431 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2431 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2431 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2431 are further described hereinbelow with reference to Table 1.

[33917] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2431 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[33918] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2432 (GAM2432) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[33919] GAM2432 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2432 was detected is described hereinabove with reference to Figs. 2-8.

[33920] GAM2432 gene, herein designated GAM GENE, and GAM2432 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[33921] GAM2432 gene, herein designated GAM GENE, encodes a GAM2432 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2432 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2432 precursor RNA is designated SEQ ID:2409, and is provided hereinbelow with reference to the sequence listing part.

[33922] GAM2432 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2432 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33923] An enzyme complex designated DICER COMPLEX, dices the GAM2432 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2432 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2432 RNA is designated SEQ ID:5023, and is provided hereinbelow with reference to the sequence listing part.

[33924] GAM2432 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2432 target RNA, herein designated GAM TARGET RNA. GAM2432 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33925] GAM2432 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2432 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2432 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2432 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2432 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33926] The complementary binding of GAM2432 RNA, herein designated GAM RNA, to target binding sites on GAM2432 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2432 target RNA, herein designated GAM TARGET RNA, into GAM2432 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33927] It is appreciated that GAM2432 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2432 target genes. The mRNA of each one of this plurality of GAM2432 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2432 RNA, herein designated GAM RNA, and which when bound by GAM2432 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2432 target proteins.

[33928] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2432 gene, herein designated GAM GENE, on one or more GAM2432 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33929] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2432 correlate with, and may be deduced from, the identity of the target genes which GAM2432 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33930] Nucleotide sequences of the GAM2432 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2432 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2432 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2432 are further described hereinbelow with reference to Table 1.

[33931] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2432 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[33932] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2433 (GAM2433) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[33933] GAM2433 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2433 was detected is described hereinabove with reference to Figs. 2-8.

[33934] GAM2433 gene, herein designated GAM GENE, and GAM2433 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[33935] GAM2433 gene, herein designated GAM GENE, encodes a GAM2433 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2433 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2433 precursor RNA is designated SEQ ID:2410, and is provided hereinbelow with reference to the sequence listing part.

[33936] GAM2433 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2433 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.



- [33937] An enzyme complex designated DICER COMPLEX, dices the GAM2433 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2433 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 87%) nucleotide sequence of GAM2433 RNA is designated SEQ ID:5024, and is provided hereinbelow with reference to the sequence listing part.
- [33938] GAM2433 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2433 target RNA, herein designated GAM TARGET RNA. GAM2433 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [33939] GAM2433 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2433 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2433 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2433 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2433 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33940] The complementary binding of GAM2433 RNA, herein designated GAM RNA, to target binding sites on GAM2433 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2433 target RNA, herein designated GAM TARGET RNA, into GAM2433 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33941] It is appreciated that GAM2433 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2433 target genes. The mRNA of each one of this plurality of GAM2433 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2433 RNA, herein designated GAM RNA, and which when bound by GAM2433 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2433 target proteins.

[33942] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2433 gene, herein designated GAM GENE, on one or more GAM2433 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33943] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2433 correlate with, and may be deduced from, the identity of the target genes which GAM2433 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33944] Nucleotide sequences of the GAM2433 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2433 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2433 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2433 are further described hereinbelow with reference to Table 1.

[33945] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2433 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

- [33946] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2434 (GAM2434) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.
- [33947] GAM2434 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2434 was detected is described hereinabove with reference to Figs. 2-8.
- [33948] GAM2434 gene, herein designated GAM GENE, and GAM2434 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.
- [33949] GAM2434 gene, herein designated GAM GENE, encodes a GAM2434 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2434 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2434 precursor RNA is designated SEQ ID:2411, and is provided hereinbelow with reference to the sequence listing part.
- [33950] GAM2434 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2434 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33951] An enzyme complex designated DICER COMPLEX, dices the GAM2434 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2434 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 85%) nucleotide sequence of GAM2434 RNA is designated SEQ ID:5025, and is provided hereinbelow with reference to the sequence listing part.

[33952] GAM2434 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2434 target RNA, herein designated GAM TARGET RNA. GAM2434 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33953] GAM2434 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2434 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2434 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2434 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2434 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33954] The complementary binding of GAM2434 RNA, herein designated GAM RNA, to target binding sites on GAM2434 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2434 target RNA, herein designated GAM TARGET RNA, into GAM2434 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33955] It is appreciated that GAM2434 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2434 target genes. The mRNA of each one of this plurality of GAM2434 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2434 RNA, herein designated GAM RNA, and which when bound by GAM2434 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2434 target proteins.

[33956] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2434 gene, herein designated GAM GENE, on one or more GAM2434 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33957] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2434 correlate with, and may be deduced from, the identity of the target genes which GAM2434 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33958] Nucleotide sequences of the GAM2434 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2434 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2434 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2434 are further described hereinbelow with reference to Table 1.

- [33959] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2434 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.
- [33960] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2435 (GAM2435) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.
- [33961] GAM2435 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2435 was detected is described hereinabove with reference to Figs. 2-8.
- [33962] GAM2435 gene, herein designated GAM GENE, and GAM2435 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.
- [33963] GAM2435 gene, herein designated GAM GENE, encodes a GAM2435 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2435 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2435 precursor RNA is designated SEQ ID:2412, and is provided hereinbelow with reference to the sequence listing part.



[33964] GAM2435 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2435 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33965] An enzyme complex designated DICER COMPLEX, dices the GAM2435 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2435 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 84%) nucleotide sequence of GAM2435 RNA is designated SEQ ID:5026, and is provided hereinbelow with reference to the sequence listing part.

[33966] GAM2435 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2435 target RNA, herein designated GAM TARGET RNA. GAM2435 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33967] GAM2435 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2435 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2435 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2435 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2435 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33968] The complementary binding of GAM2435 RNA, herein designated GAM RNA, to target binding sites on GAM2435 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2435 target RNA, herein designated GAM TARGET RNA, into GAM2435 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33969] It is appreciated that GAM2435 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2435 target genes. The

mRNA of each one of this plurality of GAM2435 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2435 RNA, herein designated GAM RNA, and which when bound by GAM2435 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2435 target proteins.

[33970] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2435 gene, herein designated GAM GENE, on one or more GAM2435 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33971] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2435 correlate with, and may be deduced from, the identity of the target genes which GAM2435 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33972] Nucleotide sequences of the GAM2435 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2435 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2435 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2435 are further described hereinbelow with reference to Table 1.

[33973] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2435 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[33974] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2436 (GAM2436) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[33975] GAM2436 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2436 was detected is described hereinabove with reference to Figs. 2-8.

[33976] GAM2436 gene, herein designated GAM GENE, and GAM2436 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[33977] GAM2436 gene, herein designated GAM GENE, encodes a GAM2436 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2436 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2436 precursor RNA is designated SEQ ID:2413, and is provided hereinbelow with reference to the sequence listing part.

[33978] GAM2436 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2436 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33979] An enzyme complex designated DICER COMPLEX, dices the GAM2436 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2436 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 84%) nucleotide sequence of GAM2436 RNA is designated SEQ ID:5027, and is provided hereinbelow with reference to the sequence listing part.

[33980] GAM2436 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2436 target RNA, herein designated GAM TARGET RNA. GAM2436 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33981] GAM2436 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2436 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2436 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2436 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2436 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33982] The complementary binding of GAM2436 RNA, herein designated GAM RNA, to target binding sites on GAM2436 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2436 target RNA, herein designated GAM TARGET RNA, into GAM2436 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33983] It is appreciated that GAM2436 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2436 target genes. The mRNA of each one of this plurality of GAM2436 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2436 RNA, herein designated GAM RNA, and which when bound by GAM2436 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2436 target proteins.

[33984] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2436 gene, herein designated GAM GENE, on one or more GAM2436 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33985] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2436 correlate with, and may be deduced from, the identity of the target

genes which GAM2436 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[33986] Nucleotide sequences of the GAM2436 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2436 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2436 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2436 are further described hereinbelow with reference to Table 1.

[33987] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2436 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[33988] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2437 (GAM2437) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[33989] GAM2437 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2437 was detected is described hereinabove with reference to Figs. 2-8.

[33990] GAM2437 gene, herein designated GAM GENE, and GAM2437 target gene, herein designated GAM TARGET GENE, are human genes contained in the



human genome.

[33991] GAM2437 gene, herein designated GAM GENE, encodes a GAM2437 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2437 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2437 precursor RNA is designated SEQ ID:2414, and is provided hereinbelow with reference to the sequence listing part.

[33992] GAM2437 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2437 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[33993] An enzyme complex designated DICER COMPLEX, dices the GAM2437 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2437 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2437 RNA is designated SEQ ID:5028, and is provided

hereinbelow with reference to the sequence listing part.

[33994] GAM2437 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2437 target RNA, herein designated GAM TARGET RNA. GAM2437 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[33995] GAM2437 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2437 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2437 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2437 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2437 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[33996] The complementary binding of GAM2437 RNA, herein designated GAM RNA, to target binding sites on GAM2437 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2437 target RNA, herein designated GAM TARGET RNA, into GAM2437 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[33997] It is appreciated that GAM2437 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2437 target genes. The mRNA of each one of this plurality of GAM2437 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2437 RNA, herein designated GAM RNA, and which when bound by GAM2437 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2437 target proteins.

[33998] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2437 gene, herein designated GAM GENE, on one or more GAM2437 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[33999] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2437 correlate with, and may be deduced from, the identity of the target genes which GAM2437 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34000] Nucleotide sequences of the GAM2437 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2437 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2437 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2437 are further described hereinbelow with reference to Table 1.

[34001] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2437 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[34002] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2438 (GAM2438) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[34003] GAM2438 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2438 was detected is described hereinabove with reference to Figs. 2-8.

[34004] GAM2438 gene, herein designated GAM GENE, and GAM2438 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[34005] GAM2438 gene, herein designated GAM GENE, encodes a GAM2438 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2438 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2438 precursor RNA is designated SEQ ID:2415, and is provided hereinbelow with reference to the sequence listing part.

[34006] GAM2438 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2438 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34007] An enzyme complex designated DICER COMPLEX, dices the GAM2438 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2438 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of GAM2438 RNA is designated SEQ ID:5029, and is provided hereinbelow with reference to the sequence listing part.

[34008] GAM2438 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2438 target RNA, herein designated GAM TARGET RNA. GAM2438 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34009] GAM2438 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2438 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2438 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2438 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2438 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34010] The complementary binding of GAM2438 RNA, herein designated GAM RNA, to target binding sites on GAM2438 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2438 target RNA, herein designated GAM TARGET RNA, into GAM2438 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34011] It is appreciated that GAM2438 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2438 target genes. The mRNA of each one of this plurality of GAM2438 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2438 RNA, herein designated GAM RNA, and which when bound by GAM2438 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2438 target proteins.

[34012] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2438 gene, herein designated GAM GENE, on one or more GAM2438 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34013] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2438 correlate with, and may be deduced from, the identity of the target genes which GAM2438 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34014] Nucleotide sequences of the GAM2438 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2438 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2438 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2438 are further described hereinbelow with reference to Table 1.

[34015] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2438 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[34016] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2439 (GAM2439) gene, which modulates



expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[34017] GAM2439 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2439 was detected is described hereinabove with reference to Figs. 2-8.

[34018] GAM2439 gene, herein designated GAM GENE, and GAM2439 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[34019] GAM2439 gene, herein designated GAM GENE, encodes a GAM2439 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2439 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2439 precursor RNA is designated SEQ ID:2416, and is provided hereinbelow with reference to the sequence listing part.

[34020] GAM2439 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2439 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

- [34021] An enzyme complex designated DICER COMPLEX, dices the GAM2439 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2439 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of GAM2439 RNA is designated SEQ ID:5030, and is provided hereinbelow with reference to the sequence listing part.
- [34022] GAM2439 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2439 target RNA, herein designated GAM TARGET RNA. GAM2439 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [34023] GAM2439 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2439 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2439 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2439 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2439 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34024] The complementary binding of GAM2439 RNA, herein designated GAM RNA, to target binding sites on GAM2439 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2439 target RNA, herein designated GAM TARGET RNA, into GAM2439 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34025] It is appreciated that GAM2439 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2439 target genes. The mRNA of each one of this plurality of GAM2439 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2439 RNA, herein designated GAM RNA, and which when bound by GAM2439 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2439 target proteins.

[34026] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2439 gene, herein designated GAM GENE, on one or more GAM2439 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34027] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2439 correlate with, and may be deduced from, the identity of the target genes which GAM2439 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34028] Nucleotide sequences of the GAM2439 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2439 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2439 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2439 are further described hereinbelow with reference to Table 1.

[34029] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2439 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

[34030] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2440 (GAM2440) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[34031] GAM2440 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2440 was detected is described hereinabove with reference to Figs. 2-8.

[34032] GAM2440 gene, herein designated GAM GENE, and GAM2440 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[34033] GAM2440 gene, herein designated GAM GENE, encodes a GAM2440 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2440 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2440 precursor RNA is designated SEQ ID:2417, and is provided hereinbelow with reference to the sequence listing part.

[34034] GAM2440 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2440 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34035] An enzyme complex designated DICER COMPLEX, dices the GAM2440 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2440 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 87%) nucleotide sequence of GAM2440 RNA is designated SEQ ID:5031, and is provided hereinbelow with reference to the sequence listing part.

[34036] GAM2440 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2440 target RNA, herein designated GAM TARGET RNA. GAM2440 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34037] GAM2440 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2440 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2440 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2440 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2440 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34038] The complementary binding of GAM2440 RNA, herein designated GAM RNA, to target binding sites on GAM2440 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2440 target RNA, herein designated GAM TARGET RNA, into GAM2440 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34039] It is appreciated that GAM2440 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2440 target genes. The mRNA of each one of this plurality of GAM2440 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2440 RNA, herein designated GAM RNA, and which when bound by GAM2440 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2440 target proteins.

[34040] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2440 gene, herein designated GAM GENE, on one or more GAM2440 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34041] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2440 correlate with, and may be deduced from, the identity of the target genes which GAM2440 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34042] Nucleotide sequences of the GAM2440 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2440 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2440 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2440 are further described hereinbelow with reference to Table 1.



[34043] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2440 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[34044] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2441 (GAM2441) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[34045] GAM2441 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2441 was detected is described hereinabove with reference to Figs. 2-8.

[34046] GAM2441 gene, herein designated GAM GENE, and GAM2441 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[34047] GAM2441 gene, herein designated GAM GENE, encodes a GAM2441 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2441 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2441 precursor RNA is designated SEQ ID:2418, and is provided hereinbelow with reference to the sequence listing part.

[34048] GAM2441 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2441 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34049] An enzyme complex designated DICER COMPLEX, dices the GAM2441 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2441 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 87%) nucleotide sequence of GAM2441 RNA is designated SEQ ID:5032, and is provided hereinbelow with reference to the sequence listing part.

[34050] GAM2441 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2441 target RNA, herein designated GAM TARGET RNA. GAM2441 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34051] GAM2441 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2441 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2441 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2441 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2441 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34052] The complementary binding of GAM2441 RNA, herein designated GAM RNA, to target binding sites on GAM2441 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2441 target RNA, herein designated GAM TARGET RNA, into GAM2441 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34053] It is appreciated that GAM2441 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2441 target genes. The

mRNA of each one of this plurality of GAM2441 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2441 RNA, herein designated GAM RNA, and which when bound by GAM2441 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2441 target proteins.

[34054] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2441 gene, herein designated GAM GENE, on one or more GAM2441 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34055] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2441 correlate with, and may be deduced from, the identity of the target genes which GAM2441 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34056] Nucleotide sequences of the GAM2441 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2441 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2441 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2441 are further described hereinbelow with reference to Table 1.

[34057] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2441 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[34058] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2442 (GAM2442) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[34059] GAM2442 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2442 was detected is described hereinabove with reference to Figs. 2-8.

[34060] GAM2442 gene, herein designated GAM GENE, and GAM2442 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[34061] GAM2442 gene, herein designated GAM GENE, encodes a GAM2442 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2442 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2442 precursor RNA is designated SEQ ID:2419, and is provided hereinbelow with reference to the sequence listing part.

[34062] GAM2442 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2442 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34063] An enzyme complex designated DICER COMPLEX, dices the GAM2442 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2442 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2442 RNA is designated SEQ ID:5033, and is provided hereinbelow with reference to the sequence listing part.

[34064] GAM2442 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2442 target RNA, herein designated GAM TARGET RNA. GAM2442 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34065] GAM2442 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2442 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2442 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2442 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2442 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34066] The complementary binding of GAM2442 RNA, herein designated GAM RNA, to target binding sites on GAM2442 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2442 target RNA, herein designated GAM TARGET RNA, into GAM2442 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34067] It is appreciated that GAM2442 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2442 target genes. The mRNA of each one of this plurality of GAM2442 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2442 RNA, herein designated GAM RNA, and which when bound by GAM2442 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2442 target proteins.

[34068] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2442 gene, herein designated GAM GENE, on one or more GAM2442 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34069] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2442 correlate with, and may be deduced from, the identity of the target



genes which GAM2442 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34070] Nucleotide sequences of the GAM2442 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2442 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2442 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2442 are further described hereinbelow with reference to Table 1.

[34071] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2442 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[34072] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2443 (GAM2443) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[34073] GAM2443 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2443 was detected is described hereinabove with reference to Figs. 2-8.

[34074] GAM2443 gene, herein designated GAM GENE, and GAM2443 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

[34075] GAM2443 gene, herein designated GAM GENE, encodes a GAM2443 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2443 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2443 precursor RNA is designated SEQ ID:2420, and is provided hereinbelow with reference to the sequence listing part.

[34076] GAM2443 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2443 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34077] An enzyme complex designated DICER COMPLEX, dices the GAM2443 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2443 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 87%) nucleotide sequence of GAM2443 RNA is designated SEQ ID:5034, and is provided

hereinbelow with reference to the sequence listing part.

[34078] GAM2443 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2443 target RNA, herein designated GAM TARGET RNA. GAM2443 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34079] GAM2443 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2443 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2443 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2443 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2443 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34080] The complementary binding of GAM2443 RNA, herein designated GAM RNA, to target binding sites on GAM2443 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2443 target RNA, herein designated GAM TARGET RNA, into GAM2443 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34081] It is appreciated that GAM2443 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2443 target genes. The mRNA of each one of this plurality of GAM2443 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2443 RNA, herein designated GAM RNA, and which when bound by GAM2443 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2443 target proteins.

[34082] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2443 gene, herein designated GAM GENE, on one or more GAM2443 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34083] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2443 correlate with, and may be deduced from, the identity of the target genes which GAM2443 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34084] Nucleotide sequences of the GAM2443 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2443 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2443 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2443 are further described hereinbelow with reference to Table 1.

[34085] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2443 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[34086] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2444 (GAM2444) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[34087] GAM2444 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2444 was detected is described hereinabove with reference to Figs. 2-8.

[34088] GAM2444 gene, herein designated GAM GENE, and GAM2444 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[34089] GAM2444 gene, herein designated GAM GENE, encodes a GAM2444 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2444 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2444 precursor RNA is designated SEQ ID:2421, and is provided hereinbelow with reference to the sequence listing part.

[34090] GAM2444 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2444 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34091] An enzyme complex designated DICER COMPLEX, dices the GAM2444 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2444 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 84%) nucleotide sequence of GAM2444 RNA is designated SEQ ID:5035, and is provided hereinbelow with reference to the sequence listing part.

[34092] GAM2444 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2444 target RNA, herein designated GAM TARGET RNA. GAM2444 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34093] GAM2444 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2444 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2444 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2444 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2444 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34094] The complementary binding of GAM2444 RNA, herein designated GAM RNA, to target binding sites on GAM2444 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2444 target RNA, herein designated GAM TARGET RNA, into GAM2444 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34095] It is appreciated that GAM2444 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2444 target genes. The mRNA of each one of this plurality of GAM2444 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2444 RNA, herein designated GAM RNA, and which when bound by GAM2444 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2444 target proteins.

[34096] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2444 gene, herein designated GAM GENE, on one or more GAM2444 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary



binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34097] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2444 correlate with, and may be deduced from, the identity of the target genes which GAM2444 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34098] Nucleotide sequences of the GAM2444 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2444 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2444 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2444 are further described hereinbelow with reference to Table 1.

[34099] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2444 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[34100] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2445 (GAM2445) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

- [34101] GAM2445 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2445 was detected is described hereinabove with reference to Figs. 2-8.
- [34102] GAM2445 gene, herein designated GAM GENE, and GAM2445 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.
- [34103] GAM2445 gene, herein designated GAM GENE, encodes a GAM2445 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2445 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2445 precursor RNA is designated SEQ ID:2422, and is provided hereinbelow with reference to the sequence listing part.
- [34104] GAM2445 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2445 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

- [34105] An enzyme complex designated DICER COMPLEX, dices the GAM2445 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2445 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2445 RNA is designated SEQ ID:5037, and is provided hereinbelow with reference to the sequence listing part.
- [34106] GAM2445 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2445 target RNA, herein designated GAM TARGET RNA. GAM2445 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [34107] GAM2445 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2445 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2445 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2445 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2445 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34108] The complementary binding of GAM2445 RNA, herein designated GAM RNA, to target binding sites on GAM2445 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2445 target RNA, herein designated GAM TARGET RNA, into GAM2445 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34109] It is appreciated that GAM2445 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2445 target genes. The mRNA of each one of this plurality of GAM2445 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2445 RNA, herein designated GAM RNA, and which when bound by GAM2445 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2445 target proteins.

[34110] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2445 gene, herein designated GAM GENE, on one or more GAM2445 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34111] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2445 correlate with, and may be deduced from, the identity of the target genes which GAM2445 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34112] Nucleotide sequences of the GAM2445 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2445 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2445 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2445 are further described hereinbelow with reference to Table 1.

[34113] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2445 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

- [34114] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2446 (GAM2446) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.
- [34115] GAM2446 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2446 was detected is described hereinabove with reference to Figs. 2-8.
- [34116] GAM2446 gene, herein designated GAM GENE, and GAM2446 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.
- [34117] GAM2446 gene, herein designated GAM GENE, encodes a GAM2446 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2446 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2446 precursor RNA is designated SEQ ID:2423, and is provided hereinbelow with reference to the sequence listing part.
- [34118] GAM2446 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2446 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34119] An enzyme complex designated DICER COMPLEX, dices the GAM2446 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2446 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of GAM2446 RNA is designated SEQ ID:5036, and is provided hereinbelow with reference to the sequence listing part.

[34120] GAM2446 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2446 target RNA, herein designated GAM TARGET RNA. GAM2446 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34121] GAM2446 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2446 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2446 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2446 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2446 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34122] The complementary binding of GAM2446 RNA, herein designated GAM RNA, to target binding sites on GAM2446 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2446 target RNA, herein designated GAM TARGET RNA, into GAM2446 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34123] It is appreciated that GAM2446 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2446 target genes. The mRNA of each one of this plurality of GAM2446 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2446 RNA, herein designated GAM RNA, and which when bound by GAM2446 RNA, herein designated GAM RNA,



causes inhibition of translation of respective one or more GAM2446 target proteins.

[34124] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2446 gene, herein designated GAM GENE, on one or more GAM2446 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34125] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2446 correlate with, and may be deduced from, the identity of the target genes which GAM2446 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34126] Nucleotide sequences of the GAM2446 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2446 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2446 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2446 are further described hereinbelow with reference to Table 1.

- [34127] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2446 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.
- [34128] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2447 (GAM2447) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.
- [34129] GAM2447 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2447 was detected is described hereinabove with reference to Figs. 2-8.
- [34130] GAM2447 gene, herein designated GAM GENE, and GAM2447 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.
- [34131] GAM2447 gene, herein designated GAM GENE, encodes a GAM2447 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2447 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2447 precursor RNA is designated SEQ ID:2424, and is provided hereinbelow with reference to the sequence listing part.

[34132] GAM2447 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2447 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34133] An enzyme complex designated DICER COMPLEX, dices the GAM2447 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2447 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 84%) nucleotide sequence of GAM2447 RNA is designated SEQ ID:5038, and is provided hereinbelow with reference to the sequence listing part.

[34134] GAM2447 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2447 target RNA, herein designated GAM TARGET RNA. GAM2447 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34135] GAM2447 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2447 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2447 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2447 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2447 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34136] The complementary binding of GAM2447 RNA, herein designated GAM RNA, to target binding sites on GAM2447 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2447 target RNA, herein designated GAM TARGET RNA, into GAM2447 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34137] It is appreciated that GAM2447 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2447 target genes. The

mRNA of each one of this plurality of GAM2447 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2447 RNA, herein designated GAM RNA, and which when bound by GAM2447 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2447 target proteins.

[34138] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2447 gene, herein designated GAM GENE, on one or more GAM2447 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34139] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2447 correlate with, and may be deduced from, the identity of the target genes which GAM2447 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34140] Nucleotide sequences of the GAM2447 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2447 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2447 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2447 are further described hereinbelow with reference to Table 1.

[34141] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2447 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[34142] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2448 (GAM2448) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[34143] GAM2448 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2448 was detected is described hereinabove with reference to Figs. 2-8.

[34144] GAM2448 gene, herein designated GAM GENE, and GAM2448 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[34145] GAM2448 gene, herein designated GAM GENE, encodes a GAM2448 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2448 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2448 precursor RNA is designated SEQ ID:2425, and is provided hereinbelow with reference to the sequence listing part.

[34146] GAM2448 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2448 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34147] An enzyme complex designated DICER COMPLEX, dices the GAM2448 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2448 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of GAM2448 RNA is designated SEQ ID:5039, and is provided hereinbelow with reference to the sequence listing part.

[34148] GAM2448 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2448 target RNA, herein designated GAM TARGET RNA. GAM2448 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34149] GAM2448 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2448 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2448 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2448 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2448 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34150] The complementary binding of GAM2448 RNA, herein designated GAM RNA, to target binding sites on GAM2448 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2448 target RNA, herein designated GAM TARGET RNA, into GAM2448 target protein, herein



designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34151] It is appreciated that GAM2448 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2448 target genes. The mRNA of each one of this plurality of GAM2448 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2448 RNA, herein designated GAM RNA, and which when bound by GAM2448 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2448 target proteins.

[34152] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2448 gene, herein designated GAM GENE, on one or more GAM2448 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34153] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2448 correlate with, and may be deduced from, the identity of the target

genes which GAM2448 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34154] Nucleotide sequences of the GAM2448 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2448 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2448 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2448 are further described hereinbelow with reference to Table 1.

[34155] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2448 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[34156] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2449 (GAM2449) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[34157] GAM2449 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2449 was detected is described hereinabove with reference to Figs. 2-8.

[34158] GAM2449 gene, herein designated GAM GENE, and GAM2449 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

- [34159] GAM2449 gene, herein designated GAM GENE, encodes a GAM2449 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2449 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2449 precursor RNA is designated SEQ ID:2426, and is provided hereinbelow with reference to the sequence listing part.
- [34160] GAM2449 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2449 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.
- [34161] An enzyme complex designated DICER COMPLEX, dices the GAM2449 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2449 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 87%) nucleotide sequence of GAM2449 RNA is designated SEQ ID:5040, and is provided

hereinbelow with reference to the sequence listing part.

[34162] GAM2449 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2449 target RNA, herein designated GAM TARGET RNA. GAM2449 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34163] GAM2449 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2449 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2449 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2449 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2449 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34164] The complementary binding of GAM2449 RNA, herein designated GAM RNA, to target binding sites on GAM2449 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2449 target RNA, herein designated GAM TARGET RNA, into GAM2449 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34165] It is appreciated that GAM2449 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2449 target genes. The mRNA of each one of this plurality of GAM2449 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2449 RNA, herein designated GAM RNA, and which when bound by GAM2449 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2449 target proteins.

[34166] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2449 gene, herein designated GAM GENE, on one or more GAM2449 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34167] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2449 correlate with, and may be deduced from, the identity of the target genes which GAM2449 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34168] Nucleotide sequences of the GAM2449 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2449 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2449 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2449 are further described hereinbelow with reference to Table 1.

[34169] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2449 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[34170] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2450 (GAM2450) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[34171] GAM2450 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2450 was detected is described hereinabove with reference to Figs. 2-8.

[34172] GAM2450 gene, herein designated GAM GENE, and GAM2450 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[34173] GAM2450 gene, herein designated GAM GENE, encodes a GAM2450 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2450 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2450 precursor RNA is designated SEQ ID:2427, and is provided hereinbelow with reference to the sequence listing part.

[34174] GAM2450 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2450 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34175] An enzyme complex designated DICER COMPLEX, dices the GAM2450 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2450 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 76%) nucleotide sequence of GAM2450 RNA is designated SEQ ID:5041, and is provided hereinbelow with reference to the sequence listing part.

[34176] GAM2450 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2450 target RNA, herein designated GAM TARGET RNA. GAM2450 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34177] GAM2450 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2450 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2450 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2450 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2450 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target



binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34178] The complementary binding of GAM2450 RNA, herein designated GAM RNA, to target binding sites on GAM2450 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2450 target RNA, herein designated GAM TARGET RNA, into GAM2450 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34179] It is appreciated that GAM2450 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2450 target genes. The mRNA of each one of this plurality of GAM2450 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2450 RNA, herein designated GAM RNA, and which when bound by GAM2450 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2450 target proteins.

[34180] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2450 gene, herein designated GAM GENE, on one or more GAM2450 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34181] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2450 correlate with, and may be deduced from, the identity of the target genes which GAM2450 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34182] Nucleotide sequences of the GAM2450 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2450 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2450 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2450 are further described hereinbelow with reference to Table 1.

[34183] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2450 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[34184] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2451 (GAM2451) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

- [34185] GAM2451 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2451 was detected is described hereinabove with reference to Figs. 2-8.
- [34186] GAM2451 gene, herein designated GAM GENE, and GAM2451 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.
- [34187] GAM2451 gene, herein designated GAM GENE, encodes a GAM2451 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2451 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2451 precursor RNA is designated SEQ ID:2428, and is provided hereinbelow with reference to the sequence listing part.
- [34188] GAM2451 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2451 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

- [34189] An enzyme complex designated DICER COMPLEX, dices the GAM2451 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2451 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 84%) nucleotide sequence of GAM2451 RNA is designated SEQ ID:5042, and is provided hereinbelow with reference to the sequence listing part.
- [34190] GAM2451 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2451 target RNA, herein designated GAM TARGET RNA. GAM2451 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [34191] GAM2451 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2451 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2451 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2451 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2451 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34192] The complementary binding of GAM2451 RNA, herein designated GAM RNA, to target binding sites on GAM2451 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2451 target RNA, herein designated GAM TARGET RNA, into GAM2451 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34193] It is appreciated that GAM2451 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2451 target genes. The mRNA of each one of this plurality of GAM2451 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2451 RNA, herein designated GAM RNA, and which when bound by GAM2451 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2451 target proteins.

[34194] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2451 gene, herein designated GAM GENE, on one or more GAM2451 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34195] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2451 correlate with, and may be deduced from, the identity of the target genes which GAM2451 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34196] Nucleotide sequences of the GAM2451 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2451 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2451 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2451 are further described hereinbelow with reference to Table 1.

[34197] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2451 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

[34198] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2452 (GAM2452) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[34199] GAM2452 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2452 was detected is described hereinabove with reference to Figs. 2-8.

[34200] GAM2452 gene, herein designated GAM GENE, and GAM2452 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[34201] GAM2452 gene, herein designated GAM GENE, encodes a GAM2452 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2452 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2452 precursor RNA is designated SEQ ID:2429, and is provided hereinbelow with reference to the sequence listing part.

[34202] GAM2452 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2452 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34203] An enzyme complex designated DICER COMPLEX, dices the GAM2452 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2452 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 83%) nucleotide sequence of GAM2452 RNA is designated SEQ ID:5043, and is provided hereinbelow with reference to the sequence listing part.

[34204] GAM2452 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2452 target RNA, herein designated GAM TARGET RNA. GAM2452 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34205] GAM2452 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2452 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2452 RNA,



herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2452 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2452 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34206] The complementary binding of GAM2452 RNA, herein designated GAM RNA, to target binding sites on GAM2452 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2452 target RNA, herein designated GAM TARGET RNA, into GAM2452 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34207] It is appreciated that GAM2452 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2452 target genes. The mRNA of each one of this plurality of GAM2452 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2452 RNA, herein designated GAM RNA, and which when bound by GAM2452 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2452 target proteins.

[34208] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2452 gene, herein designated GAM GENE, on one or more GAM2452 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34209] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2452 correlate with, and may be deduced from, the identity of the target genes which GAM2452 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34210] Nucleotide sequences of the GAM2452 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2452 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2452 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2452 are further described hereinbelow with reference to Table 1.

- [34211] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2452 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.
- [34212] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2453 (GAM2453) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.
- [34213] GAM2453 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2453 was detected is described hereinabove with reference to Figs. 2-8.
- [34214] GAM2453 gene, herein designated GAM GENE, and GAM2453 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.
- [34215] GAM2453 gene, herein designated GAM GENE, encodes a GAM2453 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2453 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2453 precursor RNA is designated SEQ ID:2430, and is provided hereinbelow with reference to the sequence listing part.

[34216] GAM2453 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2453 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34217] An enzyme complex designated DICER COMPLEX, dices the GAM2453 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2453 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2453 RNA is designated SEQ ID:5044, and is provided hereinbelow with reference to the sequence listing part.

[34218] GAM2453 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2453 target RNA, herein designated GAM TARGET RNA. GAM2453 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34219] GAM2453 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2453 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2453 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2453 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2453 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34220] The complementary binding of GAM2453 RNA, herein designated GAM RNA, to target binding sites on GAM2453 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2453 target RNA, herein designated GAM TARGET RNA, into GAM2453 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34221] It is appreciated that GAM2453 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2453 target genes. The

mRNA of each one of this plurality of GAM2453 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2453 RNA, herein designated GAM RNA, and which when bound by GAM2453 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2453 target proteins.

[34222] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2453 gene, herein designated GAM GENE, on one or more GAM2453 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34223] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2453 correlate with, and may be deduced from, the identity of the target genes which GAM2453 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34224] Nucleotide sequences of the GAM2453 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2453 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2453 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2453 are further described hereinbelow with reference to Table 1.

[34225] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2453 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[34226] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2454 (GAM2454) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[34227] GAM2454 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2454 was detected is described hereinabove with reference to Figs. 2-8.

[34228] GAM2454 gene, herein designated GAM GENE, and GAM2454 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[34229] GAM2454 gene, herein designated GAM GENE, encodes a GAM2454 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2454 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2454 precursor RNA is designated SEQ ID:2431, and is provided hereinbelow with reference to the sequence listing part.

[34230] GAM2454 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2454 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34231] An enzyme complex designated DICER COMPLEX, dices the GAM2454 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2454 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of GAM2454 RNA is designated SEQ ID:5045, and is provided hereinbelow with reference to the sequence listing part.

[34232] GAM2454 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2454 target RNA, herein designated GAM TARGET RNA. GAM2454 target RNA, herein designated GAM



TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34233] GAM2454 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2454 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2454 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2454 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2454 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34234] The complementary binding of GAM2454 RNA, herein designated GAM RNA, to target binding sites on GAM2454 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2454 target RNA, herein designated GAM TARGET RNA, into GAM2454 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34235] It is appreciated that GAM2454 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2454 target genes. The mRNA of each one of this plurality of GAM2454 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2454 RNA, herein designated GAM RNA, and which when bound by GAM2454 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2454 target proteins.

[34236] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2454 gene, herein designated GAM GENE, on one or more GAM2454 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34237] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2454 correlate with, and may be deduced from, the identity of the target

genes which GAM2454 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34238] Nucleotide sequences of the GAM2454 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2454 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2454 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2454 are further described hereinbelow with reference to Table 1.

[34239] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2454 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[34240] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2455 (GAM2455) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[34241] GAM2455 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2455 was detected is described hereinabove with reference to Figs. 2-8.

[34242] GAM2455 gene, herein designated GAM GENE, and GAM2455 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

[34243] GAM2455 gene, herein designated GAM GENE, encodes a GAM2455 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2455 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2455 precursor RNA is designated SEQ ID:2432, and is provided hereinbelow with reference to the sequence listing part.

[34244] GAM2455 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2455 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34245] An enzyme complex designated DICER COMPLEX, dices the GAM2455 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2455 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of GAM2455 RNA is designated SEQ ID:5046, and is provided

hereinbelow with reference to the sequence listing part.

[34246] GAM2455 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2455 target RNA, herein designated GAM TARGET RNA. GAM2455 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34247] GAM2455 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2455 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2455 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2455 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2455 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34248] The complementary binding of GAM2455 RNA, herein designated GAM RNA, to target binding sites on GAM2455 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2455 target RNA, herein designated GAM TARGET RNA, into GAM2455 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34249] It is appreciated that GAM2455 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2455 target genes. The mRNA of each one of this plurality of GAM2455 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2455 RNA, herein designated GAM RNA, and which when bound by GAM2455 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2455 target proteins.

[34250] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2455 gene, herein designated GAM GENE, on one or more GAM2455 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34251] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2455 correlate with, and may be deduced from, the identity of the target genes which GAM2455 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34252] Nucleotide sequences of the GAM2455 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2455 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2455 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2455 are further described hereinbelow with reference to Table 1.

[34253] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2455 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[34254] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2456 (GAM2456) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[34255] GAM2456 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2456 was detected is described hereinabove with reference to Figs. 2-8.

[34256] GAM2456 gene, herein designated GAM GENE, and GAM2456 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[34257] GAM2456 gene, herein designated GAM GENE, encodes a GAM2456 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2456 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2456 precursor RNA is designated SEQ ID:2433, and is provided hereinbelow with reference to the sequence listing part.

[34258] GAM2456 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2456 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34259] An enzyme complex designated DICER COMPLEX, dices the GAM2456 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2456 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin



structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM2456 RNA is designated SEQ ID:5047, and is provided hereinbelow with reference to the sequence listing part.

[34260] GAM2456 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2456 target RNA, herein designated GAM TARGET RNA. GAM2456 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34261] GAM2456 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2456 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2456 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2456 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2456 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34262] The complementary binding of GAM2456 RNA, herein designated GAM RNA, to target binding sites on GAM2456 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2456 target RNA, herein designated GAM TARGET RNA, into GAM2456 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34263] It is appreciated that GAM2456 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2456 target genes. The mRNA of each one of this plurality of GAM2456 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2456 RNA, herein designated GAM RNA, and which when bound by GAM2456 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2456 target proteins.

[34264] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2456 gene, herein designated GAM GENE, on one or more GAM2456 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34265] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2456 correlate with, and may be deduced from, the identity of the target genes which GAM2456 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34266] Nucleotide sequences of the GAM2456 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2456 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2456 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2456 are further described hereinbelow with reference to Table 1.

[34267] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2456 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[34268] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2457 (GAM2457) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[34269] GAM2457 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2457 was detected is described hereinabove with reference to Figs. 2-8.

[34270] GAM2457 gene, herein designated GAM GENE, and GAM2457 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[34271] GAM2457 gene, herein designated GAM GENE, encodes a GAM2457 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2457 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2457 precursor RNA is designated SEQ ID:2434, and is provided hereinbelow with reference to the sequence listing part.

[34272] GAM2457 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2457 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

- [34273] An enzyme complex designated DICER COMPLEX, dices the GAM2457 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2457 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 84%) nucleotide sequence of GAM2457 RNA is designated SEQ ID:5048, and is provided hereinbelow with reference to the sequence listing part.
- [34274] GAM2457 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2457 target RNA, herein designated GAM TARGET RNA. GAM2457 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [34275] GAM2457 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2457 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2457 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2457 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2457 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34276] The complementary binding of GAM2457 RNA, herein designated GAM RNA, to target binding sites on GAM2457 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2457 target RNA, herein designated GAM TARGET RNA, into GAM2457 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34277] It is appreciated that GAM2457 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2457 target genes. The mRNA of each one of this plurality of GAM2457 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2457 RNA, herein designated GAM RNA, and which when bound by GAM2457 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2457 target proteins.

[34278] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2457 gene, herein designated GAM GENE, on one or more GAM2457 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34279] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2457 correlate with, and may be deduced from, the identity of the target genes which GAM2457 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34280] Nucleotide sequences of the GAM2457 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2457 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2457 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2457 are further described hereinbelow with reference to Table 1.

[34281] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2457 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

[34282] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2458 (GAM2458) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[34283] GAM2458 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2458 was detected is described hereinabove with reference to Figs. 2-8.

[34284] GAM2458 gene, herein designated GAM GENE, and GAM2458 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[34285] GAM2458 gene, herein designated GAM GENE, encodes a GAM2458 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2458 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2458 precursor RNA is designated SEQ ID:2435, and is provided hereinbelow with reference to the sequence listing part.

[34286] GAM2458 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2458 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA



encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34287] An enzyme complex designated DICER COMPLEX, dices the GAM2458 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2458 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 86%) nucleotide sequence of GAM2458 RNA is designated SEQ ID:5049, and is provided hereinbelow with reference to the sequence listing part.

[34288] GAM2458 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2458 target RNA, herein designated GAM TARGET RNA. GAM2458 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34289] GAM2458 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2458 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2458 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2458 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2458 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34290] The complementary binding of GAM2458 RNA, herein designated GAM RNA, to target binding sites on GAM2458 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2458 target RNA, herein designated GAM TARGET RNA, into GAM2458 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34291] It is appreciated that GAM2458 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2458 target genes. The mRNA of each one of this plurality of GAM2458 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2458 RNA, herein designated GAM RNA, and which when bound by GAM2458 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2458 target proteins.

[34292] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2458 gene, herein designated GAM GENE, on one or more GAM2458 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34293] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2458 correlate with, and may be deduced from, the identity of the target genes which GAM2458 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34294] Nucleotide sequences of the GAM2458 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2458 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2458 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2458 are further described hereinbelow with reference to Table 1.

- [34295] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2458 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.
- [34296] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2459 (GAM2459) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.
- [34297] GAM2459 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2459 was detected is described hereinabove with reference to Figs. 2-8.
- [34298] GAM2459 gene, herein designated GAM GENE, and GAM2459 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.
- [34299] GAM2459 gene, herein designated GAM GENE, encodes a GAM2459 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2459 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2459 precursor RNA is designated SEQ ID:2436, and is provided hereinbelow with reference to the sequence listing part.

[34300] GAM2459 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2459 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34301] An enzyme complex designated DICER COMPLEX, dices the GAM2459 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2459 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of GAM2459 RNA is designated SEQ ID:5050, and is provided hereinbelow with reference to the sequence listing part.

[34302] GAM2459 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2459 target RNA, herein designated GAM TARGET RNA. GAM2459 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34303] GAM2459 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2459 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2459 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2459 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2459 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34304] The complementary binding of GAM2459 RNA, herein designated GAM RNA, to target binding sites on GAM2459 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2459 target RNA, herein designated GAM TARGET RNA, into GAM2459 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34305] It is appreciated that GAM2459 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2459 target genes. The

mRNA of each one of this plurality of GAM2459 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2459 RNA, herein designated GAM RNA, and which when bound by GAM2459 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2459 target proteins.

[34306] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2459 gene, herein designated GAM GENE, on one or more GAM2459 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34307] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2459 correlate with, and may be deduced from, the identity of the target genes which GAM2459 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34308] Nucleotide sequences of the GAM2459 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2459 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2459 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2459 are further described hereinbelow with reference to Table 1.

[34309] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2459 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[34310] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2460 (GAM2460) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[34311] GAM2460 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2460 was detected is described hereinabove with reference to Figs. 2-8.

[34312] GAM2460 gene, herein designated GAM GENE, and GAM2460 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[34313] GAM2460 gene, herein designated GAM GENE, encodes a GAM2460 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2460 precursor RNA,



herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2460 precursor RNA is designated SEQ ID:2437, and is provided hereinbelow with reference to the sequence listing part.

[34314] GAM2460 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2460 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34315] An enzyme complex designated DICER COMPLEX, dices the GAM2460 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2460 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 90%) nucleotide sequence of GAM2460 RNA is designated SEQ ID:5051, and is provided hereinbelow with reference to the sequence listing part.

[34316] GAM2460 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2460 target RNA, herein designated GAM TARGET RNA. GAM2460 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34317] GAM2460 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2460 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2460 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2460 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2460 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34318] The complementary binding of GAM2460 RNA, herein designated GAM RNA, to target binding sites on GAM2460 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2460 target RNA, herein designated GAM TARGET RNA, into GAM2460 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34319] It is appreciated that GAM2460 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2460 target genes. The mRNA of each one of this plurality of GAM2460 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2460 RNA, herein designated GAM RNA, and which when bound by GAM2460 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2460 target proteins.

[34320] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2460 gene, herein designated GAM GENE, on one or more GAM2460 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34321] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2460 correlate with, and may be deduced from, the identity of the target

genes which GAM2460 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34322] Nucleotide sequences of the GAM2460 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2460 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2460 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2460 are further described hereinbelow with reference to Table 1.

[34323] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2460 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[34324] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2461 (GAM2461) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[34325] GAM2461 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2461 was detected is described hereinabove with reference to Figs. 2-8.

[34326] GAM2461 gene, herein designated GAM GENE, and GAM2461 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

[34327] GAM2461 gene, herein designated GAM GENE, encodes a GAM2461 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2461 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2461 precursor RNA is designated SEQ ID:2438, and is provided hereinbelow with reference to the sequence listing part.

[34328] GAM2461 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2461 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34329] An enzyme complex designated DICER COMPLEX, dices the GAM2461 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2461 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 84%) nucleotide sequence of GAM2461 RNA is designated SEQ ID:5052, and is provided

hereinbelow with reference to the sequence listing part.

[34330] GAM2461 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2461 target RNA, herein designated GAM TARGET RNA. GAM2461 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34331] GAM2461 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2461 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2461 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2461 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2461 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34332] The complementary binding of GAM2461 RNA, herein designated GAM RNA, to target binding sites on GAM2461 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2461 target RNA, herein designated GAM TARGET RNA, into GAM2461 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34333] It is appreciated that GAM2461 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2461 target genes. The mRNA of each one of this plurality of GAM2461 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2461 RNA, herein designated GAM RNA, and which when bound by GAM2461 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2461 target proteins.

[34334] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2461 gene, herein designated GAM GENE, on one or more GAM2461 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34335] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2461 correlate with, and may be deduced from, the identity of the target genes which GAM2461 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34336] Nucleotide sequences of the GAM2461 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2461 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2461 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2461 are further described hereinbelow with reference to Table 1.

[34337] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2461 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[34338] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2462 (GAM2462) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[34339] GAM2462 is a novel bioinformatically detected regulatory, non protein



coding, micro RNA (miRNA) gene. The method by which GAM2462 was detected is described hereinabove with reference to Figs. 2-8.

[34340] GAM2462 gene, herein designated GAM GENE, and GAM2462 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[34341] GAM2462 gene, herein designated GAM GENE, encodes a GAM2462 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2462 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2462 precursor RNA is designated SEQ ID:2439, and is provided hereinbelow with reference to the sequence listing part.

[34342] GAM2462 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2462 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34343] An enzyme complex designated DICER COMPLEX, dices the GAM2462 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2462 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 86%) nucleotide sequence of GAM2462 RNA is designated SEQ ID:5054, and is provided hereinbelow with reference to the sequence listing part.

[34344] GAM2462 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2462 target RNA, herein designated GAM TARGET RNA. GAM2462 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34345] GAM2462 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2462 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2462 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2462 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2462 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34346] The complementary binding of GAM2462 RNA, herein designated GAM RNA, to target binding sites on GAM2462 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2462 target RNA, herein designated GAM TARGET RNA, into GAM2462 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34347] It is appreciated that GAM2462 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2462 target genes. The mRNA of each one of this plurality of GAM2462 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2462 RNA, herein designated GAM RNA, and which when bound by GAM2462 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2462 target proteins.

[34348] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2462 gene, herein designated GAM GENE, on one or more GAM2462 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34349] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2462 correlate with, and may be deduced from, the identity of the target genes which GAM2462 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34350] Nucleotide sequences of the GAM2462 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2462 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2462 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2462 are further described hereinbelow with reference to Table 1.

[34351] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2462 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[34352] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2463 (GAM2463) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[34353] GAM2463 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2463 was detected is described hereinabove with reference to Figs. 2-8.

[34354] GAM2463 gene, herein designated GAM GENE, and GAM2463 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[34355] GAM2463 gene, herein designated GAM GENE, encodes a GAM2463 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2463 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2463 precursor RNA is designated SEQ ID:2440, and is provided hereinbelow with reference to the sequence listing part.

[34356] GAM2463 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2463 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

- [34357] An enzyme complex designated DICER COMPLEX, dices the GAM2463 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2463 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of GAM2463 RNA is designated SEQ ID:5053, and is provided hereinbelow with reference to the sequence listing part.
- [34358] GAM2463 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2463 target RNA, herein designated GAM TARGET RNA. GAM2463 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [34359] GAM2463 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2463 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2463 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2463 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2463 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34360] The complementary binding of GAM2463 RNA, herein designated GAM RNA, to target binding sites on GAM2463 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2463 target RNA, herein designated GAM TARGET RNA, into GAM2463 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34361] It is appreciated that GAM2463 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2463 target genes. The mRNA of each one of this plurality of GAM2463 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2463 RNA, herein designated GAM RNA, and which when bound by GAM2463 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2463 target proteins.

[34362] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2463 gene, herein designated GAM GENE, on one or more GAM2463 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34363] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2463 correlate with, and may be deduced from, the identity of the target genes which GAM2463 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34364] Nucleotide sequences of the GAM2463 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2463 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2463 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2463 are further described hereinbelow with reference to Table 1.

[34365] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2463 RNA, herein designated GAM RNA, are described hereinbelow



with reference to Table 2.

[34366] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2464 (GAM2464) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[34367] GAM2464 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2464 was detected is described hereinabove with reference to Figs. 2-8.

[34368] GAM2464 gene, herein designated GAM GENE, and GAM2464 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[34369] GAM2464 gene, herein designated GAM GENE, encodes a GAM2464 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2464 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2464 precursor RNA is designated SEQ ID:2441, and is provided hereinbelow with reference to the sequence listing part.

[34370] GAM2464 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2464 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34371] An enzyme complex designated DICER COMPLEX, dices the GAM2464 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2464 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 88%) nucleotide sequence of GAM2464 RNA is designated SEQ ID:5055, and is provided hereinbelow with reference to the sequence listing part.

[34372] GAM2464 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2464 target RNA, herein designated GAM TARGET RNA. GAM2464 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34373] GAM2464 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2464 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2464 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2464 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2464 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34374] The complementary binding of GAM2464 RNA, herein designated GAM RNA, to target binding sites on GAM2464 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2464 target RNA, herein designated GAM TARGET RNA, into GAM2464 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34375] It is appreciated that GAM2464 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2464 target genes. The mRNA of each one of this plurality of GAM2464 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2464 RNA, herein designated GAM RNA, and which when bound by GAM2464 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2464 target proteins.

[34376] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2464 gene, herein designated GAM GENE, on one or more GAM2464 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34377] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2464 correlate with, and may be deduced from, the identity of the target genes which GAM2464 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34378] Nucleotide sequences of the GAM2464 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2464 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2464 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2464 are further described hereinbelow with reference to Table 1.

[34379] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2464 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[34380] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2465 (GAM2465) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[34381] GAM2465 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2465 was detected is described hereinabove with reference to Figs. 2-8.

[34382] GAM2465 gene, herein designated GAM GENE, and GAM2465 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[34383] GAM2465 gene, herein designated GAM GENE, encodes a GAM2465 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2465 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2465 precursor RNA is designated SEQ ID:2442, and is provided hereinbelow with reference to the sequence listing part.

[34384] GAM2465 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2465 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34385] An enzyme complex designated DICER COMPLEX, dices the GAM2465 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2465 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 83%) nucleotide sequence of GAM2465 RNA is designated SEQ ID:5056, and is provided hereinbelow with reference to the sequence listing part.

[34386] GAM2465 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2465 target RNA, herein designated GAM TARGET RNA. GAM2465 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34387] GAM2465 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2465 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2465 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2465 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2465 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34388] The complementary binding of GAM2465 RNA, herein designated GAM RNA, to target binding sites on GAM2465 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2465 target RNA, herein designated GAM TARGET RNA, into GAM2465 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34389] It is appreciated that GAM2465 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2465 target genes. The

mRNA of each one of this plurality of GAM2465 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2465 RNA, herein designated GAM RNA, and which when bound by GAM2465 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2465 target proteins.

[34390] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2465 gene, herein designated GAM GENE, on one or more GAM2465 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34391] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2465 correlate with, and may be deduced from, the identity of the target genes which GAM2465 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34392] Nucleotide sequences of the GAM2465 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2465 RNA, herein



designated GAM RNA, and a schematic representation of the secondary folding of GAM2465 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2465 are further described hereinbelow with reference to Table 1.

[34393] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2465 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[34394] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2466 (GAM2466) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[34395] GAM2466 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2466 was detected is described hereinabove with reference to Figs. 2-8.

[34396] GAM2466 gene, herein designated GAM GENE, and GAM2466 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[34397] GAM2466 gene, herein designated GAM GENE, encodes a GAM2466 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2466 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2466 precursor RNA is designated SEQ ID:2443, and is provided hereinbelow with reference to the sequence listing part.

[34398] GAM2466 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2466 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34399] An enzyme complex designated DICER COMPLEX, dices the GAM2466 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2466 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of GAM2466 RNA is designated SEQ ID:5058, and is provided hereinbelow with reference to the sequence listing part.

[34400] GAM2466 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2466 target RNA, herein designated GAM TARGET RNA. GAM2466 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34401] GAM2466 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2466 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2466 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2466 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2466 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34402] The complementary binding of GAM2466 RNA, herein designated GAM RNA, to target binding sites on GAM2466 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2466 target RNA, herein designated GAM TARGET RNA, into GAM2466 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34403] It is appreciated that GAM2466 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2466 target genes. The mRNA of each one of this plurality of GAM2466 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2466 RNA, herein designated GAM RNA, and which when bound by GAM2466 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2466 target proteins.

[34404] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2466 gene, herein designated GAM GENE, on one or more GAM2466 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34405] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2466 correlate with, and may be deduced from, the identity of the target

genes which GAM2466 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34406] Nucleotide sequences of the GAM2466 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2466 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2466 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2466 are further described hereinbelow with reference to Table 1.

[34407] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2466 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[34408] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2467 (GAM2467) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[34409] GAM2467 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2467 was detected is described hereinabove with reference to Figs. 2-8.

[34410] GAM2467 gene, herein designated GAM GENE, and GAM2467 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

[34411] GAM2467 gene, herein designated GAM GENE, encodes a GAM2467 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2467 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2467 precursor RNA is designated SEQ ID:2444, and is provided hereinbelow with reference to the sequence listing part.

[34412] GAM2467 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2467 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34413] An enzyme complex designated DICER COMPLEX, dices the GAM2467 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2467 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of GAM2467 RNA is designated SEQ ID:5057, and is provided

hereinbelow with reference to the sequence listing part.

[34414] GAM2467 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2467 target RNA, herein designated GAM TARGET RNA. GAM2467 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34415] GAM2467 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2467 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2467 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2467 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2467 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34416] The complementary binding of GAM2467 RNA, herein designated GAM RNA, to target binding sites on GAM2467 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2467 target RNA, herein designated GAM TARGET RNA, into GAM2467 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34417] It is appreciated that GAM2467 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2467 target genes. The mRNA of each one of this plurality of GAM2467 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2467 RNA, herein designated GAM RNA, and which when bound by GAM2467 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2467 target proteins.

[34418] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2467 gene, herein designated GAM GENE, on one or more GAM2467 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding



sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34419] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2467 correlate with, and may be deduced from, the identity of the target genes which GAM2467 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34420] Nucleotide sequences of the GAM2467 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2467 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2467 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2467 are further described hereinbelow with reference to Table 1.

[34421] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2467 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[34422] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2468 (GAM2468) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[34423] GAM2468 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2468 was detected is described hereinabove with reference to Figs. 2-8.

[34424] GAM2468 gene, herein designated GAM GENE, and GAM2468 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[34425] GAM2468 gene, herein designated GAM GENE, encodes a GAM2468 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2468 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2468 precursor RNA is designated SEQ ID:2445, and is provided hereinbelow with reference to the sequence listing part.

[34426] GAM2468 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2468 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34427] An enzyme complex designated DICER COMPLEX, dices the GAM2468 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2468 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 25%) nucleotide sequence of GAM2468 RNA is designated SEQ ID:5059, and is provided hereinbelow with reference to the sequence listing part.

[34428] GAM2468 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2468 target RNA, herein designated GAM TARGET RNA. GAM2468 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34429] GAM2468 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2468 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2468 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2468 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2468 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34430] The complementary binding of GAM2468 RNA, herein designated GAM RNA, to target binding sites on GAM2468 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2468 target RNA, herein designated GAM TARGET RNA, into GAM2468 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34431] It is appreciated that GAM2468 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2468 target genes. The mRNA of each one of this plurality of GAM2468 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2468 RNA, herein designated GAM RNA, and which when bound by GAM2468 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2468 target proteins.

[34432] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2468 gene, herein designated GAM GENE, on one or more GAM2468 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34433] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2468 correlate with, and may be deduced from, the identity of the target genes which GAM2468 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34434] Nucleotide sequences of the GAM2468 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2468 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2468 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2468 are further described hereinbelow with reference to Table 1.

[34435] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2468 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[34436] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2469 (GAM2469) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

- [34437] GAM2469 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2469 was detected is described hereinabove with reference to Figs. 2-8.
- [34438] GAM2469 gene, herein designated GAM GENE, and GAM2469 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.
- [34439] GAM2469 gene, herein designated GAM GENE, encodes a GAM2469 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2469 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2469 precursor RNA is designated SEQ ID:2446, and is provided hereinbelow with reference to the sequence listing part.
- [34440] GAM2469 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2469 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

- [34441] An enzyme complex designated DICER COMPLEX, dices the GAM2469 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2469 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 76%) nucleotide sequence of GAM2469 RNA is designated SEQ ID:5060, and is provided hereinbelow with reference to the sequence listing part.
- [34442] GAM2469 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2469 target RNA, herein designated GAM TARGET RNA. GAM2469 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [34443] GAM2469 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2469 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2469 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2469 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2469 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34444] The complementary binding of GAM2469 RNA, herein designated GAM RNA, to target binding sites on GAM2469 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2469 target RNA, herein designated GAM TARGET RNA, into GAM2469 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34445] It is appreciated that GAM2469 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2469 target genes. The mRNA of each one of this plurality of GAM2469 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2469 RNA, herein designated GAM RNA, and which when bound by GAM2469 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2469 target proteins.

[34446] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition



exerted by GAM2469 gene, herein designated GAM GENE, on one or more GAM2469 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34447] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2469 correlate with, and may be deduced from, the identity of the target genes which GAM2469 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34448] Nucleotide sequences of the GAM2469 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2469 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2469 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2469 are further described hereinbelow with reference to Table 1.

[34449] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2469 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

[34450] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2470 (GAM2470) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[34451] GAM2470 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2470 was detected is described hereinabove with reference to Figs. 2-8.

[34452] GAM2470 gene, herein designated GAM GENE, and GAM2470 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[34453] GAM2470 gene, herein designated GAM GENE, encodes a GAM2470 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2470 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2470 precursor RNA is designated SEQ ID:2447, and is provided hereinbelow with reference to the sequence listing part.

[34454] GAM2470 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2470 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34455] An enzyme complex designated DICER COMPLEX, dices the GAM2470 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2470 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 78%) nucleotide sequence of GAM2470 RNA is designated SEQ ID:5061, and is provided hereinbelow with reference to the sequence listing part.

[34456] GAM2470 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2470 target RNA, herein designated GAM TARGET RNA. GAM2470 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34457] GAM2470 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2470 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2470 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2470 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2470 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34458] The complementary binding of GAM2470 RNA, herein designated GAM RNA, to target binding sites on GAM2470 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2470 target RNA, herein designated GAM TARGET RNA, into GAM2470 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34459] It is appreciated that GAM2470 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2470 target genes. The mRNA of each one of this plurality of GAM2470 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2470 RNA, herein designated GAM RNA, and which when bound by GAM2470 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2470 target proteins.

[34460] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2470 gene, herein designated GAM GENE, on one or more GAM2470 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34461] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2470 correlate with, and may be deduced from, the identity of the target genes which GAM2470 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34462] Nucleotide sequences of the GAM2470 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2470 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2470 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2470 are further described hereinbelow with reference to Table 1.

- [34463] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2470 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.
- [34464] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2471 (GAM2471) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.
- [34465] GAM2471 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2471 was detected is described hereinabove with reference to Figs. 2-8.
- [34466] GAM2471 gene, herein designated GAM GENE, and GAM2471 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.
- [34467] GAM2471 gene, herein designated GAM GENE, encodes a GAM2471 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2471 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2471 precursor RNA is designated SEQ ID:2448, and is provided hereinbelow with reference to the sequence listing part.

[34468] GAM2471 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2471 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34469] An enzyme complex designated DICER COMPLEX, dices the GAM2471 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2471 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 78%) nucleotide sequence of GAM2471 RNA is designated SEQ ID:5062, and is provided hereinbelow with reference to the sequence listing part.

[34470] GAM2471 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2471 target RNA, herein designated GAM TARGET RNA. GAM2471 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34471] GAM2471 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2471 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2471 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2471 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2471 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34472] The complementary binding of GAM2471 RNA, herein designated GAM RNA, to target binding sites on GAM2471 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2471 target RNA, herein designated GAM TARGET RNA, into GAM2471 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34473] It is appreciated that GAM2471 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2471 target genes. The



mRNA of each one of this plurality of GAM2471 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2471 RNA, herein designated GAM RNA, and which when bound by GAM2471 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2471 target proteins.

[34474] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2471 gene, herein designated GAM GENE, on one or more GAM2471 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34475] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2471 correlate with, and may be deduced from, the identity of the target genes which GAM2471 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34476] Nucleotide sequences of the GAM2471 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2471 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2471 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2471 are further described hereinbelow with reference to Table 1.

[34477] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2471 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[34478] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2472 (GAM2472) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[34479] GAM2472 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2472 was detected is described hereinabove with reference to Figs. 2-8.

[34480] GAM2472 gene, herein designated GAM GENE, and GAM2472 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[34481] GAM2472 gene, herein designated GAM GENE, encodes a GAM2472 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2472 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2472 precursor RNA is designated SEQ ID:2449, and is provided hereinbelow with reference to the sequence listing part.

[34482] GAM2472 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2472 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34483] An enzyme complex designated DICER COMPLEX, dices the GAM2472 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2472 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 83%) nucleotide sequence of GAM2472 RNA is designated SEQ ID:5063, and is provided hereinbelow with reference to the sequence listing part.

[34484] GAM2472 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2472 target RNA, herein designated GAM TARGET RNA. GAM2472 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34485] GAM2472 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2472 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2472 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2472 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2472 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34486] The complementary binding of GAM2472 RNA, herein designated GAM RNA, to target binding sites on GAM2472 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2472 target RNA, herein designated GAM TARGET RNA, into GAM2472 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34487] It is appreciated that GAM2472 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2472 target genes. The mRNA of each one of this plurality of GAM2472 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2472 RNA, herein designated GAM RNA, and which when bound by GAM2472 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2472 target proteins.

[34488] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2472 gene, herein designated GAM GENE, on one or more GAM2472 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34489] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2472 correlate with, and may be deduced from, the identity of the target

genes which GAM2472 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34490] Nucleotide sequences of the GAM2472 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2472 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2472 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2472 are further described hereinbelow with reference to Table 1.

[34491] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2472 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[34492] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2473 (GAM2473) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[34493] GAM2473 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2473 was detected is described hereinabove with reference to Figs. 2-8.

[34494] GAM2473 gene, herein designated GAM GENE, and GAM2473 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

[34495] GAM2473 gene, herein designated GAM GENE, encodes a GAM2473 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2473 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2473 precursor RNA is designated SEQ ID:2450, and is provided hereinbelow with reference to the sequence listing part.

[34496] GAM2473 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2473 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34497] An enzyme complex designated DICER COMPLEX, dices the GAM2473 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2473 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of GAM2473 RNA is designated SEQ ID:5064, and is provided

hereinbelow with reference to the sequence listing part.

[34498] GAM2473 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2473 target RNA, herein designated GAM TARGET RNA. GAM2473 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34499] GAM2473 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2473 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2473 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2473 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2473 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.



[34500] The complementary binding of GAM2473 RNA, herein designated GAM RNA, to target binding sites on GAM2473 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2473 target RNA, herein designated GAM TARGET RNA, into GAM2473 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34501] It is appreciated that GAM2473 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2473 target genes. The mRNA of each one of this plurality of GAM2473 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2473 RNA, herein designated GAM RNA, and which when bound by GAM2473 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2473 target proteins.

[34502] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2473 gene, herein designated GAM GENE, on one or more GAM2473 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34503] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2473 correlate with, and may be deduced from, the identity of the target genes which GAM2473 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34504] Nucleotide sequences of the GAM2473 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2473 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2473 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2473 are further described hereinbelow with reference to Table 1.

[34505] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2473 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[34506] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2474 (GAM2474) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[34507] GAM2474 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2474 was detected is described hereinabove with reference to Figs. 2-8.

[34508] GAM2474 gene, herein designated GAM GENE, and GAM2474 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[34509] GAM2474 gene, herein designated GAM GENE, encodes a GAM2474 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2474 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2474 precursor RNA is designated SEQ ID:2451, and is provided hereinbelow with reference to the sequence listing part.

[34510] GAM2474 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2474 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34511] An enzyme complex designated DICER COMPLEX, dices the GAM2474 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2474 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of GAM2474 RNA is designated SEQ ID:5065, and is provided hereinbelow with reference to the sequence listing part.

[34512] GAM2474 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2474 target RNA, herein designated GAM TARGET RNA. GAM2474 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34513] GAM2474 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2474 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2474 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2474 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2474 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34514] The complementary binding of GAM2474 RNA, herein designated GAM RNA, to target binding sites on GAM2474 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2474 target RNA, herein designated GAM TARGET RNA, into GAM2474 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34515] It is appreciated that GAM2474 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2474 target genes. The mRNA of each one of this plurality of GAM2474 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2474 RNA, herein designated GAM RNA, and which when bound by GAM2474 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2474 target proteins.

[34516] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2474 gene, herein designated GAM GENE, on one or more GAM2474 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34517] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2474 correlate with, and may be deduced from, the identity of the target genes which GAM2474 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34518] Nucleotide sequences of the GAM2474 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2474 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2474 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2474 are further described hereinbelow with reference to Table 1.

[34519] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2474 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[34520] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2475 (GAM2475) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[34521] GAM2475 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2475 was detected is described hereinabove with reference to Figs. 2-8.

[34522] GAM2475 gene, herein designated GAM GENE, and GAM2475 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[34523] GAM2475 gene, herein designated GAM GENE, encodes a GAM2475 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2475 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2475 precursor RNA is designated SEQ ID:2452, and is provided hereinbelow with reference to the sequence listing part.

[34524] GAM2475 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2475 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

- [34525] An enzyme complex designated DICER COMPLEX, dices the GAM2475 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2475 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of GAM2475 RNA is designated SEQ ID:5066, and is provided hereinbelow with reference to the sequence listing part.
- [34526] GAM2475 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2475 target RNA, herein designated GAM TARGET RNA. GAM2475 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [34527] GAM2475 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2475 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2475 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an



illustration only, and is not meant to be limiting GAM2475 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2475 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34528] The complementary binding of GAM2475 RNA, herein designated GAM RNA, to target binding sites on GAM2475 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2475 target RNA, herein designated GAM TARGET RNA, into GAM2475 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34529] It is appreciated that GAM2475 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2475 target genes. The mRNA of each one of this plurality of GAM2475 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2475 RNA, herein designated GAM RNA, and which when bound by GAM2475 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2475 target proteins.

[34530] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2475 gene, herein designated GAM GENE, on one or more GAM2475 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34531] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2475 correlate with, and may be deduced from, the identity of the target genes which GAM2475 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34532] Nucleotide sequences of the GAM2475 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2475 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2475 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2475 are further described hereinbelow with reference to Table 1.

[34533] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2475 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

[34534] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2476 (GAM2476) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[34535] GAM2476 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2476 was detected is described hereinabove with reference to Figs. 2-8.

[34536] GAM2476 gene, herein designated GAM GENE, and GAM2476 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[34537] GAM2476 gene, herein designated GAM GENE, encodes a GAM2476 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2476 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2476 precursor RNA is designated SEQ ID:2453, and is provided hereinbelow with reference to the sequence listing part.

[34538] GAM2476 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2476 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34539] An enzyme complex designated DICER COMPLEX, dices the GAM2476 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2476 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 88%) nucleotide sequence of GAM2476 RNA is designated SEQ ID:5067, and is provided hereinbelow with reference to the sequence listing part.

[34540] GAM2476 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2476 target RNA, herein designated GAM TARGET RNA. GAM2476 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34541] GAM2476 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2476 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2476 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2476 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2476 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34542] The complementary binding of GAM2476 RNA, herein designated GAM RNA, to target binding sites on GAM2476 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2476 target RNA, herein designated GAM TARGET RNA, into GAM2476 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34543] It is appreciated that GAM2476 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2476 target genes. The mRNA of each one of this plurality of GAM2476 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2476 RNA, herein designated GAM RNA, and which when bound by GAM2476 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2476 target proteins.

[34544] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2476 gene, herein designated GAM GENE, on one or more GAM2476 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34545] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2476 correlate with, and may be deduced from, the identity of the target genes which GAM2476 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34546] Nucleotide sequences of the GAM2476 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2476 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2476 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2476 are further described hereinbelow with reference to Table 1.

- [34547] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2476 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.
- [34548] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2477 (GAM2477) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.
- [34549] GAM2477 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2477 was detected is described hereinabove with reference to Figs. 2-8.
- [34550] GAM2477 gene, herein designated GAM GENE, and GAM2477 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.
- [34551] GAM2477 gene, herein designated GAM GENE, encodes a GAM2477 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2477 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2477 precursor RNA is designated SEQ ID:2454, and is provided hereinbelow with reference to the sequence listing part.

[34552] GAM2477 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2477 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34553] An enzyme complex designated DICER COMPLEX, dices the GAM2477 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2477 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2477 RNA is designated SEQ ID:5068, and is provided hereinbelow with reference to the sequence listing part.

[34554] GAM2477 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2477 target RNA, herein designated GAM TARGET RNA. GAM2477 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.



[34555] GAM2477 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2477 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2477 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2477 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2477 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34556] The complementary binding of GAM2477 RNA, herein designated GAM RNA, to target binding sites on GAM2477 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2477 target RNA, herein designated GAM TARGET RNA, into GAM2477 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34557] It is appreciated that GAM2477 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2477 target genes. The

mRNA of each one of this plurality of GAM2477 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2477 RNA, herein designated GAM RNA, and which when bound by GAM2477 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2477 target proteins.

[34558] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2477 gene, herein designated GAM GENE, on one or more GAM2477 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34559] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2477 correlate with, and may be deduced from, the identity of the target genes which GAM2477 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34560] Nucleotide sequences of the GAM2477 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2477 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2477 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2477 are further described hereinbelow with reference to Table 1.

[34561] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2477 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[34562] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2478 (GAM2478) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[34563] GAM2478 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2478 was detected is described hereinabove with reference to Figs. 2-8.

[34564] GAM2478 gene, herein designated GAM GENE, and GAM2478 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[34565] GAM2478 gene, herein designated GAM GENE, encodes a GAM2478 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2478 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2478 precursor RNA is designated SEQ ID:2455, and is provided hereinbelow with reference to the sequence listing part.

[34566] GAM2478 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2478 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34567] An enzyme complex designated DICER COMPLEX, dices the GAM2478 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2478 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 78%) nucleotide sequence of GAM2478 RNA is designated SEQ ID:5070, and is provided hereinbelow with reference to the sequence listing part.

[34568] GAM2478 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2478 target RNA, herein designated GAM TARGET RNA. GAM2478 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34569] GAM2478 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2478 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2478 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2478 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2478 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34570] The complementary binding of GAM2478 RNA, herein designated GAM RNA, to target binding sites on GAM2478 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2478 target RNA, herein designated GAM TARGET RNA, into GAM2478 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34571] It is appreciated that GAM2478 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2478 target genes. The mRNA of each one of this plurality of GAM2478 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2478 RNA, herein designated GAM RNA, and which when bound by GAM2478 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2478 target proteins.

[34572] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2478 gene, herein designated GAM GENE, on one or more GAM2478 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34573] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2478 correlate with, and may be deduced from, the identity of the target

genes which GAM2478 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34574] Nucleotide sequences of the GAM2478 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2478 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2478 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2478 are further described hereinbelow with reference to Table 1.

[34575] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2478 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[34576] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2479 (GAM2479) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[34577] GAM2479 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2479 was detected is described hereinabove with reference to Figs. 2-8.

[34578] GAM2479 gene, herein designated GAM GENE, and GAM2479 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

[34579] GAM2479 gene, herein designated GAM GENE, encodes a GAM2479 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2479 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2479 precursor RNA is designated SEQ ID:2456, and is provided hereinbelow with reference to the sequence listing part.

[34580] GAM2479 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2479 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34581] An enzyme complex designated DICER COMPLEX, dices the GAM2479 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2479 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2479 RNA is designated SEQ ID:5069, and is provided



hereinbelow with reference to the sequence listing part.

[34582] GAM2479 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2479 target RNA, herein designated GAM TARGET RNA. GAM2479 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34583] GAM2479 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2479 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2479 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2479 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2479 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34584] The complementary binding of GAM2479 RNA, herein designated GAM RNA, to target binding sites on GAM2479 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2479 target RNA, herein designated GAM TARGET RNA, into GAM2479 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34585] It is appreciated that GAM2479 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2479 target genes. The mRNA of each one of this plurality of GAM2479 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2479 RNA, herein designated GAM RNA, and which when bound by GAM2479 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2479 target proteins.

[34586] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2479 gene, herein designated GAM GENE, on one or more GAM2479 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34587] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2479 correlate with, and may be deduced from, the identity of the target genes which GAM2479 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34588] Nucleotide sequences of the GAM2479 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2479 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2479 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2479 are further described hereinbelow with reference to Table 1.

[34589] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2479 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[34590] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2480 (GAM2480) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[34591] GAM2480 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2480 was detected is described hereinabove with reference to Figs. 2-8.

[34592] GAM2480 gene, herein designated GAM GENE, and GAM2480 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[34593] GAM2480 gene, herein designated GAM GENE, encodes a GAM2480 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2480 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2480 precursor RNA is designated SEQ ID:2457, and is provided hereinbelow with reference to the sequence listing part.

[34594] GAM2480 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2480 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34595] An enzyme complex designated DICER COMPLEX, dices the GAM2480 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2480 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 88%) nucleotide sequence of GAM2480 RNA is designated SEQ ID:5072, and is provided hereinbelow with reference to the sequence listing part.

[34596] GAM2480 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2480 target RNA, herein designated GAM TARGET RNA. GAM2480 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34597] GAM2480 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2480 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2480 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2480 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2480 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34598] The complementary binding of GAM2480 RNA, herein designated GAM RNA, to target binding sites on GAM2480 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2480 target RNA, herein designated GAM TARGET RNA, into GAM2480 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34599] It is appreciated that GAM2480 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2480 target genes. The mRNA of each one of this plurality of GAM2480 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2480 RNA, herein designated GAM RNA, and which when bound by GAM2480 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2480 target proteins.

[34600] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2480 gene, herein designated GAM GENE, on one or more GAM2480 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34601] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2480 correlate with, and may be deduced from, the identity of the target genes which GAM2480 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34602] Nucleotide sequences of the GAM2480 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2480 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2480 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2480 are further described hereinbelow with reference to Table 1.

[34603] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2480 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[34604] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2481 (GAM2481) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

- [34605] GAM2481 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2481 was detected is described hereinabove with reference to Figs. 2-8.
- [34606] GAM2481 gene, herein designated GAM GENE, and GAM2481 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.
- [34607] GAM2481 gene, herein designated GAM GENE, encodes a GAM2481 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2481 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2481 precursor RNA is designated SEQ ID:2458, and is provided hereinbelow with reference to the sequence listing part.
- [34608] GAM2481 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2481 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.



- [34609] An enzyme complex designated DICER COMPLEX, dices the GAM2481 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2481 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 85%) nucleotide sequence of GAM2481 RNA is designated SEQ ID:5071, and is provided hereinbelow with reference to the sequence listing part.
- [34610] GAM2481 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2481 target RNA, herein designated GAM TARGET RNA. GAM2481 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [34611] GAM2481 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2481 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2481 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2481 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2481 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34612] The complementary binding of GAM2481 RNA, herein designated GAM RNA, to target binding sites on GAM2481 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2481 target RNA, herein designated GAM TARGET RNA, into GAM2481 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34613] It is appreciated that GAM2481 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2481 target genes. The mRNA of each one of this plurality of GAM2481 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2481 RNA, herein designated GAM RNA, and which when bound by GAM2481 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2481 target proteins.

[34614] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2481 gene, herein designated GAM GENE, on one or more GAM2481 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34615] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2481 correlate with, and may be deduced from, the identity of the target genes which GAM2481 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34616] Nucleotide sequences of the GAM2481 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2481 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2481 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2481 are further described hereinbelow with reference to Table 1.

[34617] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2481 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

- [34618] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2482 (GAM2482) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.
- [34619] GAM2482 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2482 was detected is described hereinabove with reference to Figs. 2-8.
- [34620] GAM2482 gene, herein designated GAM GENE, and GAM2482 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.
- [34621] GAM2482 gene, herein designated GAM GENE, encodes a GAM2482 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2482 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2482 precursor RNA is designated SEQ ID:2459, and is provided hereinbelow with reference to the sequence listing part.
- [34622] GAM2482 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2482 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34623] An enzyme complex designated DICER COMPLEX, dices the GAM2482 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2482 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 84%) nucleotide sequence of GAM2482 RNA is designated SEQ ID:5073, and is provided hereinbelow with reference to the sequence listing part.

[34624] GAM2482 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2482 target RNA, herein designated GAM TARGET RNA. GAM2482 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34625] GAM2482 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2482 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2482 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2482 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2482 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34626] The complementary binding of GAM2482 RNA, herein designated GAM RNA, to target binding sites on GAM2482 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2482 target RNA, herein designated GAM TARGET RNA, into GAM2482 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34627] It is appreciated that GAM2482 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2482 target genes. The mRNA of each one of this plurality of GAM2482 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2482 RNA, herein designated GAM RNA, and which when bound by GAM2482 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2482 target proteins.

[34628] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2482 gene, herein designated GAM GENE, on one or more GAM2482 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34629] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2482 correlate with, and may be deduced from, the identity of the target genes which GAM2482 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34630] Nucleotide sequences of the GAM2482 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2482 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2482 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2482 are further described hereinbelow with reference to Table 1.

- [34631] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2482 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.
- [34632] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2483 (GAM2483) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.
- [34633] GAM2483 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2483 was detected is described hereinabove with reference to Figs. 2-8.
- [34634] GAM2483 gene, herein designated GAM GENE, and GAM2483 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.
- [34635] GAM2483 gene, herein designated GAM GENE, encodes a GAM2483 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2483 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2483 precursor RNA is designated SEQ ID:2460, and is provided hereinbelow with reference to the sequence listing part.



[34636] GAM2483 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2483 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34637] An enzyme complex designated DICER COMPLEX, dices the GAM2483 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2483 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of GAM2483 RNA is designated SEQ ID:5074, and is provided hereinbelow with reference to the sequence listing part.

[34638] GAM2483 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2483 target RNA, herein designated GAM TARGET RNA. GAM2483 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34639] GAM2483 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2483 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2483 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2483 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2483 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34640] The complementary binding of GAM2483 RNA, herein designated GAM RNA, to target binding sites on GAM2483 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2483 target RNA, herein designated GAM TARGET RNA, into GAM2483 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34641] It is appreciated that GAM2483 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2483 target genes. The

mRNA of each one of this plurality of GAM2483 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2483 RNA, herein designated GAM RNA, and which when bound by GAM2483 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2483 target proteins.

[34642] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2483 gene, herein designated GAM GENE, on one or more GAM2483 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34643] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2483 correlate with, and may be deduced from, the identity of the target genes which GAM2483 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34644] Nucleotide sequences of the GAM2483 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2483 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2483 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2483 are further described hereinbelow with reference to Table 1.

[34645] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2483 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[34646] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2484 (GAM2484) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[34647] GAM2484 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2484 was detected is described hereinabove with reference to Figs. 2-8.

[34648] GAM2484 gene, herein designated GAM GENE, and GAM2484 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[34649] GAM2484 gene, herein designated GAM GENE, encodes a GAM2484 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2484 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2484 precursor RNA is designated SEQ ID:2461, and is provided hereinbelow with reference to the sequence listing part.

[34650] GAM2484 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2484 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34651] An enzyme complex designated DICER COMPLEX, dices the GAM2484 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2484 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 85%) nucleotide sequence of GAM2484 RNA is designated SEQ ID:5076, and is provided hereinbelow with reference to the sequence listing part.

[34652] GAM2484 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2484 target RNA, herein designated GAM TARGET RNA. GAM2484 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34653] GAM2484 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2484 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2484 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2484 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2484 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34654] The complementary binding of GAM2484 RNA, herein designated GAM RNA, to target binding sites on GAM2484 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2484 target RNA, herein designated GAM TARGET RNA, into GAM2484 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34655] It is appreciated that GAM2484 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2484 target genes. The mRNA of each one of this plurality of GAM2484 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2484 RNA, herein designated GAM RNA, and which when bound by GAM2484 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2484 target proteins.

[34656] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2484 gene, herein designated GAM GENE, on one or more GAM2484 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34657] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2484 correlate with, and may be deduced from, the identity of the target

genes which GAM2484 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34658] Nucleotide sequences of the GAM2484 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2484 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2484 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2484 are further described hereinbelow with reference to Table 1.

[34659] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2484 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[34660] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2485 (GAM2485) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[34661] GAM2485 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2485 was detected is described hereinabove with reference to Figs. 2-8.

[34662] GAM2485 gene, herein designated GAM GENE, and GAM2485 target gene, herein designated GAM TARGET GENE, are human genes contained in the



human genome.

[34663] GAM2485 gene, herein designated GAM GENE, encodes a GAM2485 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2485 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2485 precursor RNA is designated SEQ ID:2462, and is provided hereinbelow with reference to the sequence listing part.

[34664] GAM2485 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2485 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34665] An enzyme complex designated DICER COMPLEX, dices the GAM2485 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2485 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of GAM2485 RNA is designated SEQ ID:5075, and is provided

hereinbelow with reference to the sequence listing part.

[34666] GAM2485 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2485 target RNA, herein designated GAM TARGET RNA. GAM2485 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34667] GAM2485 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2485 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2485 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2485 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2485 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34668] The complementary binding of GAM2485 RNA, herein designated GAM RNA, to target binding sites on GAM2485 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2485 target RNA, herein designated GAM TARGET RNA, into GAM2485 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34669] It is appreciated that GAM2485 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2485 target genes. The mRNA of each one of this plurality of GAM2485 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2485 RNA, herein designated GAM RNA, and which when bound by GAM2485 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2485 target proteins.

[34670] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2485 gene, herein designated GAM GENE, on one or more GAM2485 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G.,  
Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34671] It is yet further appreciated that specific functions, and accordingly utilities, of  
GAM2485 correlate with, and may be deduced from, the identity of the target  
genes which GAM2485 binds and inhibits, and the function of these target  
genes, as elaborated hereinbelow.

[34672] Nucleotide sequences of the GAM2485 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2485 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2485 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2485 are further described hereinbelow with reference to Table 1.

[34673] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2485 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[34674] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2486 (GAM2486) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[34675] GAM2486 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2486 was detected is described hereinabove with reference to Figs. 2-8.

[34676] GAM2486 gene, herein designated GAM GENE, and GAM2486 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[34677] GAM2486 gene, herein designated GAM GENE, encodes a GAM2486

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2486 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2486 precursor RNA is designated SEQ ID:2463, and is provided hereinbelow with reference to the sequence listing part.

[34678] GAM2486 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2486 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34679] An enzyme complex designated DICER COMPLEX, dices the GAM2486 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2486 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 78%) nucleotide sequence of GAM2486 RNA is designated SEQ ID:5077, and is provided hereinbelow with reference to the sequence listing part.

[34680] GAM2486 target gene, herein designated GAM TARGET GENE, encodes a

corresponding messenger RNA, GAM2486 target RNA, herein designated GAM TARGET RNA. GAM2486 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34681] GAM2486 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2486 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2486 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2486 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2486 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34682] The complementary binding of GAM2486 RNA, herein designated GAM RNA, to target binding sites on GAM2486 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and

BINDING SITE III, inhibits translation of GAM2486 target RNA, herein designated GAM TARGET RNA, into GAM2486 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34683] It is appreciated that GAM2486 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2486 target genes. The mRNA of each one of this plurality of GAM2486 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2486 RNA, herein designated GAM RNA, and which when bound by GAM2486 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2486 target proteins.

[34684] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2486 gene, herein designated GAM GENE, on one or more GAM2486 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).



[34685] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2486 correlate with, and may be deduced from, the identity of the target genes which GAM2486 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34686] Nucleotide sequences of the GAM2486 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2486 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2486 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2486 are further described hereinbelow with reference to Table 1.

[34687] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2486 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[34688] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2487 (GAM2487) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[34689] GAM2487 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2487 was detected is described hereinabove with reference to Figs. 2-8.

[34690] GAM2487 gene, herein designated GAM GENE, and GAM2487 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[34691] GAM2487 gene, herein designated GAM GENE, encodes a GAM2487 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2487 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2487 precursor RNA is designated SEQ ID:2464, and is provided hereinbelow with reference to the sequence listing part.

[34692] GAM2487 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2487 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34693] An enzyme complex designated DICER COMPLEX, dices the GAM2487 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2487 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer

together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2487 RNA is designated SEQ ID:5079, and is provided hereinbelow with reference to the sequence listing part.

[34694] GAM2487 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2487 target RNA, herein designated GAM TARGET RNA. GAM2487 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34695] GAM2487 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2487 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2487 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2487 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2487 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or

in both 3UTR and 5UTR regions.

[34696] The complementary binding of GAM2487 RNA, herein designated GAM RNA, to target binding sites on GAM2487 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2487 target RNA, herein designated GAM TARGET RNA, into GAM2487 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34697] It is appreciated that GAM2487 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2487 target genes. The mRNA of each one of this plurality of GAM2487 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2487 RNA, herein designated GAM RNA, and which when bound by GAM2487 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2487 target proteins.

[34698] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2487 gene, herein designated GAM GENE, on one or more GAM2487 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes

are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34699] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2487 correlate with, and may be deduced from, the identity of the target genes which GAM2487 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34700] Nucleotide sequences of the GAM2487 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2487 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2487 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2487 are further described hereinbelow with reference to Table 1.

[34701] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2487 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[34702] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2488 (GAM2488) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

- [34703] GAM2488 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2488 was detected is described hereinabove with reference to Figs. 2-8.
- [34704] GAM2488 gene, herein designated GAM GENE, and GAM2488 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.
- [34705] GAM2488 gene, herein designated GAM GENE, encodes a GAM2488 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2488 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2488 precursor RNA is designated SEQ ID:2465, and is provided hereinbelow with reference to the sequence listing part.
- [34706] GAM2488 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2488 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.
- [34707] An enzyme complex designated DICER COMPLEX, dices the GAM2488 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2488 RNA, herein designated GAM RNA, a single stranded

~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of GAM2488 RNA is designated SEQ ID:5078, and is provided hereinbelow with reference to the sequence listing part.

[34708] GAM2488 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2488 target RNA, herein designated GAM TARGET RNA. GAM2488 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34709] GAM2488 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2488 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2488 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2488 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2488 target RNA, herein designated GAM

TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34710] The complementary binding of GAM2488 RNA, herein designated GAM RNA, to target binding sites on GAM2488 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2488 target RNA, herein designated GAM TARGET RNA, into GAM2488 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34711] It is appreciated that GAM2488 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2488 target genes. The mRNA of each one of this plurality of GAM2488 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2488 RNA, herein designated GAM RNA, and which when bound by GAM2488 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2488 target proteins.

[34712] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2488 gene, herein designated GAM GENE, on one or more GAM2488 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with



reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34713] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2488 correlate with, and may be deduced from, the identity of the target genes which GAM2488 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34714] Nucleotide sequences of the GAM2488 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2488 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2488 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2488 are further described hereinbelow with reference to Table 1.

[34715] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2488 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[34716] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as

Genomic Address Messenger 2489 (GAM2489) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

- [34717] GAM2489 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2489 was detected is described hereinabove with reference to Figs. 2-8.
- [34718] GAM2489 gene, herein designated GAM GENE, and GAM2489 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.
- [34719] GAM2489 gene, herein designated GAM GENE, encodes a GAM2489 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2489 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2489 precursor RNA is designated SEQ ID:2466, and is provided hereinbelow with reference to the sequence listing part.
- [34720] GAM2489 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2489 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

- [34721] An enzyme complex designated DICER COMPLEX, dices the GAM2489 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2489 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of GAM2489 RNA is designated SEQ ID:5080, and is provided hereinbelow with reference to the sequence listing part.
- [34722] GAM2489 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2489 target RNA, herein designated GAM TARGET RNA. GAM2489 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [34723] GAM2489 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2489 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2489 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2489 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2489 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34724] The complementary binding of GAM2489 RNA, herein designated GAM RNA, to target binding sites on GAM2489 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2489 target RNA, herein designated GAM TARGET RNA, into GAM2489 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34725] It is appreciated that GAM2489 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2489 target genes. The mRNA of each one of this plurality of GAM2489 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2489 RNA, herein designated GAM RNA, and which when bound by GAM2489 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2489 target proteins.

[34726] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2489 gene, herein designated GAM GENE, on one or more GAM2489 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34727] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2489 correlate with, and may be deduced from, the identity of the target genes which GAM2489 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34728] Nucleotide sequences of the GAM2489 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2489 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2489 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2489 are further described hereinbelow with reference to Table 1.

[34729] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2489 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

[34730] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2490 (GAM2490) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[34731] GAM2490 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2490 was detected is described hereinabove with reference to Figs. 2-8.

[34732] GAM2490 gene, herein designated GAM GENE, and GAM2490 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[34733] GAM2490 gene, herein designated GAM GENE, encodes a GAM2490 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2490 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2490 precursor RNA is designated SEQ ID:2467, and is provided hereinbelow with reference to the sequence listing part.

[34734] GAM2490 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2490 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34735] An enzyme complex designated DICER COMPLEX, dices the GAM2490 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2490 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2490 RNA is designated SEQ ID:5081, and is provided hereinbelow with reference to the sequence listing part.

[34736] GAM2490 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2490 target RNA, herein designated GAM TARGET RNA. GAM2490 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34737] GAM2490 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2490 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2490 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2490 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2490 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34738] The complementary binding of GAM2490 RNA, herein designated GAM RNA, to target binding sites on GAM2490 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2490 target RNA, herein designated GAM TARGET RNA, into GAM2490 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34739] It is appreciated that GAM2490 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2490 target genes. The mRNA of each one of this plurality of GAM2490 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2490 RNA, herein designated GAM RNA, and which when bound by GAM2490 RNA, herein designated GAM RNA,



causes inhibition of translation of respective one or more GAM2490 target proteins.

[34740] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2490 gene, herein designated GAM GENE, on one or more GAM2490 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34741] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2490 correlate with, and may be deduced from, the identity of the target genes which GAM2490 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34742] Nucleotide sequences of the GAM2490 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2490 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2490 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2490 are further described hereinbelow with reference to Table 1.

[34743] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2490 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[34744] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2491 (GAM2491) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[34745] GAM2491 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2491 was detected is described hereinabove with reference to Figs. 2-8.

[34746] GAM2491 gene, herein designated GAM GENE, and GAM2491 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[34747] GAM2491 gene, herein designated GAM GENE, encodes a GAM2491 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2491 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2491 precursor RNA is designated SEQ ID:2468, and is provided hereinbelow with reference to the sequence listing part.

[34748] GAM2491 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2491 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34749] An enzyme complex designated DICER COMPLEX, dices the GAM2491 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2491 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 86%) nucleotide sequence of GAM2491 RNA is designated SEQ ID:5082, and is provided hereinbelow with reference to the sequence listing part.

[34750] GAM2491 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2491 target RNA, herein designated GAM TARGET RNA. GAM2491 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34751] GAM2491 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2491 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2491 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2491 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2491 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34752] The complementary binding of GAM2491 RNA, herein designated GAM RNA, to target binding sites on GAM2491 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2491 target RNA, herein designated GAM TARGET RNA, into GAM2491 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34753] It is appreciated that GAM2491 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2491 target genes. The

mRNA of each one of this plurality of GAM2491 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2491 RNA, herein designated GAM RNA, and which when bound by GAM2491 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2491 target proteins.

[34754] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2491 gene, herein designated GAM GENE, on one or more GAM2491 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34755] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2491 correlate with, and may be deduced from, the identity of the target genes which GAM2491 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34756] Nucleotide sequences of the GAM2491 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2491 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2491 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2491 are further described hereinbelow with reference to Table 1.

[34757] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2491 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[34758] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2492 (GAM2492) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[34759] GAM2492 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2492 was detected is described hereinabove with reference to Figs. 2-8.

[34760] GAM2492 gene, herein designated GAM GENE, and GAM2492 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[34761] GAM2492 gene, herein designated GAM GENE, encodes a GAM2492 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2492 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2492 precursor RNA is designated SEQ ID:2469, and is provided hereinbelow with reference to the sequence listing part.

[34762] GAM2492 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2492 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34763] An enzyme complex designated DICER COMPLEX, dices the GAM2492 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2492 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of GAM2492 RNA is designated SEQ ID:5083, and is provided hereinbelow with reference to the sequence listing part.

[34764] GAM2492 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2492 target RNA, herein designated GAM TARGET RNA. GAM2492 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34765] GAM2492 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2492 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2492 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2492 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2492 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34766] The complementary binding of GAM2492 RNA, herein designated GAM RNA, to target binding sites on GAM2492 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2492 target RNA, herein designated GAM TARGET RNA, into GAM2492 target protein, herein



designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34767] It is appreciated that GAM2492 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2492 target genes. The mRNA of each one of this plurality of GAM2492 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2492 RNA, herein designated GAM RNA, and which when bound by GAM2492 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2492 target proteins.

[34768] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2492 gene, herein designated GAM GENE, on one or more GAM2492 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34769] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2492 correlate with, and may be deduced from, the identity of the target

genes which GAM2492 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34770] Nucleotide sequences of the GAM2492 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2492 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2492 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2492 are further described hereinbelow with reference to Table 1.

[34771] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2492 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[34772] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2493 (GAM2493) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[34773] GAM2493 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2493 was detected is described hereinabove with reference to Figs. 2-8.

[34774] GAM2493 gene, herein designated GAM GENE, and GAM2493 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

[34775] GAM2493 gene, herein designated GAM GENE, encodes a GAM2493 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2493 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2493 precursor RNA is designated SEQ ID:2470, and is provided hereinbelow with reference to the sequence listing part.

[34776] GAM2493 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2493 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34777] An enzyme complex designated DICER COMPLEX, dices the GAM2493 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2493 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2493 RNA is designated SEQ ID:5084, and is provided

hereinbelow with reference to the sequence listing part.

[34778] GAM2493 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2493 target RNA, herein designated GAM TARGET RNA. GAM2493 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34779] GAM2493 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2493 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2493 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2493 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2493 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34780] The complementary binding of GAM2493 RNA, herein designated GAM RNA, to target binding sites on GAM2493 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2493 target RNA, herein designated GAM TARGET RNA, into GAM2493 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34781] It is appreciated that GAM2493 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2493 target genes. The mRNA of each one of this plurality of GAM2493 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2493 RNA, herein designated GAM RNA, and which when bound by GAM2493 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2493 target proteins.

[34782] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2493 gene, herein designated GAM GENE, on one or more GAM2493 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34783] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2493 correlate with, and may be deduced from, the identity of the target genes which GAM2493 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34784] Nucleotide sequences of the GAM2493 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2493 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2493 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2493 are further described hereinbelow with reference to Table 1.

[34785] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2493 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[34786] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2494 (GAM2494) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[34787] GAM2494 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2494 was detected is described hereinabove with reference to Figs. 2-8.

[34788] GAM2494 gene, herein designated GAM GENE, and GAM2494 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[34789] GAM2494 gene, herein designated GAM GENE, encodes a GAM2494 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2494 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2494 precursor RNA is designated SEQ ID:2471, and is provided hereinbelow with reference to the sequence listing part.

[34790] GAM2494 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2494 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34791] An enzyme complex designated DICER COMPLEX, dices the GAM2494 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2494 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 86%) nucleotide sequence of GAM2494 RNA is designated SEQ ID:5085, and is provided hereinbelow with reference to the sequence listing part.

[34792] GAM2494 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2494 target RNA, herein designated GAM TARGET RNA. GAM2494 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34793] GAM2494 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2494 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2494 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2494 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2494 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target



binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34794] The complementary binding of GAM2494 RNA, herein designated GAM RNA, to target binding sites on GAM2494 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2494 target RNA, herein designated GAM TARGET RNA, into GAM2494 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34795] It is appreciated that GAM2494 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2494 target genes. The mRNA of each one of this plurality of GAM2494 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2494 RNA, herein designated GAM RNA, and which when bound by GAM2494 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2494 target proteins.

[34796] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2494 gene, herein designated GAM GENE, on one or more GAM2494 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34797] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2494 correlate with, and may be deduced from, the identity of the target genes which GAM2494 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34798] Nucleotide sequences of the GAM2494 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2494 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2494 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2494 are further described hereinbelow with reference to Table 1.

[34799] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2494 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[34800] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2495 (GAM2495) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[34801] GAM2495 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2495 was detected is described hereinabove with reference to Figs. 2-8.

[34802] GAM2495 gene, herein designated GAM GENE, and GAM2495 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[34803] GAM2495 gene, herein designated GAM GENE, encodes a GAM2495 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2495 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2495 precursor RNA is designated SEQ ID:2472, and is provided hereinbelow with reference to the sequence listing part.

[34804] GAM2495 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2495 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

- [34805] An enzyme complex designated DICER COMPLEX, dices the GAM2495 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2495 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2495 RNA is designated SEQ ID:5086, and is provided hereinbelow with reference to the sequence listing part.
- [34806] GAM2495 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2495 target RNA, herein designated GAM TARGET RNA. GAM2495 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [34807] GAM2495 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2495 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2495 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2495 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2495 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34808] The complementary binding of GAM2495 RNA, herein designated GAM RNA, to target binding sites on GAM2495 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2495 target RNA, herein designated GAM TARGET RNA, into GAM2495 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34809] It is appreciated that GAM2495 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2495 target genes. The mRNA of each one of this plurality of GAM2495 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2495 RNA, herein designated GAM RNA, and which when bound by GAM2495 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2495 target proteins.

[34810] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2495 gene, herein designated GAM GENE, on one or more GAM2495 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34811] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2495 correlate with, and may be deduced from, the identity of the target genes which GAM2495 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34812] Nucleotide sequences of the GAM2495 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2495 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2495 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2495 are further described hereinbelow with reference to Table 1.

[34813] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2495 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

- [34814] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2496 (GAM2496) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.
- [34815] GAM2496 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2496 was detected is described hereinabove with reference to Figs. 2-8.
- [34816] GAM2496 gene, herein designated GAM GENE, and GAM2496 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.
- [34817] GAM2496 gene, herein designated GAM GENE, encodes a GAM2496 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2496 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2496 precursor RNA is designated SEQ ID:2473, and is provided hereinbelow with reference to the sequence listing part.
- [34818] GAM2496 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2496 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34819] An enzyme complex designated DICER COMPLEX, dices the GAM2496 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2496 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 85%) nucleotide sequence of GAM2496 RNA is designated SEQ ID:5087, and is provided hereinbelow with reference to the sequence listing part.

[34820] GAM2496 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2496 target RNA, herein designated GAM TARGET RNA. GAM2496 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34821] GAM2496 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2496 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2496 RNA,



herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2496 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2496 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34822] The complementary binding of GAM2496 RNA, herein designated GAM RNA, to target binding sites on GAM2496 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2496 target RNA, herein designated GAM TARGET RNA, into GAM2496 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34823] It is appreciated that GAM2496 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2496 target genes. The mRNA of each one of this plurality of GAM2496 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2496 RNA, herein designated GAM RNA, and which when bound by GAM2496 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2496 target proteins.

[34824] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2496 gene, herein designated GAM GENE, on one or more GAM2496 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34825] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2496 correlate with, and may be deduced from, the identity of the target genes which GAM2496 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34826] Nucleotide sequences of the GAM2496 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2496 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2496 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2496 are further described hereinbelow with reference to Table 1.

[34827] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2496 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[34828] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2497 (GAM2497) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[34829] GAM2497 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2497 was detected is described hereinabove with reference to Figs. 2-8.

[34830] GAM2497 gene, herein designated GAM GENE, and GAM2497 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[34831] GAM2497 gene, herein designated GAM GENE, encodes a GAM2497 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2497 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2497 precursor RNA is designated SEQ ID:2474, and is provided hereinbelow with reference to the sequence listing part.

[34832] GAM2497 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2497 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34833] An enzyme complex designated DICER COMPLEX, dices the GAM2497 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2497 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2497 RNA is designated SEQ ID:5088, and is provided hereinbelow with reference to the sequence listing part.

[34834] GAM2497 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2497 target RNA, herein designated GAM TARGET RNA. GAM2497 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34835] GAM2497 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2497 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2497 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2497 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2497 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34836] The complementary binding of GAM2497 RNA, herein designated GAM RNA, to target binding sites on GAM2497 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2497 target RNA, herein designated GAM TARGET RNA, into GAM2497 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34837] It is appreciated that GAM2497 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2497 target genes. The

mRNA of each one of this plurality of GAM2497 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2497 RNA, herein designated GAM RNA, and which when bound by GAM2497 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2497 target proteins.

[34838] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2497 gene, herein designated GAM GENE, on one or more GAM2497 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34839] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2497 correlate with, and may be deduced from, the identity of the target genes which GAM2497 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34840] Nucleotide sequences of the GAM2497 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2497 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2497 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2497 are further described hereinbelow with reference to Table 1.

[34841] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2497 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[34842] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2498 (GAM2498) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[34843] GAM2498 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2498 was detected is described hereinabove with reference to Figs. 2-8.

[34844] GAM2498 gene, herein designated GAM GENE, and GAM2498 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[34845] GAM2498 gene, herein designated GAM GENE, encodes a GAM2498 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2498 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2498 precursor RNA is designated SEQ ID:2475, and is provided hereinbelow with reference to the sequence listing part.

[34846] GAM2498 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2498 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34847] An enzyme complex designated DICER COMPLEX, dices the GAM2498 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2498 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of GAM2498 RNA is designated SEQ ID:5089, and is provided hereinbelow with reference to the sequence listing part.

[34848] GAM2498 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2498 target RNA, herein designated GAM TARGET RNA. GAM2498 target RNA, herein designated GAM



TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34849] GAM2498 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2498 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2498 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2498 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2498 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34850] The complementary binding of GAM2498 RNA, herein designated GAM RNA, to target binding sites on GAM2498 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2498 target RNA, herein designated GAM TARGET RNA, into GAM2498 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34851] It is appreciated that GAM2498 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2498 target genes. The mRNA of each one of this plurality of GAM2498 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2498 RNA, herein designated GAM RNA, and which when bound by GAM2498 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2498 target proteins.

[34852] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2498 gene, herein designated GAM GENE, on one or more GAM2498 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34853] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2498 correlate with, and may be deduced from, the identity of the target

genes which GAM2498 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34854] Nucleotide sequences of the GAM2498 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2498 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2498 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2498 are further described hereinbelow with reference to Table 1.

[34855] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2498 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[34856] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2499 (GAM2499) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[34857] GAM2499 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2499 was detected is described hereinabove with reference to Figs. 2-8.

[34858] GAM2499 gene, herein designated GAM GENE, and GAM2499 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

[34859] GAM2499 gene, herein designated GAM GENE, encodes a GAM2499 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2499 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2499 precursor RNA is designated SEQ ID:2476, and is provided hereinbelow with reference to the sequence listing part.

[34860] GAM2499 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2499 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34861] An enzyme complex designated DICER COMPLEX, dices the GAM2499 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2499 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2499 RNA is designated SEQ ID:5090, and is provided

hereinbelow with reference to the sequence listing part.

[34862] GAM2499 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2499 target RNA, herein designated GAM TARGET RNA. GAM2499 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34863] GAM2499 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2499 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2499 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2499 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2499 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34864] The complementary binding of GAM2499 RNA, herein designated GAM RNA, to target binding sites on GAM2499 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2499 target RNA, herein designated GAM TARGET RNA, into GAM2499 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34865] It is appreciated that GAM2499 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2499 target genes. The mRNA of each one of this plurality of GAM2499 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2499 RNA, herein designated GAM RNA, and which when bound by GAM2499 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2499 target proteins.

[34866] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2499 gene, herein designated GAM GENE, on one or more GAM2499 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34867] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2499 correlate with, and may be deduced from, the identity of the target genes which GAM2499 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34868] Nucleotide sequences of the GAM2499 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2499 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2499 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2499 are further described hereinbelow with reference to Table 1.

[34869] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2499 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[34870] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2500 (GAM2500) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[34871] GAM2500 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2500 was detected is described hereinabove with reference to Figs. 2-8.

[34872] GAM2500 gene, herein designated GAM GENE, and GAM2500 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[34873] GAM2500 gene, herein designated GAM GENE, encodes a GAM2500 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2500 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2500 precursor RNA is designated SEQ ID:2477, and is provided hereinbelow with reference to the sequence listing part.

[34874] GAM2500 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2500 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34875] An enzyme complex designated DICER COMPLEX, dices the GAM2500 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2500 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin



structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2500 RNA is designated SEQ ID:5091, and is provided hereinbelow with reference to the sequence listing part.

[34876] GAM2500 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2500 target RNA, herein designated GAM TARGET RNA. GAM2500 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34877] GAM2500 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2500 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2500 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2500 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2500 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34878] The complementary binding of GAM2500 RNA, herein designated GAM RNA, to target binding sites on GAM2500 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2500 target RNA, herein designated GAM TARGET RNA, into GAM2500 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34879] It is appreciated that GAM2500 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2500 target genes. The mRNA of each one of this plurality of GAM2500 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2500 RNA, herein designated GAM RNA, and which when bound by GAM2500 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2500 target proteins.

[34880] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2500 gene, herein designated GAM GENE, on one or more GAM2500 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34881] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2500 correlate with, and may be deduced from, the identity of the target genes which GAM2500 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34882] Nucleotide sequences of the GAM2500 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2500 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2500 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2500 are further described hereinbelow with reference to Table 1.

[34883] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2500 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[34884] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2501 (GAM2501) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

- [34885] GAM2501 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2501 was detected is described hereinabove with reference to Figs. 2-8.
- [34886] GAM2501 gene, herein designated GAM GENE, and GAM2501 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.
- [34887] GAM2501 gene, herein designated GAM GENE, encodes a GAM2501 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2501 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2501 precursor RNA is designated SEQ ID:2478, and is provided hereinbelow with reference to the sequence listing part.
- [34888] GAM2501 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2501 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

- [34889] An enzyme complex designated DICER COMPLEX, dices the GAM2501 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2501 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of GAM2501 RNA is designated SEQ ID:5092, and is provided hereinbelow with reference to the sequence listing part.
- [34890] GAM2501 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2501 target RNA, herein designated GAM TARGET RNA. GAM2501 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [34891] GAM2501 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2501 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2501 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2501 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2501 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34892] The complementary binding of GAM2501 RNA, herein designated GAM RNA, to target binding sites on GAM2501 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2501 target RNA, herein designated GAM TARGET RNA, into GAM2501 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34893] It is appreciated that GAM2501 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2501 target genes. The mRNA of each one of this plurality of GAM2501 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2501 RNA, herein designated GAM RNA, and which when bound by GAM2501 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2501 target proteins.

[34894] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2501 gene, herein designated GAM GENE, on one or more GAM2501 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34895] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2501 correlate with, and may be deduced from, the identity of the target genes which GAM2501 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34896] Nucleotide sequences of the GAM2501 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2501 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2501 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2501 are further described hereinbelow with reference to Table 1.

[34897] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2501 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

[34898] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2502 (GAM2502) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[34899] GAM2502 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2502 was detected is described hereinabove with reference to Figs. 2-8.

[34900] GAM2502 gene, herein designated GAM GENE, and GAM2502 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[34901] GAM2502 gene, herein designated GAM GENE, encodes a GAM2502 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2502 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2502 precursor RNA is designated SEQ ID:2479, and is provided hereinbelow with reference to the sequence listing part.

[34902] GAM2502 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2502 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA



encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34903] An enzyme complex designated DICER COMPLEX, dices the GAM2502 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2502 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of GAM2502 RNA is designated SEQ ID:5093, and is provided hereinbelow with reference to the sequence listing part.

[34904] GAM2502 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2502 target RNA, herein designated GAM TARGET RNA. GAM2502 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34905] GAM2502 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2502 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2502 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2502 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2502 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34906] The complementary binding of GAM2502 RNA, herein designated GAM RNA, to target binding sites on GAM2502 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2502 target RNA, herein designated GAM TARGET RNA, into GAM2502 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34907] It is appreciated that GAM2502 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2502 target genes. The mRNA of each one of this plurality of GAM2502 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2502 RNA, herein designated GAM RNA, and which when bound by GAM2502 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2502 target proteins.

[34908] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2502 gene, herein designated GAM GENE, on one or more GAM2502 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34909] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2502 correlate with, and may be deduced from, the identity of the target genes which GAM2502 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34910] Nucleotide sequences of the GAM2502 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2502 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2502 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2502 are further described hereinbelow with reference to Table 1.

- [34911] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2502 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.
- [34912] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2503 (GAM2503) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.
- [34913] GAM2503 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2503 was detected is described hereinabove with reference to Figs. 2-8.
- [34914] GAM2503 gene, herein designated GAM GENE, and GAM2503 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.
- [34915] GAM2503 gene, herein designated GAM GENE, encodes a GAM2503 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2503 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2503 precursor RNA is designated SEQ ID:2480, and is provided hereinbelow with reference to the sequence listing part.

[34916] GAM2503 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2503 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34917] An enzyme complex designated DICER COMPLEX, dices the GAM2503 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2503 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 86%) nucleotide sequence of GAM2503 RNA is designated SEQ ID:5094, and is provided hereinbelow with reference to the sequence listing part.

[34918] GAM2503 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2503 target RNA, herein designated GAM TARGET RNA. GAM2503 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34919] GAM2503 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2503 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2503 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2503 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2503 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34920] The complementary binding of GAM2503 RNA, herein designated GAM RNA, to target binding sites on GAM2503 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2503 target RNA, herein designated GAM TARGET RNA, into GAM2503 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34921] It is appreciated that GAM2503 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2503 target genes. The

mRNA of each one of this plurality of GAM2503 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2503 RNA, herein designated GAM RNA, and which when bound by GAM2503 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2503 target proteins.

[34922] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2503 gene, herein designated GAM GENE, on one or more GAM2503 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34923] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2503 correlate with, and may be deduced from, the identity of the target genes which GAM2503 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34924] Nucleotide sequences of the GAM2503 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2503 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2503 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2503 are further described hereinbelow with reference to Table 1.

[34925] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2503 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[34926] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2504 (GAM2504) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[34927] GAM2504 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2504 was detected is described hereinabove with reference to Figs. 2-8.

[34928] GAM2504 gene, herein designated GAM GENE, and GAM2504 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[34929] GAM2504 gene, herein designated GAM GENE, encodes a GAM2504 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2504 precursor RNA,



herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2504 precursor RNA is designated SEQ ID:2481, and is provided hereinbelow with reference to the sequence listing part.

[34930] GAM2504 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2504 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34931] An enzyme complex designated DICER COMPLEX, dices the GAM2504 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2504 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of GAM2504 RNA is designated SEQ ID:5095, and is provided hereinbelow with reference to the sequence listing part.

[34932] GAM2504 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2504 target RNA, herein designated GAM TARGET RNA. GAM2504 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34933] GAM2504 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2504 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2504 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2504 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2504 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34934] The complementary binding of GAM2504 RNA, herein designated GAM RNA, to target binding sites on GAM2504 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2504 target RNA, herein designated GAM TARGET RNA, into GAM2504 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34935] It is appreciated that GAM2504 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2504 target genes. The mRNA of each one of this plurality of GAM2504 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2504 RNA, herein designated GAM RNA, and which when bound by GAM2504 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2504 target proteins.

[34936] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2504 gene, herein designated GAM GENE, on one or more GAM2504 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34937] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2504 correlate with, and may be deduced from, the identity of the target

genes which GAM2504 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34938] Nucleotide sequences of the GAM2504 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2504 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2504 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2504 are further described hereinbelow with reference to Table 1.

[34939] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2504 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[34940] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2505 (GAM2505) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[34941] GAM2505 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2505 was detected is described hereinabove with reference to Figs. 2-8.

[34942] GAM2505 gene, herein designated GAM GENE, and GAM2505 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

[34943] GAM2505 gene, herein designated GAM GENE, encodes a GAM2505 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2505 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2505 precursor RNA is designated SEQ ID:2482, and is provided hereinbelow with reference to the sequence listing part.

[34944] GAM2505 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2505 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34945] An enzyme complex designated DICER COMPLEX, dices the GAM2505 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2505 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 83%) nucleotide sequence of GAM2505 RNA is designated SEQ ID:5096, and is provided

hereinbelow with reference to the sequence listing part.

[34946] GAM2505 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2505 target RNA, herein designated GAM TARGET RNA. GAM2505 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34947] GAM2505 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2505 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2505 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2505 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2505 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34948] The complementary binding of GAM2505 RNA, herein designated GAM RNA, to target binding sites on GAM2505 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2505 target RNA, herein designated GAM TARGET RNA, into GAM2505 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34949] It is appreciated that GAM2505 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2505 target genes. The mRNA of each one of this plurality of GAM2505 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2505 RNA, herein designated GAM RNA, and which when bound by GAM2505 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2505 target proteins.

[34950] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2505 gene, herein designated GAM GENE, on one or more GAM2505 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34951] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2505 correlate with, and may be deduced from, the identity of the target genes which GAM2505 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34952] Nucleotide sequences of the GAM2505 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2505 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2505 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2505 are further described hereinbelow with reference to Table 1.

[34953] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2505 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[34954] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2506 (GAM2506) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[34955] GAM2506 is a novel bioinformatically detected regulatory, non protein



coding, micro RNA (miRNA) gene. The method by which GAM2506 was detected is described hereinabove with reference to Figs. 2-8.

[34956] GAM2506 gene, herein designated GAM GENE, and GAM2506 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[34957] GAM2506 gene, herein designated GAM GENE, encodes a GAM2506 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2506 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2506 precursor RNA is designated SEQ ID:2483, and is provided hereinbelow with reference to the sequence listing part.

[34958] GAM2506 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2506 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34959] An enzyme complex designated DICER COMPLEX, dices the GAM2506 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2506 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2506 RNA is designated SEQ ID:5097, and is provided hereinbelow with reference to the sequence listing part.

[34960] GAM2506 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2506 target RNA, herein designated GAM TARGET RNA. GAM2506 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34961] GAM2506 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2506 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2506 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2506 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2506 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34962] The complementary binding of GAM2506 RNA, herein designated GAM RNA, to target binding sites on GAM2506 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2506 target RNA, herein designated GAM TARGET RNA, into GAM2506 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34963] It is appreciated that GAM2506 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2506 target genes. The mRNA of each one of this plurality of GAM2506 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2506 RNA, herein designated GAM RNA, and which when bound by GAM2506 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2506 target proteins.

[34964] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2506 gene, herein designated GAM GENE, on one or more GAM2506 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34965] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2506 correlate with, and may be deduced from, the identity of the target genes which GAM2506 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34966] Nucleotide sequences of the GAM2506 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2506 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2506 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2506 are further described hereinbelow with reference to Table 1.

[34967] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2506 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[34968] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2507 (GAM2507) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[34969] GAM2507 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2507 was detected is described hereinabove with reference to Figs. 2-8.

[34970] GAM2507 gene, herein designated GAM GENE, and GAM2507 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[34971] GAM2507 gene, herein designated GAM GENE, encodes a GAM2507 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2507 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2507 precursor RNA is designated SEQ ID:2484, and is provided hereinbelow with reference to the sequence listing part.

[34972] GAM2507 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2507 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

- [34973] An enzyme complex designated DICER COMPLEX, dices the GAM2507 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2507 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2507 RNA is designated SEQ ID:5098, and is provided hereinbelow with reference to the sequence listing part.
- [34974] GAM2507 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2507 target RNA, herein designated GAM TARGET RNA. GAM2507 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [34975] GAM2507 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2507 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2507 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2507 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2507 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34976] The complementary binding of GAM2507 RNA, herein designated GAM RNA, to target binding sites on GAM2507 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2507 target RNA, herein designated GAM TARGET RNA, into GAM2507 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34977] It is appreciated that GAM2507 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2507 target genes. The mRNA of each one of this plurality of GAM2507 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2507 RNA, herein designated GAM RNA, and which when bound by GAM2507 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2507 target proteins.

[34978] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2507 gene, herein designated GAM GENE, on one or more GAM2507 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34979] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2507 correlate with, and may be deduced from, the identity of the target genes which GAM2507 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34980] Nucleotide sequences of the GAM2507 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2507 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2507 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2507 are further described hereinbelow with reference to Table 1.

[34981] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2507 RNA, herein designated GAM RNA, are described hereinbelow



with reference to Table 2.

[34982] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2508 (GAM2508) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[34983] GAM2508 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2508 was detected is described hereinabove with reference to Figs. 2-8.

[34984] GAM2508 gene, herein designated GAM GENE, and GAM2508 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[34985] GAM2508 gene, herein designated GAM GENE, encodes a GAM2508 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2508 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2508 precursor RNA is designated SEQ ID:2485, and is provided hereinbelow with reference to the sequence listing part.

[34986] GAM2508 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2508 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[34987] An enzyme complex designated DICER COMPLEX, dices the GAM2508 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2508 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2508 RNA is designated SEQ ID:5099, and is provided hereinbelow with reference to the sequence listing part.

[34988] GAM2508 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2508 target RNA, herein designated GAM TARGET RNA. GAM2508 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[34989] GAM2508 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2508 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2508 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2508 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2508 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[34990] The complementary binding of GAM2508 RNA, herein designated GAM RNA, to target binding sites on GAM2508 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2508 target RNA, herein designated GAM TARGET RNA, into GAM2508 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[34991] It is appreciated that GAM2508 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2508 target genes. The mRNA of each one of this plurality of GAM2508 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2508 RNA, herein designated GAM RNA, and which when bound by GAM2508 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2508 target proteins.

[34992] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2508 gene, herein designated GAM GENE, on one or more GAM2508 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[34993] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2508 correlate with, and may be deduced from, the identity of the target genes which GAM2508 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[34994] Nucleotide sequences of the GAM2508 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2508 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2508 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2508 are further described hereinbelow with reference to Table 1.

[34995] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2508 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[34996] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2509 (GAM2509) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[34997] GAM2509 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2509 was detected is described hereinabove with reference to Figs. 2-8.

[34998] GAM2509 gene, herein designated GAM GENE, and GAM2509 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[34999] GAM2509 gene, herein designated GAM GENE, encodes a GAM2509 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2509 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2509 precursor RNA is designated SEQ ID:2486, and is provided hereinbelow with reference to the sequence listing part.

[35000] GAM2509 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2509 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35001] An enzyme complex designated DICER COMPLEX, dices the GAM2509 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2509 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 94%) nucleotide sequence of GAM2509 RNA is designated SEQ ID:5100, and is provided hereinbelow with reference to the sequence listing part.

[35002] GAM2509 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2509 target RNA, herein designated GAM TARGET RNA. GAM2509 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35003] GAM2509 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2509 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2509 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2509 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2509 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35004] The complementary binding of GAM2509 RNA, herein designated GAM RNA, to target binding sites on GAM2509 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2509 target RNA, herein designated GAM TARGET RNA, into GAM2509 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35005] It is appreciated that GAM2509 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2509 target genes. The

mRNA of each one of this plurality of GAM2509 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2509 RNA, herein designated GAM RNA, and which when bound by GAM2509 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2509 target proteins.

[35006] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2509 gene, herein designated GAM GENE, on one or more GAM2509 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35007] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2509 correlate with, and may be deduced from, the identity of the target genes which GAM2509 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35008] Nucleotide sequences of the GAM2509 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2509 RNA, herein



designated GAM RNA, and a schematic representation of the secondary folding of GAM2509 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2509 are further described hereinbelow with reference to Table 1.

[35009] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2509 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[35010] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2510 (GAM2510) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35011] GAM2510 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2510 was detected is described hereinabove with reference to Figs. 2-8.

[35012] GAM2510 gene, herein designated GAM GENE, and GAM2510 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[35013] GAM2510 gene, herein designated GAM GENE, encodes a GAM2510 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2510 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2510 precursor RNA is designated SEQ ID:2487, and is provided hereinbelow with reference to the sequence listing part.

[35014] GAM2510 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2510 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35015] An enzyme complex designated DICER COMPLEX, dices the GAM2510 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2510 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of GAM2510 RNA is designated SEQ ID:5101, and is provided hereinbelow with reference to the sequence listing part.

[35016] GAM2510 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2510 target RNA, herein designated GAM TARGET RNA. GAM2510 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35017] GAM2510 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2510 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2510 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2510 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2510 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35018] The complementary binding of GAM2510 RNA, herein designated GAM RNA, to target binding sites on GAM2510 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2510 target RNA, herein designated GAM TARGET RNA, into GAM2510 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35019] It is appreciated that GAM2510 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2510 target genes. The mRNA of each one of this plurality of GAM2510 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2510 RNA, herein designated GAM RNA, and which when bound by GAM2510 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2510 target proteins.

[35020] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2510 gene, herein designated GAM GENE, on one or more GAM2510 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35021] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2510 correlate with, and may be deduced from, the identity of the target

genes which GAM2510 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35022] Nucleotide sequences of the GAM2510 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2510 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2510 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2510 are further described hereinbelow with reference to Table 1.

[35023] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2510 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[35024] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2511 (GAM2511) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35025] GAM2511 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2511 was detected is described hereinabove with reference to Figs. 2-8.

[35026] GAM2511 gene, herein designated GAM GENE, and GAM2511 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

[35027] GAM2511 gene, herein designated GAM GENE, encodes a GAM2511 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2511 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2511 precursor RNA is designated SEQ ID:2488, and is provided hereinbelow with reference to the sequence listing part.

[35028] GAM2511 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2511 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35029] An enzyme complex designated DICER COMPLEX, dices the GAM2511 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2511 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 76%) nucleotide sequence of GAM2511 RNA is designated SEQ ID:5102, and is provided

hereinbelow with reference to the sequence listing part.

[35030] GAM2511 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2511 target RNA, herein designated GAM TARGET RNA. GAM2511 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35031] GAM2511 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2511 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2511 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2511 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2511 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35032] The complementary binding of GAM2511 RNA, herein designated GAM RNA, to target binding sites on GAM2511 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2511 target RNA, herein designated GAM TARGET RNA, into GAM2511 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35033] It is appreciated that GAM2511 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2511 target genes. The mRNA of each one of this plurality of GAM2511 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2511 RNA, herein designated GAM RNA, and which when bound by GAM2511 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2511 target proteins.

[35034] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2511 gene, herein designated GAM GENE, on one or more GAM2511 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding



sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35035] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2511 correlate with, and may be deduced from, the identity of the target genes which GAM2511 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35036] Nucleotide sequences of the GAM2511 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2511 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2511 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2511 are further described hereinbelow with reference to Table 1.

[35037] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2511 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[35038] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2512 (GAM2512) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35039] GAM2512 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2512 was detected is described hereinabove with reference to Figs. 2-8.

[35040] GAM2512 gene, herein designated GAM GENE, and GAM2512 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[35041] GAM2512 gene, herein designated GAM GENE, encodes a GAM2512 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2512 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2512 precursor RNA is designated SEQ ID:2489, and is provided hereinbelow with reference to the sequence listing part.

[35042] GAM2512 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2512 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35043] An enzyme complex designated DICER COMPLEX, dices the GAM2512 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2512 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of GAM2512 RNA is designated SEQ ID:5103, and is provided hereinbelow with reference to the sequence listing part.

[35044] GAM2512 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2512 target RNA, herein designated GAM TARGET RNA. GAM2512 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35045] GAM2512 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2512 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2512 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2512 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2512 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35046] The complementary binding of GAM2512 RNA, herein designated GAM RNA, to target binding sites on GAM2512 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2512 target RNA, herein designated GAM TARGET RNA, into GAM2512 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35047] It is appreciated that GAM2512 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2512 target genes. The mRNA of each one of this plurality of GAM2512 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2512 RNA, herein designated GAM RNA, and which when bound by GAM2512 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2512 target proteins.

[35048] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2512 gene, herein designated GAM GENE, on one or more GAM2512 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35049] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2512 correlate with, and may be deduced from, the identity of the target genes which GAM2512 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35050] Nucleotide sequences of the GAM2512 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2512 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2512 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2512 are further described hereinbelow with reference to Table 1.

[35051] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2512 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[35052] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2513 (GAM2513) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35053] GAM2513 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2513 was detected is described hereinabove with reference to Figs. 2-8.

[35054] GAM2513 gene, herein designated GAM GENE, and GAM2513 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[35055] GAM2513 gene, herein designated GAM GENE, encodes a GAM2513 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2513 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2513 precursor RNA is designated SEQ ID:2490, and is provided hereinbelow with reference to the sequence listing part.

[35056] GAM2513 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2513 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

- [35057] An enzyme complex designated DICER COMPLEX, dices the GAM2513 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2513 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of GAM2513 RNA is designated SEQ ID:5104, and is provided hereinbelow with reference to the sequence listing part.
- [35058] GAM2513 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2513 target RNA, herein designated GAM TARGET RNA. GAM2513 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [35059] GAM2513 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2513 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2513 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2513 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2513 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35060] The complementary binding of GAM2513 RNA, herein designated GAM RNA, to target binding sites on GAM2513 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2513 target RNA, herein designated GAM TARGET RNA, into GAM2513 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35061] It is appreciated that GAM2513 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2513 target genes. The mRNA of each one of this plurality of GAM2513 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2513 RNA, herein designated GAM RNA, and which when bound by GAM2513 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2513 target proteins.

[35062] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition



exerted by GAM2513 gene, herein designated GAM GENE, on one or more GAM2513 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35063] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2513 correlate with, and may be deduced from, the identity of the target genes which GAM2513 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35064] Nucleotide sequences of the GAM2513 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2513 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2513 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2513 are further described hereinbelow with reference to Table 1.

[35065] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2513 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

[35066] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2514 (GAM2514) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35067] GAM2514 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2514 was detected is described hereinabove with reference to Figs. 2-8.

[35068] GAM2514 gene, herein designated GAM GENE, and GAM2514 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[35069] GAM2514 gene, herein designated GAM GENE, encodes a GAM2514 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2514 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2514 precursor RNA is designated SEQ ID:2491, and is provided hereinbelow with reference to the sequence listing part.

[35070] GAM2514 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2514 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35071] An enzyme complex designated DICER COMPLEX, dices the GAM2514 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2514 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2514 RNA is designated SEQ ID:5105, and is provided hereinbelow with reference to the sequence listing part.

[35072] GAM2514 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2514 target RNA, herein designated GAM TARGET RNA. GAM2514 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35073] GAM2514 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2514 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2514 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2514 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2514 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35074] The complementary binding of GAM2514 RNA, herein designated GAM RNA, to target binding sites on GAM2514 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2514 target RNA, herein designated GAM TARGET RNA, into GAM2514 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35075] It is appreciated that GAM2514 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2514 target genes. The mRNA of each one of this plurality of GAM2514 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2514 RNA, herein designated GAM RNA, and which when bound by GAM2514 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2514 target proteins.

[35076] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2514 gene, herein designated GAM GENE, on one or more GAM2514 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35077] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2514 correlate with, and may be deduced from, the identity of the target genes which GAM2514 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35078] Nucleotide sequences of the GAM2514 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2514 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2514 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2514 are further described hereinbelow with reference to Table 1.

[35079] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2514 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[35080] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2515 (GAM2515) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35081] GAM2515 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2515 was detected is described hereinabove with reference to Figs. 2-8.

[35082] GAM2515 gene, herein designated GAM GENE, and GAM2515 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[35083] GAM2515 gene, herein designated GAM GENE, encodes a GAM2515 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2515 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2515 precursor RNA is designated SEQ ID:2492, and is provided hereinbelow with reference to the sequence listing part.

[35084] GAM2515 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2515 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35085] An enzyme complex designated DICER COMPLEX, dices the GAM2515 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2515 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2515 RNA is designated SEQ ID:5106, and is provided hereinbelow with reference to the sequence listing part.

[35086] GAM2515 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2515 target RNA, herein designated GAM TARGET RNA. GAM2515 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35087] GAM2515 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2515 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2515 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2515 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2515 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35088] The complementary binding of GAM2515 RNA, herein designated GAM RNA, to target binding sites on GAM2515 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2515 target RNA, herein designated GAM TARGET RNA, into GAM2515 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35089] It is appreciated that GAM2515 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2515 target genes. The



mRNA of each one of this plurality of GAM2515 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2515 RNA, herein designated GAM RNA, and which when bound by GAM2515 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2515 target proteins.

[35090] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2515 gene, herein designated GAM GENE, on one or more GAM2515 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35091] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2515 correlate with, and may be deduced from, the identity of the target genes which GAM2515 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35092] Nucleotide sequences of the GAM2515 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2515 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2515 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2515 are further described hereinbelow with reference to Table 1.

[35093] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2515 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[35094] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2516 (GAM2516) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35095] GAM2516 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2516 was detected is described hereinabove with reference to Figs. 2-8.

[35096] GAM2516 gene, herein designated GAM GENE, and GAM2516 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[35097] GAM2516 gene, herein designated GAM GENE, encodes a GAM2516 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2516 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2516 precursor RNA is designated SEQ ID:2493, and is provided hereinbelow with reference to the sequence listing part.

[35098] GAM2516 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2516 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35099] An enzyme complex designated DICER COMPLEX, dices the GAM2516 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2516 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of GAM2516 RNA is designated SEQ ID:5107, and is provided hereinbelow with reference to the sequence listing part.

[35100] GAM2516 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2516 target RNA, herein designated GAM TARGET RNA. GAM2516 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35101] GAM2516 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2516 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2516 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2516 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2516 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35102] The complementary binding of GAM2516 RNA, herein designated GAM RNA, to target binding sites on GAM2516 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2516 target RNA, herein designated GAM TARGET RNA, into GAM2516 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35103] It is appreciated that GAM2516 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2516 target genes. The mRNA of each one of this plurality of GAM2516 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2516 RNA, herein designated GAM RNA, and which when bound by GAM2516 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2516 target proteins.

[35104] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2516 gene, herein designated GAM GENE, on one or more GAM2516 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35105] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2516 correlate with, and may be deduced from, the identity of the target

genes which GAM2516 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35106] Nucleotide sequences of the GAM2516 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2516 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2516 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2516 are further described hereinbelow with reference to Table 1.

[35107] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2516 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[35108] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2517 (GAM2517) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35109] GAM2517 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2517 was detected is described hereinabove with reference to Figs. 2-8.

[35110] GAM2517 gene, herein designated GAM GENE, and GAM2517 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

- [35111] GAM2517 gene, herein designated GAM GENE, encodes a GAM2517 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2517 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2517 precursor RNA is designated SEQ ID:2494, and is provided hereinbelow with reference to the sequence listing part.
- [35112] GAM2517 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2517 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.
- [35113] An enzyme complex designated DICER COMPLEX, dices the GAM2517 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2517 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 92%) nucleotide sequence of GAM2517 RNA is designated SEQ ID:5108, and is provided

hereinbelow with reference to the sequence listing part.

[35114] GAM2517 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2517 target RNA, herein designated GAM TARGET RNA. GAM2517 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35115] GAM2517 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2517 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2517 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2517 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2517 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.



[35116] The complementary binding of GAM2517 RNA, herein designated GAM RNA, to target binding sites on GAM2517 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2517 target RNA, herein designated GAM TARGET RNA, into GAM2517 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35117] It is appreciated that GAM2517 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2517 target genes. The mRNA of each one of this plurality of GAM2517 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2517 RNA, herein designated GAM RNA, and which when bound by GAM2517 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2517 target proteins.

[35118] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2517 gene, herein designated GAM GENE, on one or more GAM2517 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35119] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2517 correlate with, and may be deduced from, the identity of the target genes which GAM2517 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35120] Nucleotide sequences of the GAM2517 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2517 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2517 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2517 are further described hereinbelow with reference to Table 1.

[35121] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2517 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[35122] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2518 (GAM2518) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35123] GAM2518 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2518 was detected is described hereinabove with reference to Figs. 2-8.

[35124] GAM2518 gene, herein designated GAM GENE, and GAM2518 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[35125] GAM2518 gene, herein designated GAM GENE, encodes a GAM2518 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2518 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2518 precursor RNA is designated SEQ ID:2495, and is provided hereinbelow with reference to the sequence listing part.

[35126] GAM2518 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2518 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35127] An enzyme complex designated DICER COMPLEX, dices the GAM2518 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2518 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 92%) nucleotide sequence of GAM2518 RNA is designated SEQ ID:5109, and is provided hereinbelow with reference to the sequence listing part.

[35128] GAM2518 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2518 target RNA, herein designated GAM TARGET RNA. GAM2518 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35129] GAM2518 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2518 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2518 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2518 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2518 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35130] The complementary binding of GAM2518 RNA, herein designated GAM RNA, to target binding sites on GAM2518 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2518 target RNA, herein designated GAM TARGET RNA, into GAM2518 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35131] It is appreciated that GAM2518 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2518 target genes. The mRNA of each one of this plurality of GAM2518 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2518 RNA, herein designated GAM RNA, and which when bound by GAM2518 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2518 target proteins.

[35132] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2518 gene, herein designated GAM GENE, on one or more GAM2518 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35133] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2518 correlate with, and may be deduced from, the identity of the target genes which GAM2518 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35134] Nucleotide sequences of the GAM2518 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2518 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2518 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2518 are further described hereinbelow with reference to Table 1.

[35135] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2518 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[35136] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2519 (GAM2519) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35137] GAM2519 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2519 was detected is described hereinabove with reference to Figs. 2-8.

[35138] GAM2519 gene, herein designated GAM GENE, and GAM2519 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[35139] GAM2519 gene, herein designated GAM GENE, encodes a GAM2519 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2519 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2519 precursor RNA is designated SEQ ID:2496, and is provided hereinbelow with reference to the sequence listing part.

[35140] GAM2519 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2519 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

- [35141] An enzyme complex designated DICER COMPLEX, dices the GAM2519 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2519 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 76%) nucleotide sequence of GAM2519 RNA is designated SEQ ID:5110, and is provided hereinbelow with reference to the sequence listing part.
- [35142] GAM2519 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2519 target RNA, herein designated GAM TARGET RNA. GAM2519 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [35143] GAM2519 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2519 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2519 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an



illustration only, and is not meant to be limiting GAM2519 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2519 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35144] The complementary binding of GAM2519 RNA, herein designated GAM RNA, to target binding sites on GAM2519 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2519 target RNA, herein designated GAM TARGET RNA, into GAM2519 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35145] It is appreciated that GAM2519 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2519 target genes. The mRNA of each one of this plurality of GAM2519 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2519 RNA, herein designated GAM RNA, and which when bound by GAM2519 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2519 target proteins.

[35146] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2519 gene, herein designated GAM GENE, on one or more GAM2519 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35147] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2519 correlate with, and may be deduced from, the identity of the target genes which GAM2519 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35148] Nucleotide sequences of the GAM2519 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2519 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2519 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2519 are further described hereinbelow with reference to Table 1.

[35149] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2519 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

[35150] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2520 (GAM2520) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35151] GAM2520 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2520 was detected is described hereinabove with reference to Figs. 2-8.

[35152] GAM2520 gene, herein designated GAM GENE, and GAM2520 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[35153] GAM2520 gene, herein designated GAM GENE, encodes a GAM2520 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2520 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2520 precursor RNA is designated SEQ ID:2497, and is provided hereinbelow with reference to the sequence listing part.

[35154] GAM2520 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2520 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35155] An enzyme complex designated DICER COMPLEX, dices the GAM2520 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2520 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of GAM2520 RNA is designated SEQ ID:5111, and is provided hereinbelow with reference to the sequence listing part.

[35156] GAM2520 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2520 target RNA, herein designated GAM TARGET RNA. GAM2520 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35157] GAM2520 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2520 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2520 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2520 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2520 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35158] The complementary binding of GAM2520 RNA, herein designated GAM RNA, to target binding sites on GAM2520 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2520 target RNA, herein designated GAM TARGET RNA, into GAM2520 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35159] It is appreciated that GAM2520 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2520 target genes. The mRNA of each one of this plurality of GAM2520 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2520 RNA, herein designated GAM RNA, and which when bound by GAM2520 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2520 target proteins.

[35160] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2520 gene, herein designated GAM GENE, on one or more GAM2520 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35161] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2520 correlate with, and may be deduced from, the identity of the target genes which GAM2520 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35162] Nucleotide sequences of the GAM2520 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2520 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2520 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2520 are further described hereinbelow with reference to Table 1.

- [35163] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2520 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.
- [35164] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2521 (GAM2521) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.
- [35165] GAM2521 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2521 was detected is described hereinabove with reference to Figs. 2-8.
- [35166] GAM2521 gene, herein designated GAM GENE, and GAM2521 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.
- [35167] GAM2521 gene, herein designated GAM GENE, encodes a GAM2521 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2521 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2521 precursor RNA is designated SEQ ID:2498, and is provided hereinbelow with reference to the sequence listing part.

[35168] GAM2521 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2521 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35169] An enzyme complex designated DICER COMPLEX, dices the GAM2521 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2521 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of GAM2521 RNA is designated SEQ ID:5112, and is provided hereinbelow with reference to the sequence listing part.

[35170] GAM2521 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2521 target RNA, herein designated GAM TARGET RNA. GAM2521 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.



[35171] GAM2521 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2521 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2521 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2521 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2521 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35172] The complementary binding of GAM2521 RNA, herein designated GAM RNA, to target binding sites on GAM2521 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2521 target RNA, herein designated GAM TARGET RNA, into GAM2521 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35173] It is appreciated that GAM2521 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2521 target genes. The

mRNA of each one of this plurality of GAM2521 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2521 RNA, herein designated GAM RNA, and which when bound by GAM2521 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2521 target proteins.

[35174] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2521 gene, herein designated GAM GENE, on one or more GAM2521 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35175] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2521 correlate with, and may be deduced from, the identity of the target genes which GAM2521 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35176] Nucleotide sequences of the GAM2521 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2521 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2521 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2521 are further described hereinbelow with reference to Table 1.

[35177] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2521 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[35178] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2522 (GAM2522) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35179] GAM2522 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2522 was detected is described hereinabove with reference to Figs. 2-8.

[35180] GAM2522 gene, herein designated GAM GENE, and GAM2522 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[35181] GAM2522 gene, herein designated GAM GENE, encodes a GAM2522 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2522 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2522 precursor RNA is designated SEQ ID:2499, and is provided hereinbelow with reference to the sequence listing part.

[35182] GAM2522 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2522 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35183] An enzyme complex designated DICER COMPLEX, dices the GAM2522 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2522 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of GAM2522 RNA is designated SEQ ID:5113, and is provided hereinbelow with reference to the sequence listing part.

[35184] GAM2522 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2522 target RNA, herein designated GAM TARGET RNA. GAM2522 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35185] GAM2522 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2522 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2522 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2522 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2522 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35186] The complementary binding of GAM2522 RNA, herein designated GAM RNA, to target binding sites on GAM2522 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2522 target RNA, herein designated GAM TARGET RNA, into GAM2522 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35187] It is appreciated that GAM2522 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2522 target genes. The mRNA of each one of this plurality of GAM2522 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2522 RNA, herein designated GAM RNA, and which when bound by GAM2522 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2522 target proteins.

[35188] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2522 gene, herein designated GAM GENE, on one or more GAM2522 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35189] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2522 correlate with, and may be deduced from, the identity of the target

genes which GAM2522 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35190] Nucleotide sequences of the GAM2522 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2522 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2522 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2522 are further described hereinbelow with reference to Table 1.

[35191] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2522 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[35192] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2523 (GAM2523) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35193] GAM2523 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2523 was detected is described hereinabove with reference to Figs. 2-8.

[35194] GAM2523 gene, herein designated GAM GENE, and GAM2523 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

[35195] GAM2523 gene, herein designated GAM GENE, encodes a GAM2523 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2523 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2523 precursor RNA is designated SEQ ID:2500, and is provided hereinbelow with reference to the sequence listing part.

[35196] GAM2523 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2523 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35197] An enzyme complex designated DICER COMPLEX, dices the GAM2523 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2523 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of GAM2523 RNA is designated SEQ ID:5115, and is provided



hereinbelow with reference to the sequence listing part.

[35198] GAM2523 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2523 target RNA, herein designated GAM TARGET RNA. GAM2523 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35199] GAM2523 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2523 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2523 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2523 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2523 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35200] The complementary binding of GAM2523 RNA, herein designated GAM RNA, to target binding sites on GAM2523 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2523 target RNA, herein designated GAM TARGET RNA, into GAM2523 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35201] It is appreciated that GAM2523 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2523 target genes. The mRNA of each one of this plurality of GAM2523 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2523 RNA, herein designated GAM RNA, and which when bound by GAM2523 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2523 target proteins.

[35202] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2523 gene, herein designated GAM GENE, on one or more GAM2523 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35203] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2523 correlate with, and may be deduced from, the identity of the target genes which GAM2523 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35204] Nucleotide sequences of the GAM2523 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2523 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2523 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2523 are further described hereinbelow with reference to Table 1.

[35205] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2523 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[35206] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2524 (GAM2524) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35207] GAM2524 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2524 was detected is described hereinabove with reference to Figs. 2-8.

[35208] GAM2524 gene, herein designated GAM GENE, and GAM2524 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[35209] GAM2524 gene, herein designated GAM GENE, encodes a GAM2524 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2524 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2524 precursor RNA is designated SEQ ID:2501, and is provided hereinbelow with reference to the sequence listing part.

[35210] GAM2524 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2524 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35211] An enzyme complex designated DICER COMPLEX, dices the GAM2524 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2524 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of GAM2524 RNA is designated SEQ ID:5114, and is provided hereinbelow with reference to the sequence listing part.

[35212] GAM2524 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2524 target RNA, herein designated GAM TARGET RNA. GAM2524 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35213] GAM2524 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2524 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2524 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2524 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2524 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35214] The complementary binding of GAM2524 RNA, herein designated GAM RNA, to target binding sites on GAM2524 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2524 target RNA, herein designated GAM TARGET RNA, into GAM2524 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35215] It is appreciated that GAM2524 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2524 target genes. The mRNA of each one of this plurality of GAM2524 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2524 RNA, herein designated GAM RNA, and which when bound by GAM2524 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2524 target proteins.

[35216] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2524 gene, herein designated GAM GENE, on one or more GAM2524 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35217] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2524 correlate with, and may be deduced from, the identity of the target genes which GAM2524 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35218] Nucleotide sequences of the GAM2524 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2524 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2524 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2524 are further described hereinbelow with reference to Table 1.

[35219] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2524 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[35220] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2525 (GAM2525) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35221] GAM2525 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2525 was detected is described hereinabove with reference to Figs. 2-8.

[35222] GAM2525 gene, herein designated GAM GENE, and GAM2525 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[35223] GAM2525 gene, herein designated GAM GENE, encodes a GAM2525 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2525 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2525 precursor RNA is designated SEQ ID:2502, and is provided hereinbelow with reference to the sequence listing part.

[35224] GAM2525 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2525 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.



- [35225] An enzyme complex designated DICER COMPLEX, dices the GAM2525 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2525 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of GAM2525 RNA is designated SEQ ID:5116, and is provided hereinbelow with reference to the sequence listing part.
- [35226] GAM2525 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2525 target RNA, herein designated GAM TARGET RNA. GAM2525 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [35227] GAM2525 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2525 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2525 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2525 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2525 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35228] The complementary binding of GAM2525 RNA, herein designated GAM RNA, to target binding sites on GAM2525 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2525 target RNA, herein designated GAM TARGET RNA, into GAM2525 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35229] It is appreciated that GAM2525 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2525 target genes. The mRNA of each one of this plurality of GAM2525 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2525 RNA, herein designated GAM RNA, and which when bound by GAM2525 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2525 target proteins.

[35230] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2525 gene, herein designated GAM GENE, on one or more GAM2525 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35231] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2525 correlate with, and may be deduced from, the identity of the target genes which GAM2525 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35232] Nucleotide sequences of the GAM2525 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2525 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2525 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2525 are further described hereinbelow with reference to Table 1.

[35233] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2525 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

[35234] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2526 (GAM2526) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35235] GAM2526 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2526 was detected is described hereinabove with reference to Figs. 2-8.

[35236] GAM2526 gene, herein designated GAM GENE, and GAM2526 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[35237] GAM2526 gene, herein designated GAM GENE, encodes a GAM2526 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2526 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2526 precursor RNA is designated SEQ ID:2503, and is provided hereinbelow with reference to the sequence listing part.

[35238] GAM2526 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2526 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35239] An enzyme complex designated DICER COMPLEX, dices the GAM2526 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2526 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 87%) nucleotide sequence of GAM2526 RNA is designated SEQ ID:5117, and is provided hereinbelow with reference to the sequence listing part.

[35240] GAM2526 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2526 target RNA, herein designated GAM TARGET RNA. GAM2526 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35241] GAM2526 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2526 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2526 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2526 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2526 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35242] The complementary binding of GAM2526 RNA, herein designated GAM RNA, to target binding sites on GAM2526 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2526 target RNA, herein designated GAM TARGET RNA, into GAM2526 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35243] It is appreciated that GAM2526 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2526 target genes. The mRNA of each one of this plurality of GAM2526 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2526 RNA, herein designated GAM RNA, and which when bound by GAM2526 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2526 target proteins.

[35244] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2526 gene, herein designated GAM GENE, on one or more GAM2526 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35245] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2526 correlate with, and may be deduced from, the identity of the target genes which GAM2526 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35246] Nucleotide sequences of the GAM2526 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2526 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2526 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2526 are further described hereinbelow with reference to Table 1.

[35247] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2526 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[35248] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2527 (GAM2527) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35249] GAM2527 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2527 was detected is described hereinabove with reference to Figs. 2-8.

[35250] GAM2527 gene, herein designated GAM GENE, and GAM2527 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[35251] GAM2527 gene, herein designated GAM GENE, encodes a GAM2527 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2527 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2527 precursor RNA is designated SEQ ID:2504, and is provided hereinbelow with reference to the sequence listing part.



[35252] GAM2527 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2527 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35253] An enzyme complex designated DICER COMPLEX, dices the GAM2527 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2527 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 86%) nucleotide sequence of GAM2527 RNA is designated SEQ ID:5118, and is provided hereinbelow with reference to the sequence listing part.

[35254] GAM2527 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2527 target RNA, herein designated GAM TARGET RNA. GAM2527 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35255] GAM2527 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2527 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2527 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2527 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2527 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35256] The complementary binding of GAM2527 RNA, herein designated GAM RNA, to target binding sites on GAM2527 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2527 target RNA, herein designated GAM TARGET RNA, into GAM2527 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35257] It is appreciated that GAM2527 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2527 target genes. The

mRNA of each one of this plurality of GAM2527 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2527 RNA, herein designated GAM RNA, and which when bound by GAM2527 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2527 target proteins.

[35258] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2527 gene, herein designated GAM GENE, on one or more GAM2527 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35259] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2527 correlate with, and may be deduced from, the identity of the target genes which GAM2527 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35260] Nucleotide sequences of the GAM2527 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2527 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2527 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2527 are further described hereinbelow with reference to Table 1.

[35261] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2527 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[35262] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2528 (GAM2528) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35263] GAM2528 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2528 was detected is described hereinabove with reference to Figs. 2-8.

[35264] GAM2528 gene, herein designated GAM GENE, and GAM2528 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[35265] GAM2528 gene, herein designated GAM GENE, encodes a GAM2528 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2528 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2528 precursor RNA is designated SEQ ID:2505, and is provided hereinbelow with reference to the sequence listing part.

[35266] GAM2528 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2528 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35267] An enzyme complex designated DICER COMPLEX, dices the GAM2528 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2528 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2528 RNA is designated SEQ ID:5119, and is provided hereinbelow with reference to the sequence listing part.

[35268] GAM2528 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2528 target RNA, herein designated GAM TARGET RNA. GAM2528 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35269] GAM2528 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2528 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2528 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2528 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2528 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35270] The complementary binding of GAM2528 RNA, herein designated GAM RNA, to target binding sites on GAM2528 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2528 target RNA, herein designated GAM TARGET RNA, into GAM2528 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35271] It is appreciated that GAM2528 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2528 target genes. The mRNA of each one of this plurality of GAM2528 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2528 RNA, herein designated GAM RNA, and which when bound by GAM2528 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2528 target proteins.

[35272] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2528 gene, herein designated GAM GENE, on one or more GAM2528 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35273] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2528 correlate with, and may be deduced from, the identity of the target

genes which GAM2528 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35274] Nucleotide sequences of the GAM2528 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2528 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2528 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2528 are further described hereinbelow with reference to Table 1.

[35275] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2528 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[35276] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2529 (GAM2529) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35277] GAM2529 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2529 was detected is described hereinabove with reference to Figs. 2-8.

[35278] GAM2529 gene, herein designated GAM GENE, and GAM2529 target gene, herein designated GAM TARGET GENE, are human genes contained in the



human genome.

[35279] GAM2529 gene, herein designated GAM GENE, encodes a GAM2529 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2529 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2529 precursor RNA is designated SEQ ID:2506, and is provided hereinbelow with reference to the sequence listing part.

[35280] GAM2529 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2529 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35281] An enzyme complex designated DICER COMPLEX, dices the GAM2529 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2529 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of GAM2529 RNA is designated SEQ ID:5120, and is provided

hereinbelow with reference to the sequence listing part.

[35282] GAM2529 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2529 target RNA, herein designated GAM TARGET RNA. GAM2529 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35283] GAM2529 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2529 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2529 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2529 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2529 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35284] The complementary binding of GAM2529 RNA, herein designated GAM RNA, to target binding sites on GAM2529 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2529 target RNA, herein designated GAM TARGET RNA, into GAM2529 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35285] It is appreciated that GAM2529 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2529 target genes. The mRNA of each one of this plurality of GAM2529 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2529 RNA, herein designated GAM RNA, and which when bound by GAM2529 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2529 target proteins.

[35286] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2529 gene, herein designated GAM GENE, on one or more GAM2529 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35287] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2529 correlate with, and may be deduced from, the identity of the target genes which GAM2529 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35288] Nucleotide sequences of the GAM2529 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2529 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2529 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2529 are further described hereinbelow with reference to Table 1.

[35289] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2529 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[35290] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2530 (GAM2530) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35291] GAM2530 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2530 was detected is described hereinabove with reference to Figs. 2-8.

[35292] GAM2530 gene, herein designated GAM GENE, and GAM2530 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[35293] GAM2530 gene, herein designated GAM GENE, encodes a GAM2530 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2530 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2530 precursor RNA is designated SEQ ID:2507, and is provided hereinbelow with reference to the sequence listing part.

[35294] GAM2530 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2530 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35295] An enzyme complex designated DICER COMPLEX, dices the GAM2530 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2530 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2530 RNA is designated SEQ ID:5121, and is provided hereinbelow with reference to the sequence listing part.

[35296] GAM2530 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2530 target RNA, herein designated GAM TARGET RNA. GAM2530 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35297] GAM2530 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2530 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2530 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2530 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2530 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35298] The complementary binding of GAM2530 RNA, herein designated GAM RNA, to target binding sites on GAM2530 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2530 target RNA, herein designated GAM TARGET RNA, into GAM2530 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35299] It is appreciated that GAM2530 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2530 target genes. The mRNA of each one of this plurality of GAM2530 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2530 RNA, herein designated GAM RNA, and which when bound by GAM2530 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2530 target proteins.

[35300] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2530 gene, herein designated GAM GENE, on one or more GAM2530 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35301] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2530 correlate with, and may be deduced from, the identity of the target genes which GAM2530 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35302] Nucleotide sequences of the GAM2530 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2530 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2530 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2530 are further described hereinbelow with reference to Table 1.

[35303] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2530 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[35304] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2531 (GAM2531) gene, which modulates



expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35305] GAM2531 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2531 was detected is described hereinabove with reference to Figs. 2-8.

[35306] GAM2531 gene, herein designated GAM GENE, and GAM2531 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[35307] GAM2531 gene, herein designated GAM GENE, encodes a GAM2531 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2531 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2531 precursor RNA is designated SEQ ID:2508, and is provided hereinbelow with reference to the sequence listing part.

[35308] GAM2531 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2531 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35309] An enzyme complex designated DICER COMPLEX, dices the GAM2531 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2531 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 83%) nucleotide sequence of GAM2531 RNA is designated SEQ ID:5122, and is provided hereinbelow with reference to the sequence listing part.

[35310] GAM2531 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2531 target RNA, herein designated GAM TARGET RNA. GAM2531 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35311] GAM2531 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2531 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2531 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2531 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2531 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35312] The complementary binding of GAM2531 RNA, herein designated GAM RNA, to target binding sites on GAM2531 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2531 target RNA, herein designated GAM TARGET RNA, into GAM2531 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35313] It is appreciated that GAM2531 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2531 target genes. The mRNA of each one of this plurality of GAM2531 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2531 RNA, herein designated GAM RNA, and which when bound by GAM2531 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2531 target proteins.

[35314] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2531 gene, herein designated GAM GENE, on one or more GAM2531 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35315] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2531 correlate with, and may be deduced from, the identity of the target genes which GAM2531 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35316] Nucleotide sequences of the GAM2531 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2531 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2531 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2531 are further described hereinbelow with reference to Table 1.

[35317] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2531 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

[35318] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2532 (GAM2532) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35319] GAM2532 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2532 was detected is described hereinabove with reference to Figs. 2-8.

[35320] GAM2532 gene, herein designated GAM GENE, and GAM2532 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[35321] GAM2532 gene, herein designated GAM GENE, encodes a GAM2532 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2532 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2532 precursor RNA is designated SEQ ID:2509, and is provided hereinbelow with reference to the sequence listing part.

[35322] GAM2532 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2532 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35323] An enzyme complex designated DICER COMPLEX, dices the GAM2532 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2532 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 76%) nucleotide sequence of GAM2532 RNA is designated SEQ ID:5123, and is provided hereinbelow with reference to the sequence listing part.

[35324] GAM2532 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2532 target RNA, herein designated GAM TARGET RNA. GAM2532 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35325] GAM2532 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2532 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2532 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2532 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2532 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35326] The complementary binding of GAM2532 RNA, herein designated GAM RNA, to target binding sites on GAM2532 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2532 target RNA, herein designated GAM TARGET RNA, into GAM2532 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35327] It is appreciated that GAM2532 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2532 target genes. The mRNA of each one of this plurality of GAM2532 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2532 RNA, herein designated GAM RNA, and which when bound by GAM2532 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2532 target proteins.

[35328] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2532 gene, herein designated GAM GENE, on one or more GAM2532 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35329] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2532 correlate with, and may be deduced from, the identity of the target genes which GAM2532 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35330] Nucleotide sequences of the GAM2532 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2532 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2532 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2532 are further described hereinbelow with reference to Table 1.



[35331] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2532 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[35332] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2533 (GAM2533) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35333] GAM2533 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2533 was detected is described hereinabove with reference to Figs. 2-8.

[35334] GAM2533 gene, herein designated GAM GENE, and GAM2533 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[35335] GAM2533 gene, herein designated GAM GENE, encodes a GAM2533 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2533 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2533 precursor RNA is designated SEQ ID:2510, and is provided hereinbelow with reference to the sequence listing part.

[35336] GAM2533 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2533 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35337] An enzyme complex designated DICER COMPLEX, dices the GAM2533 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2533 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2533 RNA is designated SEQ ID:5124, and is provided hereinbelow with reference to the sequence listing part.

[35338] GAM2533 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2533 target RNA, herein designated GAM TARGET RNA. GAM2533 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35339] GAM2533 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2533 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2533 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2533 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2533 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35340] The complementary binding of GAM2533 RNA, herein designated GAM RNA, to target binding sites on GAM2533 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2533 target RNA, herein designated GAM TARGET RNA, into GAM2533 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35341] It is appreciated that GAM2533 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2533 target genes. The

mRNA of each one of this plurality of GAM2533 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2533 RNA, herein designated GAM RNA, and which when bound by GAM2533 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2533 target proteins.

[35342] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2533 gene, herein designated GAM GENE, on one or more GAM2533 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35343] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2533 correlate with, and may be deduced from, the identity of the target genes which GAM2533 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35344] Nucleotide sequences of the GAM2533 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2533 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2533 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2533 are further described hereinbelow with reference to Table 1.

[35345] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2533 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[35346] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2534 (GAM2534) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35347] GAM2534 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2534 was detected is described hereinabove with reference to Figs. 2-8.

[35348] GAM2534 gene, herein designated GAM GENE, and GAM2534 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[35349] GAM2534 gene, herein designated GAM GENE, encodes a GAM2534 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2534 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2534 precursor RNA is designated SEQ ID:2511, and is provided hereinbelow with reference to the sequence listing part.

[35350] GAM2534 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2534 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35351] An enzyme complex designated DICER COMPLEX, dices the GAM2534 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2534 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 78%) nucleotide sequence of GAM2534 RNA is designated SEQ ID:5125, and is provided hereinbelow with reference to the sequence listing part.

[35352] GAM2534 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2534 target RNA, herein designated GAM TARGET RNA. GAM2534 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35353] GAM2534 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2534 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2534 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2534 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2534 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35354] The complementary binding of GAM2534 RNA, herein designated GAM RNA, to target binding sites on GAM2534 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2534 target RNA, herein designated GAM TARGET RNA, into GAM2534 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35355] It is appreciated that GAM2534 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2534 target genes. The mRNA of each one of this plurality of GAM2534 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2534 RNA, herein designated GAM RNA, and which when bound by GAM2534 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2534 target proteins.

[35356] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2534 gene, herein designated GAM GENE, on one or more GAM2534 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35357] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2534 correlate with, and may be deduced from, the identity of the target



genes which GAM2534 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35358] Nucleotide sequences of the GAM2534 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2534 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2534 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2534 are further described hereinbelow with reference to Table 1.

[35359] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2534 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[35360] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2535 (GAM2535) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35361] GAM2535 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2535 was detected is described hereinabove with reference to Figs. 2-8.

[35362] GAM2535 gene, herein designated GAM GENE, and GAM2535 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

[35363] GAM2535 gene, herein designated GAM GENE, encodes a GAM2535 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2535 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2535 precursor RNA is designated SEQ ID:2512, and is provided hereinbelow with reference to the sequence listing part.

[35364] GAM2535 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2535 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35365] An enzyme complex designated DICER COMPLEX, dices the GAM2535 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2535 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 85%) nucleotide sequence of GAM2535 RNA is designated SEQ ID:5126, and is provided

hereinbelow with reference to the sequence listing part.

[35366] GAM2535 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2535 target RNA, herein designated GAM TARGET RNA. GAM2535 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35367] GAM2535 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2535 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2535 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2535 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2535 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35368] The complementary binding of GAM2535 RNA, herein designated GAM RNA, to target binding sites on GAM2535 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2535 target RNA, herein designated GAM TARGET RNA, into GAM2535 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35369] It is appreciated that GAM2535 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2535 target genes. The mRNA of each one of this plurality of GAM2535 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2535 RNA, herein designated GAM RNA, and which when bound by GAM2535 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2535 target proteins.

[35370] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2535 gene, herein designated GAM GENE, on one or more GAM2535 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35371] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2535 correlate with, and may be deduced from, the identity of the target genes which GAM2535 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35372] Nucleotide sequences of the GAM2535 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2535 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2535 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2535 are further described hereinbelow with reference to Table 1.

[35373] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2535 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[35374] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2536 (GAM2536) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35375] GAM2536 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2536 was detected is described hereinabove with reference to Figs. 2-8.

[35376] GAM2536 gene, herein designated GAM GENE, and GAM2536 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[35377] GAM2536 gene, herein designated GAM GENE, encodes a GAM2536 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2536 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2536 precursor RNA is designated SEQ ID:2513, and is provided hereinbelow with reference to the sequence listing part.

[35378] GAM2536 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2536 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35379] An enzyme complex designated DICER COMPLEX, dices the GAM2536 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2536 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of GAM2536 RNA is designated SEQ ID:5127, and is provided hereinbelow with reference to the sequence listing part.

[35380] GAM2536 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2536 target RNA, herein designated GAM TARGET RNA. GAM2536 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35381] GAM2536 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2536 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2536 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2536 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2536 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35382] The complementary binding of GAM2536 RNA, herein designated GAM RNA, to target binding sites on GAM2536 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2536 target RNA, herein designated GAM TARGET RNA, into GAM2536 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35383] It is appreciated that GAM2536 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2536 target genes. The mRNA of each one of this plurality of GAM2536 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2536 RNA, herein designated GAM RNA, and which when bound by GAM2536 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2536 target proteins.

[35384] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2536 gene, herein designated GAM GENE, on one or more GAM2536 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary



binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35385] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2536 correlate with, and may be deduced from, the identity of the target genes which GAM2536 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35386] Nucleotide sequences of the GAM2536 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2536 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2536 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2536 are further described hereinbelow with reference to Table 1.

[35387] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2536 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[35388] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2537 (GAM2537) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35389] GAM2537 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2537 was detected is described hereinabove with reference to Figs. 2-8.

[35390] GAM2537 gene, herein designated GAM GENE, and GAM2537 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[35391] GAM2537 gene, herein designated GAM GENE, encodes a GAM2537 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2537 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2537 precursor RNA is designated SEQ ID:2514, and is provided hereinbelow with reference to the sequence listing part.

[35392] GAM2537 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2537 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

- [35393] An enzyme complex designated DICER COMPLEX, dices the GAM2537 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2537 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM2537 RNA is designated SEQ ID:5128, and is provided hereinbelow with reference to the sequence listing part.
- [35394] GAM2537 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2537 target RNA, herein designated GAM TARGET RNA. GAM2537 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [35395] GAM2537 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2537 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2537 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2537 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2537 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35396] The complementary binding of GAM2537 RNA, herein designated GAM RNA, to target binding sites on GAM2537 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2537 target RNA, herein designated GAM TARGET RNA, into GAM2537 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35397] It is appreciated that GAM2537 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2537 target genes. The mRNA of each one of this plurality of GAM2537 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2537 RNA, herein designated GAM RNA, and which when bound by GAM2537 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2537 target proteins.

[35398] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2537 gene, herein designated GAM GENE, on one or more GAM2537 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35399] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2537 correlate with, and may be deduced from, the identity of the target genes which GAM2537 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35400] Nucleotide sequences of the GAM2537 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2537 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2537 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2537 are further described hereinbelow with reference to Table 1.

[35401] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2537 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

[35402] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2538 (GAM2538) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35403] GAM2538 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2538 was detected is described hereinabove with reference to Figs. 2-8.

[35404] GAM2538 gene, herein designated GAM GENE, and GAM2538 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[35405] GAM2538 gene, herein designated GAM GENE, encodes a GAM2538 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2538 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2538 precursor RNA is designated SEQ ID:2515, and is provided hereinbelow with reference to the sequence listing part.

[35406] GAM2538 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2538 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35407] An enzyme complex designated DICER COMPLEX, dices the GAM2538 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2538 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 83%) nucleotide sequence of GAM2538 RNA is designated SEQ ID:5129, and is provided hereinbelow with reference to the sequence listing part.

[35408] GAM2538 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2538 target RNA, herein designated GAM TARGET RNA. GAM2538 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35409] GAM2538 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2538 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2538 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2538 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2538 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35410] The complementary binding of GAM2538 RNA, herein designated GAM RNA, to target binding sites on GAM2538 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2538 target RNA, herein designated GAM TARGET RNA, into GAM2538 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35411] It is appreciated that GAM2538 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2538 target genes. The mRNA of each one of this plurality of GAM2538 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2538 RNA, herein designated GAM RNA, and which when bound by GAM2538 RNA, herein designated GAM RNA,



causes inhibition of translation of respective one or more GAM2538 target proteins.

[35412] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2538 gene, herein designated GAM GENE, on one or more GAM2538 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35413] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2538 correlate with, and may be deduced from, the identity of the target genes which GAM2538 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35414] Nucleotide sequences of the GAM2538 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2538 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2538 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2538 are further described hereinbelow with reference to Table 1.

- [35415] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2538 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.
- [35416] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2539 (GAM2539) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.
- [35417] GAM2539 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2539 was detected is described hereinabove with reference to Figs. 2-8.
- [35418] GAM2539 gene, herein designated GAM GENE, and GAM2539 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.
- [35419] GAM2539 gene, herein designated GAM GENE, encodes a GAM2539 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2539 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2539 precursor RNA is designated SEQ ID:2516, and is provided hereinbelow with reference to the sequence listing part.

[35420] GAM2539 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2539 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35421] An enzyme complex designated DICER COMPLEX, dices the GAM2539 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2539 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 85%) nucleotide sequence of GAM2539 RNA is designated SEQ ID:5130, and is provided hereinbelow with reference to the sequence listing part.

[35422] GAM2539 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2539 target RNA, herein designated GAM TARGET RNA. GAM2539 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35423] GAM2539 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2539 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2539 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2539 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2539 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35424] The complementary binding of GAM2539 RNA, herein designated GAM RNA, to target binding sites on GAM2539 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2539 target RNA, herein designated GAM TARGET RNA, into GAM2539 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35425] It is appreciated that GAM2539 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2539 target genes. The

mRNA of each one of this plurality of GAM2539 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2539 RNA, herein designated GAM RNA, and which when bound by GAM2539 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2539 target proteins.

[35426] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2539 gene, herein designated GAM GENE, on one or more GAM2539 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35427] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2539 correlate with, and may be deduced from, the identity of the target genes which GAM2539 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35428] Nucleotide sequences of the GAM2539 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2539 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2539 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2539 are further described hereinbelow with reference to Table 1.

[35429] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2539 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[35430] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2540 (GAM2540) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35431] GAM2540 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2540 was detected is described hereinabove with reference to Figs. 2-8.

[35432] GAM2540 gene, herein designated GAM GENE, and GAM2540 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[35433] GAM2540 gene, herein designated GAM GENE, encodes a GAM2540 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2540 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2540 precursor RNA is designated SEQ ID:2517, and is provided hereinbelow with reference to the sequence listing part.

[35434] GAM2540 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2540 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35435] An enzyme complex designated DICER COMPLEX, dices the GAM2540 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2540 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 78%) nucleotide sequence of GAM2540 RNA is designated SEQ ID:5131, and is provided hereinbelow with reference to the sequence listing part.

[35436] GAM2540 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2540 target RNA, herein designated GAM TARGET RNA. GAM2540 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35437] GAM2540 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2540 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2540 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2540 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2540 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35438] The complementary binding of GAM2540 RNA, herein designated GAM RNA, to target binding sites on GAM2540 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2540 target RNA, herein designated GAM TARGET RNA, into GAM2540 target protein, herein



designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35439] It is appreciated that GAM2540 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2540 target genes. The mRNA of each one of this plurality of GAM2540 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2540 RNA, herein designated GAM RNA, and which when bound by GAM2540 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2540 target proteins.

[35440] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2540 gene, herein designated GAM GENE, on one or more GAM2540 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35441] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2540 correlate with, and may be deduced from, the identity of the target

genes which GAM2540 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35442] Nucleotide sequences of the GAM2540 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2540 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2540 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2540 are further described hereinbelow with reference to Table 1.

[35443] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2540 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[35444] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2541 (GAM2541) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35445] GAM2541 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2541 was detected is described hereinabove with reference to Figs. 2-8.

[35446] GAM2541 gene, herein designated GAM GENE, and GAM2541 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

[35447] GAM2541 gene, herein designated GAM GENE, encodes a GAM2541 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2541 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2541 precursor RNA is designated SEQ ID:2518, and is provided hereinbelow with reference to the sequence listing part.

[35448] GAM2541 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2541 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35449] An enzyme complex designated DICER COMPLEX, dices the GAM2541 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2541 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of GAM2541 RNA is designated SEQ ID:5132, and is provided

hereinbelow with reference to the sequence listing part.

[35450] GAM2541 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2541 target RNA, herein designated GAM TARGET RNA. GAM2541 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35451] GAM2541 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2541 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2541 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2541 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2541 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35452] The complementary binding of GAM2541 RNA, herein designated GAM RNA, to target binding sites on GAM2541 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2541 target RNA, herein designated GAM TARGET RNA, into GAM2541 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35453] It is appreciated that GAM2541 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2541 target genes. The mRNA of each one of this plurality of GAM2541 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2541 RNA, herein designated GAM RNA, and which when bound by GAM2541 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2541 target proteins.

[35454] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2541 gene, herein designated GAM GENE, on one or more GAM2541 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35455] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2541 correlate with, and may be deduced from, the identity of the target genes which GAM2541 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35456] Nucleotide sequences of the GAM2541 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2541 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2541 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2541 are further described hereinbelow with reference to Table 1.

[35457] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2541 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[35458] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2542 (GAM2542) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35459] GAM2542 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2542 was detected is described hereinabove with reference to Figs. 2-8.

[35460] GAM2542 gene, herein designated GAM GENE, and GAM2542 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[35461] GAM2542 gene, herein designated GAM GENE, encodes a GAM2542 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2542 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2542 precursor RNA is designated SEQ ID:2519, and is provided hereinbelow with reference to the sequence listing part.

[35462] GAM2542 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2542 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35463] An enzyme complex designated DICER COMPLEX, dices the GAM2542 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2542 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM2542 RNA is designated SEQ ID:5133, and is provided hereinbelow with reference to the sequence listing part.

[35464] GAM2542 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2542 target RNA, herein designated GAM TARGET RNA. GAM2542 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35465] GAM2542 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2542 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2542 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2542 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2542 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target



binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35466] The complementary binding of GAM2542 RNA, herein designated GAM RNA, to target binding sites on GAM2542 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2542 target RNA, herein designated GAM TARGET RNA, into GAM2542 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35467] It is appreciated that GAM2542 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2542 target genes. The mRNA of each one of this plurality of GAM2542 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2542 RNA, herein designated GAM RNA, and which when bound by GAM2542 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2542 target proteins.

[35468] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2542 gene, herein designated GAM GENE, on one or more GAM2542 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35469] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2542 correlate with, and may be deduced from, the identity of the target genes which GAM2542 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35470] Nucleotide sequences of the GAM2542 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2542 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2542 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2542 are further described hereinbelow with reference to Table 1.

[35471] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2542 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[35472] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2543 (GAM2543) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35473] GAM2543 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2543 was detected is described hereinabove with reference to Figs. 2-8.

[35474] GAM2543 gene, herein designated GAM GENE, and GAM2543 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[35475] GAM2543 gene, herein designated GAM GENE, encodes a GAM2543 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2543 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2543 precursor RNA is designated SEQ ID:2520, and is provided hereinbelow with reference to the sequence listing part.

[35476] GAM2543 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2543 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

- [35477] An enzyme complex designated DICER COMPLEX, dices the GAM2543 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2543 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of GAM2543 RNA is designated SEQ ID:5134, and is provided hereinbelow with reference to the sequence listing part.
- [35478] GAM2543 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2543 target RNA, herein designated GAM TARGET RNA. GAM2543 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [35479] GAM2543 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2543 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2543 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2543 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2543 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35480] The complementary binding of GAM2543 RNA, herein designated GAM RNA, to target binding sites on GAM2543 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2543 target RNA, herein designated GAM TARGET RNA, into GAM2543 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35481] It is appreciated that GAM2543 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2543 target genes. The mRNA of each one of this plurality of GAM2543 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2543 RNA, herein designated GAM RNA, and which when bound by GAM2543 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2543 target proteins.

[35482] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2543 gene, herein designated GAM GENE, on one or more GAM2543 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35483] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2543 correlate with, and may be deduced from, the identity of the target genes which GAM2543 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35484] Nucleotide sequences of the GAM2543 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2543 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2543 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2543 are further described hereinbelow with reference to Table 1.

[35485] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2543 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

[35486] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2544 (GAM2544) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35487] GAM2544 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2544 was detected is described hereinabove with reference to Figs. 2-8.

[35488] GAM2544 gene, herein designated GAM GENE, and GAM2544 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[35489] GAM2544 gene, herein designated GAM GENE, encodes a GAM2544 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2544 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2544 precursor RNA is designated SEQ ID:2521, and is provided hereinbelow with reference to the sequence listing part.

[35490] GAM2544 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2544 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35491] An enzyme complex designated DICER COMPLEX, dices the GAM2544 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2544 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 25%) nucleotide sequence of GAM2544 RNA is designated SEQ ID:5135, and is provided hereinbelow with reference to the sequence listing part.

[35492] GAM2544 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2544 target RNA, herein designated GAM TARGET RNA. GAM2544 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35493] GAM2544 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2544 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2544 RNA,



herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2544 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2544 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35494] The complementary binding of GAM2544 RNA, herein designated GAM RNA, to target binding sites on GAM2544 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2544 target RNA, herein designated GAM TARGET RNA, into GAM2544 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35495] It is appreciated that GAM2544 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2544 target genes. The mRNA of each one of this plurality of GAM2544 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2544 RNA, herein designated GAM RNA, and which when bound by GAM2544 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2544 target proteins.

[35496] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2544 gene, herein designated GAM GENE, on one or more GAM2544 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35497] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2544 correlate with, and may be deduced from, the identity of the target genes which GAM2544 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35498] Nucleotide sequences of the GAM2544 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2544 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2544 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2544 are further described hereinbelow with reference to Table 1.

[35499] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2544 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[35500] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2545 (GAM2545) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35501] GAM2545 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2545 was detected is described hereinabove with reference to Figs. 2-8.

[35502] GAM2545 gene, herein designated GAM GENE, and GAM2545 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[35503] GAM2545 gene, herein designated GAM GENE, encodes a GAM2545 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2545 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2545 precursor RNA is designated SEQ ID:2522, and is provided hereinbelow with reference to the sequence listing part.

[35504] GAM2545 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2545 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35505] An enzyme complex designated DICER COMPLEX, dices the GAM2545 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2545 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 84%) nucleotide sequence of GAM2545 RNA is designated SEQ ID:5136, and is provided hereinbelow with reference to the sequence listing part.

[35506] GAM2545 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2545 target RNA, herein designated GAM TARGET RNA. GAM2545 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35507] GAM2545 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2545 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2545 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2545 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2545 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35508] The complementary binding of GAM2545 RNA, herein designated GAM RNA, to target binding sites on GAM2545 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2545 target RNA, herein designated GAM TARGET RNA, into GAM2545 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35509] It is appreciated that GAM2545 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2545 target genes. The

mRNA of each one of this plurality of GAM2545 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2545 RNA, herein designated GAM RNA, and which when bound by GAM2545 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2545 target proteins.

[35510] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2545 gene, herein designated GAM GENE, on one or more GAM2545 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35511] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2545 correlate with, and may be deduced from, the identity of the target genes which GAM2545 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35512] Nucleotide sequences of the GAM2545 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2545 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2545 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2545 are further described hereinbelow with reference to Table 1.

[35513] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2545 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[35514] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2546 (GAM2546) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35515] GAM2546 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2546 was detected is described hereinabove with reference to Figs. 2-8.

[35516] GAM2546 gene, herein designated GAM GENE, and GAM2546 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[35517] GAM2546 gene, herein designated GAM GENE, encodes a GAM2546 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2546 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2546 precursor RNA is designated SEQ ID:2523, and is provided hereinbelow with reference to the sequence listing part.

[35518] GAM2546 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2546 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35519] An enzyme complex designated DICER COMPLEX, dices the GAM2546 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2546 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of GAM2546 RNA is designated SEQ ID:5137, and is provided hereinbelow with reference to the sequence listing part.

[35520] GAM2546 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2546 target RNA, herein designated GAM TARGET RNA. GAM2546 target RNA, herein designated GAM



TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35521] GAM2546 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2546 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2546 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2546 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2546 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35522] The complementary binding of GAM2546 RNA, herein designated GAM RNA, to target binding sites on GAM2546 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2546 target RNA, herein designated GAM TARGET RNA, into GAM2546 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35523] It is appreciated that GAM2546 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2546 target genes. The mRNA of each one of this plurality of GAM2546 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2546 RNA, herein designated GAM RNA, and which when bound by GAM2546 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2546 target proteins.

[35524] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2546 gene, herein designated GAM GENE, on one or more GAM2546 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35525] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2546 correlate with, and may be deduced from, the identity of the target

genes which GAM2546 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35526] Nucleotide sequences of the GAM2546 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2546 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2546 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2546 are further described hereinbelow with reference to Table 1.

[35527] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2546 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[35528] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2547 (GAM2547) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35529] GAM2547 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2547 was detected is described hereinabove with reference to Figs. 2-8.

[35530] GAM2547 gene, herein designated GAM GENE, and GAM2547 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

[35531] GAM2547 gene, herein designated GAM GENE, encodes a GAM2547 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2547 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2547 precursor RNA is designated SEQ ID:2524, and is provided hereinbelow with reference to the sequence listing part.

[35532] GAM2547 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2547 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35533] An enzyme complex designated DICER COMPLEX, dices the GAM2547 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2547 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 87%) nucleotide sequence of GAM2547 RNA is designated SEQ ID:5138, and is provided

hereinbelow with reference to the sequence listing part.

[35534] GAM2547 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2547 target RNA, herein designated GAM TARGET RNA. GAM2547 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35535] GAM2547 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2547 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2547 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2547 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2547 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35536] The complementary binding of GAM2547 RNA, herein designated GAM RNA, to target binding sites on GAM2547 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2547 target RNA, herein designated GAM TARGET RNA, into GAM2547 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35537] It is appreciated that GAM2547 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2547 target genes. The mRNA of each one of this plurality of GAM2547 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2547 RNA, herein designated GAM RNA, and which when bound by GAM2547 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2547 target proteins.

[35538] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2547 gene, herein designated GAM GENE, on one or more GAM2547 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35539] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2547 correlate with, and may be deduced from, the identity of the target genes which GAM2547 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35540] Nucleotide sequences of the GAM2547 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2547 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2547 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2547 are further described hereinbelow with reference to Table 1.

[35541] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2547 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[35542] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2548 (GAM2548) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35543] GAM2548 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2548 was detected is described hereinabove with reference to Figs. 2-8.

[35544] GAM2548 gene, herein designated GAM GENE, and GAM2548 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[35545] GAM2548 gene, herein designated GAM GENE, encodes a GAM2548 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2548 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2548 precursor RNA is designated SEQ ID:2525, and is provided hereinbelow with reference to the sequence listing part.

[35546] GAM2548 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2548 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35547] An enzyme complex designated DICER COMPLEX, dices the GAM2548 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2548 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin



structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2548 RNA is designated SEQ ID:5139, and is provided hereinbelow with reference to the sequence listing part.

[35548] GAM2548 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2548 target RNA, herein designated GAM TARGET RNA. GAM2548 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35549] GAM2548 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2548 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2548 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2548 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2548 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35550] The complementary binding of GAM2548 RNA, herein designated GAM RNA, to target binding sites on GAM2548 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2548 target RNA, herein designated GAM TARGET RNA, into GAM2548 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35551] It is appreciated that GAM2548 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2548 target genes. The mRNA of each one of this plurality of GAM2548 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2548 RNA, herein designated GAM RNA, and which when bound by GAM2548 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2548 target proteins.

[35552] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2548 gene, herein designated GAM GENE, on one or more GAM2548 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35553] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2548 correlate with, and may be deduced from, the identity of the target genes which GAM2548 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35554] Nucleotide sequences of the GAM2548 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2548 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2548 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2548 are further described hereinbelow with reference to Table 1.

[35555] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2548 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[35556] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2549 (GAM2549) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35557] GAM2549 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2549 was detected is described hereinabove with reference to Figs. 2-8.

[35558] GAM2549 gene, herein designated GAM GENE, and GAM2549 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[35559] GAM2549 gene, herein designated GAM GENE, encodes a GAM2549 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2549 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2549 precursor RNA is designated SEQ ID:2526, and is provided hereinbelow with reference to the sequence listing part.

[35560] GAM2549 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2549 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

- [35561] An enzyme complex designated DICER COMPLEX, dices the GAM2549 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2549 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 87%) nucleotide sequence of GAM2549 RNA is designated SEQ ID:5140, and is provided hereinbelow with reference to the sequence listing part.
- [35562] GAM2549 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2549 target RNA, herein designated GAM TARGET RNA. GAM2549 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [35563] GAM2549 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2549 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2549 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2549 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2549 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35564] The complementary binding of GAM2549 RNA, herein designated GAM RNA, to target binding sites on GAM2549 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2549 target RNA, herein designated GAM TARGET RNA, into GAM2549 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35565] It is appreciated that GAM2549 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2549 target genes. The mRNA of each one of this plurality of GAM2549 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2549 RNA, herein designated GAM RNA, and which when bound by GAM2549 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2549 target proteins.

[35566] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2549 gene, herein designated GAM GENE, on one or more GAM2549 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35567] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2549 correlate with, and may be deduced from, the identity of the target genes which GAM2549 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35568] Nucleotide sequences of the GAM2549 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2549 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2549 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2549 are further described hereinbelow with reference to Table 1.

[35569] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2549 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

[35570] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2550 (GAM2550) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35571] GAM2550 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2550 was detected is described hereinabove with reference to Figs. 2-8.

[35572] GAM2550 gene, herein designated GAM GENE, and GAM2550 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[35573] GAM2550 gene, herein designated GAM GENE, encodes a GAM2550 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2550 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2550 precursor RNA is designated SEQ ID:2527, and is provided hereinbelow with reference to the sequence listing part.

[35574] GAM2550 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2550 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA



encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35575] An enzyme complex designated DICER COMPLEX, dices the GAM2550 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2550 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 86%) nucleotide sequence of GAM2550 RNA is designated SEQ ID:5142, and is provided hereinbelow with reference to the sequence listing part.

[35576] GAM2550 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2550 target RNA, herein designated GAM TARGET RNA. GAM2550 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35577] GAM2550 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2550 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2550 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2550 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2550 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35578] The complementary binding of GAM2550 RNA, herein designated GAM RNA, to target binding sites on GAM2550 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2550 target RNA, herein designated GAM TARGET RNA, into GAM2550 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35579] It is appreciated that GAM2550 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2550 target genes. The mRNA of each one of this plurality of GAM2550 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2550 RNA, herein designated GAM RNA, and which when bound by GAM2550 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2550 target proteins.

[35580] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2550 gene, herein designated GAM GENE, on one or more GAM2550 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35581] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2550 correlate with, and may be deduced from, the identity of the target genes which GAM2550 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35582] Nucleotide sequences of the GAM2550 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2550 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2550 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2550 are further described hereinbelow with reference to Table 1.

[35583] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2550 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[35584] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2551 (GAM2551) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35585] GAM2551 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2551 was detected is described hereinabove with reference to Figs. 2-8.

[35586] GAM2551 gene, herein designated GAM GENE, and GAM2551 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[35587] GAM2551 gene, herein designated GAM GENE, encodes a GAM2551 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2551 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2551 precursor RNA is designated SEQ ID:2528, and is provided hereinbelow with reference to the sequence listing part.

[35588] GAM2551 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2551 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35589] An enzyme complex designated DICER COMPLEX, dices the GAM2551 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2551 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 88%) nucleotide sequence of GAM2551 RNA is designated SEQ ID:5141, and is provided hereinbelow with reference to the sequence listing part.

[35590] GAM2551 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2551 target RNA, herein designated GAM TARGET RNA. GAM2551 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35591] GAM2551 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2551 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2551 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2551 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2551 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35592] The complementary binding of GAM2551 RNA, herein designated GAM RNA, to target binding sites on GAM2551 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2551 target RNA, herein designated GAM TARGET RNA, into GAM2551 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35593] It is appreciated that GAM2551 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2551 target genes. The

mRNA of each one of this plurality of GAM2551 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2551 RNA, herein designated GAM RNA, and which when bound by GAM2551 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2551 target proteins.

[35594] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2551 gene, herein designated GAM GENE, on one or more GAM2551 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35595] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2551 correlate with, and may be deduced from, the identity of the target genes which GAM2551 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35596] Nucleotide sequences of the GAM2551 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2551 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2551 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2551 are further described hereinbelow with reference to Table 1.

[35597] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2551 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[35598] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2552 (GAM2552) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35599] GAM2552 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2552 was detected is described hereinabove with reference to Figs. 2-8.

[35600] GAM2552 gene, herein designated GAM GENE, and GAM2552 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[35601] GAM2552 gene, herein designated GAM GENE, encodes a GAM2552 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2552 precursor RNA,



herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2552 precursor RNA is designated SEQ ID:2529, and is provided hereinbelow with reference to the sequence listing part.

[35602] GAM2552 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2552 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35603] An enzyme complex designated DICER COMPLEX, dices the GAM2552 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2552 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2552 RNA is designated SEQ ID:5143, and is provided hereinbelow with reference to the sequence listing part.

[35604] GAM2552 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2552 target RNA, herein designated GAM TARGET RNA. GAM2552 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35605] GAM2552 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2552 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2552 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2552 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2552 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35606] The complementary binding of GAM2552 RNA, herein designated GAM RNA, to target binding sites on GAM2552 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2552 target RNA, herein designated GAM TARGET RNA, into GAM2552 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35607] It is appreciated that GAM2552 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2552 target genes. The mRNA of each one of this plurality of GAM2552 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2552 RNA, herein designated GAM RNA, and which when bound by GAM2552 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2552 target proteins.

[35608] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2552 gene, herein designated GAM GENE, on one or more GAM2552 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35609] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2552 correlate with, and may be deduced from, the identity of the target

genes which GAM2552 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35610] Nucleotide sequences of the GAM2552 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2552 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2552 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2552 are further described hereinbelow with reference to Table 1.

[35611] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2552 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[35612] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2553 (GAM2553) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35613] GAM2553 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2553 was detected is described hereinabove with reference to Figs. 2-8.

[35614] GAM2553 gene, herein designated GAM GENE, and GAM2553 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

[35615] GAM2553 gene, herein designated GAM GENE, encodes a GAM2553 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2553 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2553 precursor RNA is designated SEQ ID:2530, and is provided hereinbelow with reference to the sequence listing part.

[35616] GAM2553 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2553 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35617] An enzyme complex designated DICER COMPLEX, dices the GAM2553 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2553 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 84%) nucleotide sequence of GAM2553 RNA is designated SEQ ID:5144, and is provided

hereinbelow with reference to the sequence listing part.

[35618] GAM2553 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2553 target RNA, herein designated GAM TARGET RNA. GAM2553 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35619] GAM2553 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2553 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2553 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2553 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2553 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35620] The complementary binding of GAM2553 RNA, herein designated GAM RNA, to target binding sites on GAM2553 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2553 target RNA, herein designated GAM TARGET RNA, into GAM2553 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35621] It is appreciated that GAM2553 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2553 target genes. The mRNA of each one of this plurality of GAM2553 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2553 RNA, herein designated GAM RNA, and which when bound by GAM2553 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2553 target proteins.

[35622] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2553 gene, herein designated GAM GENE, on one or more GAM2553 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35623] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2553 correlate with, and may be deduced from, the identity of the target genes which GAM2553 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35624] Nucleotide sequences of the GAM2553 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2553 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2553 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2553 are further described hereinbelow with reference to Table 1.

[35625] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2553 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[35626] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2554 (GAM2554) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35627] GAM2554 is a novel bioinformatically detected regulatory, non protein



coding, micro RNA (miRNA) gene. The method by which GAM2554 was detected is described hereinabove with reference to Figs. 2-8.

[35628] GAM2554 gene, herein designated GAM GENE, and GAM2554 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[35629] GAM2554 gene, herein designated GAM GENE, encodes a GAM2554 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2554 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2554 precursor RNA is designated SEQ ID:2531, and is provided hereinbelow with reference to the sequence listing part.

[35630] GAM2554 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2554 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35631] An enzyme complex designated DICER COMPLEX, dices the GAM2554 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2554 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of GAM2554 RNA is designated SEQ ID:5145, and is provided hereinbelow with reference to the sequence listing part.

[35632] GAM2554 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2554 target RNA, herein designated GAM TARGET RNA. GAM2554 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35633] GAM2554 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2554 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2554 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2554 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2554 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35634] The complementary binding of GAM2554 RNA, herein designated GAM RNA, to target binding sites on GAM2554 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2554 target RNA, herein designated GAM TARGET RNA, into GAM2554 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35635] It is appreciated that GAM2554 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2554 target genes. The mRNA of each one of this plurality of GAM2554 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2554 RNA, herein designated GAM RNA, and which when bound by GAM2554 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2554 target proteins.

[35636] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2554 gene, herein designated GAM GENE, on one or more GAM2554 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35637] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2554 correlate with, and may be deduced from, the identity of the target genes which GAM2554 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35638] Nucleotide sequences of the GAM2554 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2554 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2554 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2554 are further described hereinbelow with reference to Table 1.

[35639] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2554 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[35640] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2555 (GAM2555) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

- [35641] GAM2555 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2555 was detected is described hereinabove with reference to Figs. 2-8.
- [35642] GAM2555 gene, herein designated GAM GENE, and GAM2555 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.
- [35643] GAM2555 gene, herein designated GAM GENE, encodes a GAM2555 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2555 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2555 precursor RNA is designated SEQ ID:2532, and is provided hereinbelow with reference to the sequence listing part.
- [35644] GAM2555 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2555 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

- [35645] An enzyme complex designated DICER COMPLEX, dices the GAM2555 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2555 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM2555 RNA is designated SEQ ID:5146, and is provided hereinbelow with reference to the sequence listing part.
- [35646] GAM2555 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2555 target RNA, herein designated GAM TARGET RNA. GAM2555 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [35647] GAM2555 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2555 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2555 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2555 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2555 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35648] The complementary binding of GAM2555 RNA, herein designated GAM RNA, to target binding sites on GAM2555 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2555 target RNA, herein designated GAM TARGET RNA, into GAM2555 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35649] It is appreciated that GAM2555 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2555 target genes. The mRNA of each one of this plurality of GAM2555 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2555 RNA, herein designated GAM RNA, and which when bound by GAM2555 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2555 target proteins.

[35650] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2555 gene, herein designated GAM GENE, on one or more GAM2555 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35651] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2555 correlate with, and may be deduced from, the identity of the target genes which GAM2555 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35652] Nucleotide sequences of the GAM2555 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2555 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2555 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2555 are further described hereinbelow with reference to Table 1.

[35653] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2555 RNA, herein designated GAM RNA, are described hereinbelow



with reference to Table 2.

[35654] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2556 (GAM2556) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35655] GAM2556 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2556 was detected is described hereinabove with reference to Figs. 2-8.

[35656] GAM2556 gene, herein designated GAM GENE, and GAM2556 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[35657] GAM2556 gene, herein designated GAM GENE, encodes a GAM2556 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2556 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2556 precursor RNA is designated SEQ ID:2533, and is provided hereinbelow with reference to the sequence listing part.

[35658] GAM2556 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2556 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35659] An enzyme complex designated DICER COMPLEX, dices the GAM2556 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2556 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of GAM2556 RNA is designated SEQ ID:5147, and is provided hereinbelow with reference to the sequence listing part.

[35660] GAM2556 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2556 target RNA, herein designated GAM TARGET RNA. GAM2556 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35661] GAM2556 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2556 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2556 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2556 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2556 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35662] The complementary binding of GAM2556 RNA, herein designated GAM RNA, to target binding sites on GAM2556 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2556 target RNA, herein designated GAM TARGET RNA, into GAM2556 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35663] It is appreciated that GAM2556 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2556 target genes. The mRNA of each one of this plurality of GAM2556 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2556 RNA, herein designated GAM RNA, and which when bound by GAM2556 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2556 target proteins.

[35664] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2556 gene, herein designated GAM GENE, on one or more GAM2556 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35665] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2556 correlate with, and may be deduced from, the identity of the target genes which GAM2556 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35666] Nucleotide sequences of the GAM2556 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2556 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2556 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2556 are further described hereinbelow with reference to Table 1.

[35667] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2556 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[35668] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2557 (GAM2557) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35669] GAM2557 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2557 was detected is described hereinabove with reference to Figs. 2-8.

[35670] GAM2557 gene, herein designated GAM GENE, and GAM2557 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[35671] GAM2557 gene, herein designated GAM GENE, encodes a GAM2557 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2557 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2557 precursor RNA is designated SEQ ID:2534, and is provided hereinbelow with reference to the sequence listing part.

[35672] GAM2557 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2557 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35673] An enzyme complex designated DICER COMPLEX, dices the GAM2557 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2557 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 83%) nucleotide sequence of GAM2557 RNA is designated SEQ ID:5148, and is provided hereinbelow with reference to the sequence listing part.

[35674] GAM2557 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2557 target RNA, herein designated GAM TARGET RNA. GAM2557 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35675] GAM2557 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2557 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2557 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2557 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2557 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35676] The complementary binding of GAM2557 RNA, herein designated GAM RNA, to target binding sites on GAM2557 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2557 target RNA, herein designated GAM TARGET RNA, into GAM2557 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35677] It is appreciated that GAM2557 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2557 target genes. The

mRNA of each one of this plurality of GAM2557 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2557 RNA, herein designated GAM RNA, and which when bound by GAM2557 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2557 target proteins.

[35678] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2557 gene, herein designated GAM GENE, on one or more GAM2557 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35679] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2557 correlate with, and may be deduced from, the identity of the target genes which GAM2557 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35680] Nucleotide sequences of the GAM2557 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2557 RNA, herein



designated GAM RNA, and a schematic representation of the secondary folding of GAM2557 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2557 are further described hereinbelow with reference to Table 1.

[35681] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2557 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[35682] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2558 (GAM2558) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35683] GAM2558 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2558 was detected is described hereinabove with reference to Figs. 2-8.

[35684] GAM2558 gene, herein designated GAM GENE, and GAM2558 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[35685] GAM2558 gene, herein designated GAM GENE, encodes a GAM2558 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2558 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2558 precursor RNA is designated SEQ ID:2535, and is provided hereinbelow with reference to the sequence listing part.

[35686] GAM2558 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2558 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35687] An enzyme complex designated DICER COMPLEX, dices the GAM2558 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2558 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of GAM2558 RNA is designated SEQ ID:5149, and is provided hereinbelow with reference to the sequence listing part.

[35688] GAM2558 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2558 target RNA, herein designated GAM TARGET RNA. GAM2558 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35689] GAM2558 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2558 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2558 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2558 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2558 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35690] The complementary binding of GAM2558 RNA, herein designated GAM RNA, to target binding sites on GAM2558 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2558 target RNA, herein designated GAM TARGET RNA, into GAM2558 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35691] It is appreciated that GAM2558 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2558 target genes. The mRNA of each one of this plurality of GAM2558 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2558 RNA, herein designated GAM RNA, and which when bound by GAM2558 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2558 target proteins.

[35692] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2558 gene, herein designated GAM GENE, on one or more GAM2558 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35693] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2558 correlate with, and may be deduced from, the identity of the target genes which GAM2558 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35694] Nucleotide sequences of the GAM2558 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2558 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2558 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2558 are further described hereinbelow with reference to Table 1.

[35695] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2558 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[35696] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2559 (GAM2559) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35697] GAM2559 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2559 was detected is described hereinabove with reference to Figs. 2-8.

[35698] GAM2559 gene, herein designated GAM GENE, and GAM2559 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[35699] GAM2559 gene, herein designated GAM GENE, encodes a GAM2559

precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2559 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2559 precursor RNA is designated SEQ ID:2536, and is provided hereinbelow with reference to the sequence listing part.

[35700] GAM2559 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2559 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35701] An enzyme complex designated DICER COMPLEX, dices the GAM2559 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2559 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 83%) nucleotide sequence of GAM2559 RNA is designated SEQ ID:5150, and is provided hereinbelow with reference to the sequence listing part.

[35702] GAM2559 target gene, herein designated GAM TARGET GENE, encodes a

corresponding messenger RNA, GAM2559 target RNA, herein designated GAM TARGET RNA. GAM2559 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35703] GAM2559 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2559 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2559 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2559 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2559 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35704] The complementary binding of GAM2559 RNA, herein designated GAM RNA, to target binding sites on GAM2559 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and



BINDING SITE III, inhibits translation of GAM2559 target RNA, herein designated GAM TARGET RNA, into GAM2559 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35705] It is appreciated that GAM2559 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2559 target genes. The mRNA of each one of this plurality of GAM2559 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2559 RNA, herein designated GAM RNA, and which when bound by GAM2559 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2559 target proteins.

[35706] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2559 gene, herein designated GAM GENE, on one or more GAM2559 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35707] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2559 correlate with, and may be deduced from, the identity of the target genes which GAM2559 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35708] Nucleotide sequences of the GAM2559 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2559 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2559 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2559 are further described hereinbelow with reference to Table 1.

[35709] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2559 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[35710] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2560 (GAM2560) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35711] GAM2560 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2560 was detected is described hereinabove with reference to Figs. 2-8.

[35712] GAM2560 gene, herein designated GAM GENE, and GAM2560 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[35713] GAM2560 gene, herein designated GAM GENE, encodes a GAM2560 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2560 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2560 precursor RNA is designated SEQ ID:2537, and is provided hereinbelow with reference to the sequence listing part.

[35714] GAM2560 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2560 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35715] An enzyme complex designated DICER COMPLEX, dices the GAM2560 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2560 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer

together with other necessary proteins. A probable (over 93%) nucleotide sequence of GAM2560 RNA is designated SEQ ID:5151, and is provided hereinbelow with reference to the sequence listing part.

[35716] GAM2560 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2560 target RNA, herein designated GAM TARGET RNA. GAM2560 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35717] GAM2560 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2560 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2560 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2560 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2560 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or

in both 3UTR and 5UTR regions.

[35718] The complementary binding of GAM2560 RNA, herein designated GAM RNA, to target binding sites on GAM2560 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2560 target RNA, herein designated GAM TARGET RNA, into GAM2560 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35719] It is appreciated that GAM2560 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2560 target genes. The mRNA of each one of this plurality of GAM2560 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2560 RNA, herein designated GAM RNA, and which when bound by GAM2560 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2560 target proteins.

[35720] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2560 gene, herein designated GAM GENE, on one or more GAM2560 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes

are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35721] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2560 correlate with, and may be deduced from, the identity of the target genes which GAM2560 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35722] Nucleotide sequences of the GAM2560 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2560 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2560 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2560 are further described hereinbelow with reference to Table 1.

[35723] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2560 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[35724] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2561 (GAM2561) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

- [35725] GAM2561 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2561 was detected is described hereinabove with reference to Figs. 2-8.
- [35726] GAM2561 gene, herein designated GAM GENE, and GAM2561 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.
- [35727] GAM2561 gene, herein designated GAM GENE, encodes a GAM2561 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2561 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2561 precursor RNA is designated SEQ ID:2538, and is provided hereinbelow with reference to the sequence listing part.
- [35728] GAM2561 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2561 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.
- [35729] An enzyme complex designated DICER COMPLEX, dices the GAM2561 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2561 RNA, herein designated GAM RNA, a single stranded

~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2561 RNA is designated SEQ ID:5152, and is provided hereinbelow with reference to the sequence listing part.

[35730] GAM2561 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2561 target RNA, herein designated GAM TARGET RNA. GAM2561 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35731] GAM2561 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2561 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2561 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2561 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2561 target RNA, herein designated GAM



TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35732] The complementary binding of GAM2561 RNA, herein designated GAM RNA, to target binding sites on GAM2561 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2561 target RNA, herein designated GAM TARGET RNA, into GAM2561 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35733] It is appreciated that GAM2561 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2561 target genes. The mRNA of each one of this plurality of GAM2561 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2561 RNA, herein designated GAM RNA, and which when bound by GAM2561 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2561 target proteins.

[35734] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2561 gene, herein designated GAM GENE, on one or more GAM2561 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with

reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35735] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2561 correlate with, and may be deduced from, the identity of the target genes which GAM2561 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35736] Nucleotide sequences of the GAM2561 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2561 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2561 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2561 are further described hereinbelow with reference to Table 1.

[35737] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2561 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[35738] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as

Genomic Address Messenger 2562 (GAM2562) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35739] GAM2562 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2562 was detected is described hereinabove with reference to Figs. 2-8.

[35740] GAM2562 gene, herein designated GAM GENE, and GAM2562 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[35741] GAM2562 gene, herein designated GAM GENE, encodes a GAM2562 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2562 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2562 precursor RNA is designated SEQ ID:2539, and is provided hereinbelow with reference to the sequence listing part.

[35742] GAM2562 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2562 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

- [35743] An enzyme complex designated DICER COMPLEX, dices the GAM2562 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2562 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 85%) nucleotide sequence of GAM2562 RNA is designated SEQ ID:5153, and is provided hereinbelow with reference to the sequence listing part.
- [35744] GAM2562 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2562 target RNA, herein designated GAM TARGET RNA. GAM2562 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [35745] GAM2562 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2562 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2562 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2562 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2562 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35746] The complementary binding of GAM2562 RNA, herein designated GAM RNA, to target binding sites on GAM2562 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2562 target RNA, herein designated GAM TARGET RNA, into GAM2562 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35747] It is appreciated that GAM2562 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2562 target genes. The mRNA of each one of this plurality of GAM2562 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2562 RNA, herein designated GAM RNA, and which when bound by GAM2562 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2562 target proteins.

[35748] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2562 gene, herein designated GAM GENE, on one or more GAM2562 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35749] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2562 correlate with, and may be deduced from, the identity of the target genes which GAM2562 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35750] Nucleotide sequences of the GAM2562 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2562 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2562 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2562 are further described hereinbelow with reference to Table 1.

[35751] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2562 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

[35752] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2563 (GAM2563) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35753] GAM2563 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2563 was detected is described hereinabove with reference to Figs. 2-8.

[35754] GAM2563 gene, herein designated GAM GENE, and GAM2563 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[35755] GAM2563 gene, herein designated GAM GENE, encodes a GAM2563 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2563 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2563 precursor RNA is designated SEQ ID:2540, and is provided hereinbelow with reference to the sequence listing part.

[35756] GAM2563 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2563 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35757] An enzyme complex designated DICER COMPLEX, dices the GAM2563 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2563 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 83%) nucleotide sequence of GAM2563 RNA is designated SEQ ID:5154, and is provided hereinbelow with reference to the sequence listing part.

[35758] GAM2563 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2563 target RNA, herein designated GAM TARGET RNA. GAM2563 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35759] GAM2563 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2563 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2563 RNA,



herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2563 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2563 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35760] The complementary binding of GAM2563 RNA, herein designated GAM RNA, to target binding sites on GAM2563 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2563 target RNA, herein designated GAM TARGET RNA, into GAM2563 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35761] It is appreciated that GAM2563 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2563 target genes. The mRNA of each one of this plurality of GAM2563 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2563 RNA, herein designated GAM RNA, and which when bound by GAM2563 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2563 target proteins.

[35762] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2563 gene, herein designated GAM GENE, on one or more GAM2563 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35763] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2563 correlate with, and may be deduced from, the identity of the target genes which GAM2563 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35764] Nucleotide sequences of the GAM2563 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2563 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2563 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2563 are further described hereinbelow with reference to Table 1.

[35765] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2563 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[35766] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2564 (GAM2564) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35767] GAM2564 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2564 was detected is described hereinabove with reference to Figs. 2-8.

[35768] GAM2564 gene, herein designated GAM GENE, and GAM2564 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[35769] GAM2564 gene, herein designated GAM GENE, encodes a GAM2564 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2564 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2564 precursor RNA is designated SEQ ID:2541, and is provided hereinbelow with reference to the sequence listing part.

[35770] GAM2564 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2564 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35771] An enzyme complex designated DICER COMPLEX, dices the GAM2564 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2564 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 83%) nucleotide sequence of GAM2564 RNA is designated SEQ ID:5155, and is provided hereinbelow with reference to the sequence listing part.

[35772] GAM2564 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2564 target RNA, herein designated GAM TARGET RNA. GAM2564 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35773] GAM2564 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2564 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2564 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2564 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2564 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35774] The complementary binding of GAM2564 RNA, herein designated GAM RNA, to target binding sites on GAM2564 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2564 target RNA, herein designated GAM TARGET RNA, into GAM2564 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35775] It is appreciated that GAM2564 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2564 target genes. The

mRNA of each one of this plurality of GAM2564 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2564 RNA, herein designated GAM RNA, and which when bound by GAM2564 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2564 target proteins.

[35776] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2564 gene, herein designated GAM GENE, on one or more GAM2564 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35777] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2564 correlate with, and may be deduced from, the identity of the target genes which GAM2564 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35778] Nucleotide sequences of the GAM2564 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2564 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2564 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2564 are further described hereinbelow with reference to Table 1.

[35779] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2564 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[35780] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2565 (GAM2565) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35781] GAM2565 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2565 was detected is described hereinabove with reference to Figs. 2-8.

[35782] GAM2565 gene, herein designated GAM GENE, and GAM2565 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[35783] GAM2565 gene, herein designated GAM GENE, encodes a GAM2565 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2565 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2565 precursor RNA is designated SEQ ID:2542, and is provided hereinbelow with reference to the sequence listing part.

[35784] GAM2565 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2565 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35785] An enzyme complex designated DICER COMPLEX, dices the GAM2565 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2565 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 87%) nucleotide sequence of GAM2565 RNA is designated SEQ ID:5156, and is provided hereinbelow with reference to the sequence listing part.

[35786] GAM2565 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2565 target RNA, herein designated GAM TARGET RNA. GAM2565 target RNA, herein designated GAM



TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35787] GAM2565 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2565 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2565 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2565 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2565 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35788] The complementary binding of GAM2565 RNA, herein designated GAM RNA, to target binding sites on GAM2565 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2565 target RNA, herein designated GAM TARGET RNA, into GAM2565 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35789] It is appreciated that GAM2565 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2565 target genes. The mRNA of each one of this plurality of GAM2565 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2565 RNA, herein designated GAM RNA, and which when bound by GAM2565 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2565 target proteins.

[35790] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2565 gene, herein designated GAM GENE, on one or more GAM2565 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35791] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2565 correlate with, and may be deduced from, the identity of the target

genes which GAM2565 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35792] Nucleotide sequences of the GAM2565 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2565 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2565 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2565 are further described hereinbelow with reference to Table 1.

[35793] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2565 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[35794] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2566 (GAM2566) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35795] GAM2566 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2566 was detected is described hereinabove with reference to Figs. 2-8.

[35796] GAM2566 gene, herein designated GAM GENE, and GAM2566 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

[35797] GAM2566 gene, herein designated GAM GENE, encodes a GAM2566 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2566 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2566 precursor RNA is designated SEQ ID:2543, and is provided hereinbelow with reference to the sequence listing part.

[35798] GAM2566 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2566 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35799] An enzyme complex designated DICER COMPLEX, dices the GAM2566 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2566 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 87%) nucleotide sequence of GAM2566 RNA is designated SEQ ID:5157, and is provided

hereinbelow with reference to the sequence listing part.

[35800] GAM2566 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2566 target RNA, herein designated GAM TARGET RNA. GAM2566 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35801] GAM2566 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2566 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2566 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2566 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2566 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35802] The complementary binding of GAM2566 RNA, herein designated GAM RNA, to target binding sites on GAM2566 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2566 target RNA, herein designated GAM TARGET RNA, into GAM2566 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35803] It is appreciated that GAM2566 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2566 target genes. The mRNA of each one of this plurality of GAM2566 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2566 RNA, herein designated GAM RNA, and which when bound by GAM2566 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2566 target proteins.

[35804] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2566 gene, herein designated GAM GENE, on one or more GAM2566 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35805] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2566 correlate with, and may be deduced from, the identity of the target genes which GAM2566 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35806] Nucleotide sequences of the GAM2566 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2566 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2566 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2566 are further described hereinbelow with reference to Table 1.

[35807] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2566 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[35808] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2567 (GAM2567) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35809] GAM2567 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2567 was detected is described hereinabove with reference to Figs. 2-8.

[35810] GAM2567 gene, herein designated GAM GENE, and GAM2567 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[35811] GAM2567 gene, herein designated GAM GENE, encodes a GAM2567 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2567 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2567 precursor RNA is designated SEQ ID:2544, and is provided hereinbelow with reference to the sequence listing part.

[35812] GAM2567 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2567 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35813] An enzyme complex designated DICER COMPLEX, dices the GAM2567 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2567 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin



structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of GAM2567 RNA is designated SEQ ID:5158, and is provided hereinbelow with reference to the sequence listing part.

[35814] GAM2567 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2567 target RNA, herein designated GAM TARGET RNA. GAM2567 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35815] GAM2567 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2567 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2567 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2567 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2567 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35816] The complementary binding of GAM2567 RNA, herein designated GAM RNA, to target binding sites on GAM2567 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2567 target RNA, herein designated GAM TARGET RNA, into GAM2567 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35817] It is appreciated that GAM2567 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2567 target genes. The mRNA of each one of this plurality of GAM2567 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2567 RNA, herein designated GAM RNA, and which when bound by GAM2567 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2567 target proteins.

[35818] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2567 gene, herein designated GAM GENE, on one or more GAM2567 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35819] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2567 correlate with, and may be deduced from, the identity of the target genes which GAM2567 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35820] Nucleotide sequences of the GAM2567 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2567 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2567 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2567 are further described hereinbelow with reference to Table 1.

[35821] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2567 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[35822] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2568 (GAM2568) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35823] GAM2568 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2568 was detected is described hereinabove with reference to Figs. 2-8.

[35824] GAM2568 gene, herein designated GAM GENE, and GAM2568 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[35825] GAM2568 gene, herein designated GAM GENE, encodes a GAM2568 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2568 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2568 precursor RNA is designated SEQ ID:2545, and is provided hereinbelow with reference to the sequence listing part.

[35826] GAM2568 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2568 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

- [35827] An enzyme complex designated DICER COMPLEX, dices the GAM2568 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2568 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of GAM2568 RNA is designated SEQ ID:5159, and is provided hereinbelow with reference to the sequence listing part.
- [35828] GAM2568 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2568 target RNA, herein designated GAM TARGET RNA. GAM2568 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [35829] GAM2568 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2568 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2568 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2568 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2568 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35830] The complementary binding of GAM2568 RNA, herein designated GAM RNA, to target binding sites on GAM2568 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2568 target RNA, herein designated GAM TARGET RNA, into GAM2568 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35831] It is appreciated that GAM2568 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2568 target genes. The mRNA of each one of this plurality of GAM2568 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2568 RNA, herein designated GAM RNA, and which when bound by GAM2568 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2568 target proteins.

[35832] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2568 gene, herein designated GAM GENE, on one or more GAM2568 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35833] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2568 correlate with, and may be deduced from, the identity of the target genes which GAM2568 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35834] Nucleotide sequences of the GAM2568 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2568 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2568 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2568 are further described hereinbelow with reference to Table 1.

[35835] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2568 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

[35836] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2569 (GAM2569) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35837] GAM2569 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2569 was detected is described hereinabove with reference to Figs. 2-8.

[35838] GAM2569 gene, herein designated GAM GENE, and GAM2569 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[35839] GAM2569 gene, herein designated GAM GENE, encodes a GAM2569 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2569 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2569 precursor RNA is designated SEQ ID:2546, and is provided hereinbelow with reference to the sequence listing part.

[35840] GAM2569 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2569 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA



encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35841] An enzyme complex designated DICER COMPLEX, dices the GAM2569 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2569 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 83%) nucleotide sequence of GAM2569 RNA is designated SEQ ID:5160, and is provided hereinbelow with reference to the sequence listing part.

[35842] GAM2569 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2569 target RNA, herein designated GAM TARGET RNA. GAM2569 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35843] GAM2569 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2569 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2569 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2569 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2569 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35844] The complementary binding of GAM2569 RNA, herein designated GAM RNA, to target binding sites on GAM2569 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2569 target RNA, herein designated GAM TARGET RNA, into GAM2569 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35845] It is appreciated that GAM2569 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2569 target genes. The mRNA of each one of this plurality of GAM2569 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2569 RNA, herein designated GAM RNA, and which when bound by GAM2569 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2569 target proteins.

[35846] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2569 gene, herein designated GAM GENE, on one or more GAM2569 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35847] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2569 correlate with, and may be deduced from, the identity of the target genes which GAM2569 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35848] Nucleotide sequences of the GAM2569 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2569 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2569 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2569 are further described hereinbelow with reference to Table 1.

[35849] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2569 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[35850] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2570 (GAM2570) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35851] GAM2570 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2570 was detected is described hereinabove with reference to Figs. 2-8.

[35852] GAM2570 gene, herein designated GAM GENE, and GAM2570 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[35853] GAM2570 gene, herein designated GAM GENE, encodes a GAM2570 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2570 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2570 precursor RNA is designated SEQ ID:2547, and is provided hereinbelow with reference to the sequence listing part.

[35854] GAM2570 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2570 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35855] An enzyme complex designated DICER COMPLEX, dices the GAM2570 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2570 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 78%) nucleotide sequence of GAM2570 RNA is designated SEQ ID:5161, and is provided hereinbelow with reference to the sequence listing part.

[35856] GAM2570 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2570 target RNA, herein designated GAM TARGET RNA. GAM2570 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35857] GAM2570 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2570 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2570 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2570 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2570 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35858] The complementary binding of GAM2570 RNA, herein designated GAM RNA, to target binding sites on GAM2570 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2570 target RNA, herein designated GAM TARGET RNA, into GAM2570 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35859] It is appreciated that GAM2570 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2570 target genes. The

mRNA of each one of this plurality of GAM2570 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2570 RNA, herein designated GAM RNA, and which when bound by GAM2570 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2570 target proteins.

[35860] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2570 gene, herein designated GAM GENE, on one or more GAM2570 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35861] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2570 correlate with, and may be deduced from, the identity of the target genes which GAM2570 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35862] Nucleotide sequences of the GAM2570 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2570 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2570 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2570 are further described hereinbelow with reference to Table 1.

[35863] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2570 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[35864] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2571 (GAM2571) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35865] GAM2571 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2571 was detected is described hereinabove with reference to Figs. 2-8.

[35866] GAM2571 gene, herein designated GAM GENE, and GAM2571 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[35867] GAM2571 gene, herein designated GAM GENE, encodes a GAM2571 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2571 precursor RNA,



herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2571 precursor RNA is designated SEQ ID:2548, and is provided hereinbelow with reference to the sequence listing part.

[35868] GAM2571 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2571 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35869] An enzyme complex designated DICER COMPLEX, dices the GAM2571 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2571 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 85%) nucleotide sequence of GAM2571 RNA is designated SEQ ID:5162, and is provided hereinbelow with reference to the sequence listing part.

[35870] GAM2571 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2571 target RNA, herein designated GAM TARGET RNA. GAM2571 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35871] GAM2571 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2571 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2571 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2571 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2571 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35872] The complementary binding of GAM2571 RNA, herein designated GAM RNA, to target binding sites on GAM2571 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2571 target RNA, herein designated GAM TARGET RNA, into GAM2571 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35873] It is appreciated that GAM2571 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2571 target genes. The mRNA of each one of this plurality of GAM2571 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2571 RNA, herein designated GAM RNA, and which when bound by GAM2571 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2571 target proteins.

[35874] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2571 gene, herein designated GAM GENE, on one or more GAM2571 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35875] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2571 correlate with, and may be deduced from, the identity of the target

genes which GAM2571 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35876] Nucleotide sequences of the GAM2571 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2571 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2571 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2571 are further described hereinbelow with reference to Table 1.

[35877] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2571 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[35878] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2572 (GAM2572) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35879] GAM2572 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2572 was detected is described hereinabove with reference to Figs. 2-8.

[35880] GAM2572 gene, herein designated GAM GENE, and GAM2572 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

[35881] GAM2572 gene, herein designated GAM GENE, encodes a GAM2572 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2572 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2572 precursor RNA is designated SEQ ID:2549, and is provided hereinbelow with reference to the sequence listing part.

[35882] GAM2572 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2572 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35883] An enzyme complex designated DICER COMPLEX, dices the GAM2572 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2572 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 88%) nucleotide sequence of GAM2572 RNA is designated SEQ ID:5163, and is provided

hereinbelow with reference to the sequence listing part.

[35884] GAM2572 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2572 target RNA, herein designated GAM TARGET RNA. GAM2572 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35885] GAM2572 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2572 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2572 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2572 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2572 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35886] The complementary binding of GAM2572 RNA, herein designated GAM RNA, to target binding sites on GAM2572 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2572 target RNA, herein designated GAM TARGET RNA, into GAM2572 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35887] It is appreciated that GAM2572 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2572 target genes. The mRNA of each one of this plurality of GAM2572 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2572 RNA, herein designated GAM RNA, and which when bound by GAM2572 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2572 target proteins.

[35888] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2572 gene, herein designated GAM GENE, on one or more GAM2572 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35889] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2572 correlate with, and may be deduced from, the identity of the target genes which GAM2572 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35890] Nucleotide sequences of the GAM2572 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2572 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2572 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2572 are further described hereinbelow with reference to Table 1.

[35891] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2572 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[35892] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2573 (GAM2573) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35893] GAM2573 is a novel bioinformatically detected regulatory, non protein



coding, micro RNA (miRNA) gene. The method by which GAM2573 was detected is described hereinabove with reference to Figs. 2-8.

[35894] GAM2573 gene, herein designated GAM GENE, and GAM2573 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[35895] GAM2573 gene, herein designated GAM GENE, encodes a GAM2573 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2573 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2573 precursor RNA is designated SEQ ID:2550, and is provided hereinbelow with reference to the sequence listing part.

[35896] GAM2573 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2573 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35897] An enzyme complex designated DICER COMPLEX, dices the GAM2573 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2573 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 76%) nucleotide sequence of GAM2573 RNA is designated SEQ ID:5164, and is provided hereinbelow with reference to the sequence listing part.

[35898] GAM2573 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2573 target RNA, herein designated GAM TARGET RNA. GAM2573 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35899] GAM2573 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2573 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2573 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2573 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2573 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35900] The complementary binding of GAM2573 RNA, herein designated GAM RNA, to target binding sites on GAM2573 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2573 target RNA, herein designated GAM TARGET RNA, into GAM2573 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35901] It is appreciated that GAM2573 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2573 target genes. The mRNA of each one of this plurality of GAM2573 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2573 RNA, herein designated GAM RNA, and which when bound by GAM2573 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2573 target proteins.

[35902] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2573 gene, herein designated GAM GENE, on one or more GAM2573 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35903] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2573 correlate with, and may be deduced from, the identity of the target genes which GAM2573 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35904] Nucleotide sequences of the GAM2573 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2573 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2573 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2573 are further described hereinbelow with reference to Table 1.

[35905] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2573 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[35906] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2574 (GAM2574) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35907] GAM2574 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2574 was detected is described hereinabove with reference to Figs. 2-8.

[35908] GAM2574 gene, herein designated GAM GENE, and GAM2574 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[35909] GAM2574 gene, herein designated GAM GENE, encodes a GAM2574 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2574 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2574 precursor RNA is designated SEQ ID:2551, and is provided hereinbelow with reference to the sequence listing part.

[35910] GAM2574 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2574 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

- [35911] An enzyme complex designated DICER COMPLEX, dices the GAM2574 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2574 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 85%) nucleotide sequence of GAM2574 RNA is designated SEQ ID:5165, and is provided hereinbelow with reference to the sequence listing part.
- [35912] GAM2574 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2574 target RNA, herein designated GAM TARGET RNA. GAM2574 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [35913] GAM2574 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2574 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2574 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2574 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2574 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35914] The complementary binding of GAM2574 RNA, herein designated GAM RNA, to target binding sites on GAM2574 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2574 target RNA, herein designated GAM TARGET RNA, into GAM2574 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35915] It is appreciated that GAM2574 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2574 target genes. The mRNA of each one of this plurality of GAM2574 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2574 RNA, herein designated GAM RNA, and which when bound by GAM2574 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2574 target proteins.

[35916] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2574 gene, herein designated GAM GENE, on one or more GAM2574 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35917] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2574 correlate with, and may be deduced from, the identity of the target genes which GAM2574 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35918] Nucleotide sequences of the GAM2574 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2574 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2574 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2574 are further described hereinbelow with reference to Table 1.

[35919] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2574 RNA, herein designated GAM RNA, are described hereinbelow



with reference to Table 2.

[35920] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2575 (GAM2575) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35921] GAM2575 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2575 was detected is described hereinabove with reference to Figs. 2-8.

[35922] GAM2575 gene, herein designated GAM GENE, and GAM2575 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[35923] GAM2575 gene, herein designated GAM GENE, encodes a GAM2575 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2575 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2575 precursor RNA is designated SEQ ID:2552, and is provided hereinbelow with reference to the sequence listing part.

[35924] GAM2575 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2575 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35925] An enzyme complex designated DICER COMPLEX, dices the GAM2575 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2575 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2575 RNA is designated SEQ ID:5167, and is provided hereinbelow with reference to the sequence listing part.

[35926] GAM2575 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2575 target RNA, herein designated GAM TARGET RNA. GAM2575 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35927] GAM2575 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2575 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2575 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2575 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2575 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35928] The complementary binding of GAM2575 RNA, herein designated GAM RNA, to target binding sites on GAM2575 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2575 target RNA, herein designated GAM TARGET RNA, into GAM2575 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35929] It is appreciated that GAM2575 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2575 target genes. The mRNA of each one of this plurality of GAM2575 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2575 RNA, herein designated GAM RNA, and which when bound by GAM2575 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2575 target proteins.

[35930] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2575 gene, herein designated GAM GENE, on one or more GAM2575 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35931] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2575 correlate with, and may be deduced from, the identity of the target genes which GAM2575 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35932] Nucleotide sequences of the GAM2575 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2575 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2575 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2575 are further described hereinbelow with reference to Table 1.

[35933] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2575 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[35934] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2576 (GAM2576) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35935] GAM2576 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2576 was detected is described hereinabove with reference to Figs. 2-8.

[35936] GAM2576 gene, herein designated GAM GENE, and GAM2576 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[35937] GAM2576 gene, herein designated GAM GENE, encodes a GAM2576 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2576 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2576 precursor RNA is designated SEQ ID:2553, and is provided hereinbelow with reference to the sequence listing part.

[35938] GAM2576 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2576 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35939] An enzyme complex designated DICER COMPLEX, dices the GAM2576 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2576 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 84%) nucleotide sequence of GAM2576 RNA is designated SEQ ID:5166, and is provided hereinbelow with reference to the sequence listing part.

[35940] GAM2576 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2576 target RNA, herein designated GAM TARGET RNA. GAM2576 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35941] GAM2576 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2576 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2576 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2576 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2576 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35942] The complementary binding of GAM2576 RNA, herein designated GAM RNA, to target binding sites on GAM2576 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2576 target RNA, herein designated GAM TARGET RNA, into GAM2576 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35943] It is appreciated that GAM2576 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2576 target genes. The

mRNA of each one of this plurality of GAM2576 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2576 RNA, herein designated GAM RNA, and which when bound by GAM2576 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2576 target proteins.

[35944] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2576 gene, herein designated GAM GENE, on one or more GAM2576 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35945] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2576 correlate with, and may be deduced from, the identity of the target genes which GAM2576 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35946] Nucleotide sequences of the GAM2576 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2576 RNA, herein



designated GAM RNA, and a schematic representation of the secondary folding of GAM2576 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2576 are further described hereinbelow with reference to Table 1.

[35947] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2576 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[35948] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2577 (GAM2577) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35949] GAM2577 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2577 was detected is described hereinabove with reference to Figs. 2-8.

[35950] GAM2577 gene, herein designated GAM GENE, and GAM2577 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[35951] GAM2577 gene, herein designated GAM GENE, encodes a GAM2577 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2577 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2577 precursor RNA is designated SEQ ID:2554, and is provided hereinbelow with reference to the sequence listing part.

[35952] GAM2577 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2577 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35953] An enzyme complex designated DICER COMPLEX, dices the GAM2577 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2577 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 87%) nucleotide sequence of GAM2577 RNA is designated SEQ ID:5168, and is provided hereinbelow with reference to the sequence listing part.

[35954] GAM2577 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2577 target RNA, herein designated GAM TARGET RNA. GAM2577 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35955] GAM2577 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2577 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2577 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2577 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2577 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35956] The complementary binding of GAM2577 RNA, herein designated GAM RNA, to target binding sites on GAM2577 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2577 target RNA, herein designated GAM TARGET RNA, into GAM2577 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35957] It is appreciated that GAM2577 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2577 target genes. The mRNA of each one of this plurality of GAM2577 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2577 RNA, herein designated GAM RNA, and which when bound by GAM2577 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2577 target proteins.

[35958] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2577 gene, herein designated GAM GENE, on one or more GAM2577 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35959] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2577 correlate with, and may be deduced from, the identity of the target

genes which GAM2577 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35960] Nucleotide sequences of the GAM2577 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2577 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2577 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2577 are further described hereinbelow with reference to Table 1.

[35961] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2577 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[35962] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2578 (GAM2578) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35963] GAM2578 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2578 was detected is described hereinabove with reference to Figs. 2-8.

[35964] GAM2578 gene, herein designated GAM GENE, and GAM2578 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

[35965] GAM2578 gene, herein designated GAM GENE, encodes a GAM2578 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2578 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2578 precursor RNA is designated SEQ ID:2555, and is provided hereinbelow with reference to the sequence listing part.

[35966] GAM2578 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2578 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35967] An enzyme complex designated DICER COMPLEX, dices the GAM2578 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2578 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of GAM2578 RNA is designated SEQ ID:5169, and is provided

hereinbelow with reference to the sequence listing part.

[35968] GAM2578 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2578 target RNA, herein designated GAM TARGET RNA. GAM2578 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35969] GAM2578 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2578 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2578 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2578 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2578 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35970] The complementary binding of GAM2578 RNA, herein designated GAM RNA, to target binding sites on GAM2578 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2578 target RNA, herein designated GAM TARGET RNA, into GAM2578 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35971] It is appreciated that GAM2578 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2578 target genes. The mRNA of each one of this plurality of GAM2578 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2578 RNA, herein designated GAM RNA, and which when bound by GAM2578 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2578 target proteins.

[35972] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2578 gene, herein designated GAM GENE, on one or more GAM2578 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding



sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35973] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2578 correlate with, and may be deduced from, the identity of the target genes which GAM2578 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35974] Nucleotide sequences of the GAM2578 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2578 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2578 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2578 are further described hereinbelow with reference to Table 1.

[35975] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2578 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[35976] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2579 (GAM2579) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35977] GAM2579 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2579 was detected is described hereinabove with reference to Figs. 2-8.

[35978] GAM2579 gene, herein designated GAM GENE, and GAM2579 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[35979] GAM2579 gene, herein designated GAM GENE, encodes a GAM2579 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2579 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2579 precursor RNA is designated SEQ ID:2556, and is provided hereinbelow with reference to the sequence listing part.

[35980] GAM2579 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2579 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[35981] An enzyme complex designated DICER COMPLEX, dices the GAM2579 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2579 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of GAM2579 RNA is designated SEQ ID:5170, and is provided hereinbelow with reference to the sequence listing part.

[35982] GAM2579 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2579 target RNA, herein designated GAM TARGET RNA. GAM2579 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[35983] GAM2579 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2579 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2579 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2579 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2579 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35984] The complementary binding of GAM2579 RNA, herein designated GAM RNA, to target binding sites on GAM2579 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2579 target RNA, herein designated GAM TARGET RNA, into GAM2579 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35985] It is appreciated that GAM2579 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2579 target genes. The mRNA of each one of this plurality of GAM2579 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2579 RNA, herein designated GAM RNA, and which when bound by GAM2579 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2579 target proteins.

[35986] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2579 gene, herein designated GAM GENE, on one or more GAM2579 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[35987] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2579 correlate with, and may be deduced from, the identity of the target genes which GAM2579 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[35988] Nucleotide sequences of the GAM2579 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2579 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2579 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2579 are further described hereinbelow with reference to Table 1.

[35989] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2579 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[35990] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2580 (GAM2580) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[35991] GAM2580 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2580 was detected is described hereinabove with reference to Figs. 2-8.

[35992] GAM2580 gene, herein designated GAM GENE, and GAM2580 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[35993] GAM2580 gene, herein designated GAM GENE, encodes a GAM2580 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2580 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2580 precursor RNA is designated SEQ ID:2557, and is provided hereinbelow with reference to the sequence listing part.

[35994] GAM2580 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2580 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

- [35995] An enzyme complex designated DICER COMPLEX, dices the GAM2580 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2580 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of GAM2580 RNA is designated SEQ ID:5171, and is provided hereinbelow with reference to the sequence listing part.
- [35996] GAM2580 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2580 target RNA, herein designated GAM TARGET RNA. GAM2580 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [35997] GAM2580 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2580 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2580 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2580 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2580 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[35998] The complementary binding of GAM2580 RNA, herein designated GAM RNA, to target binding sites on GAM2580 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2580 target RNA, herein designated GAM TARGET RNA, into GAM2580 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[35999] It is appreciated that GAM2580 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2580 target genes. The mRNA of each one of this plurality of GAM2580 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2580 RNA, herein designated GAM RNA, and which when bound by GAM2580 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2580 target proteins.

[36000] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition



exerted by GAM2580 gene, herein designated GAM GENE, on one or more GAM2580 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36001] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2580 correlate with, and may be deduced from, the identity of the target genes which GAM2580 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36002] Nucleotide sequences of the GAM2580 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2580 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2580 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2580 are further described hereinbelow with reference to Table 1.

[36003] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2580 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

[36004] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2581 (GAM2581) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[36005] GAM2581 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2581 was detected is described hereinabove with reference to Figs. 2-8.

[36006] GAM2581 gene, herein designated GAM GENE, and GAM2581 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[36007] GAM2581 gene, herein designated GAM GENE, encodes a GAM2581 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2581 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2581 precursor RNA is designated SEQ ID:2558, and is provided hereinbelow with reference to the sequence listing part.

[36008] GAM2581 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2581 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36009] An enzyme complex designated DICER COMPLEX, dices the GAM2581 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2581 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 90%) nucleotide sequence of GAM2581 RNA is designated SEQ ID:5172, and is provided hereinbelow with reference to the sequence listing part.

[36010] GAM2581 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2581 target RNA, herein designated GAM TARGET RNA. GAM2581 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36011] GAM2581 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2581 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2581 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting. GAM2581 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2581 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36012] The complementary binding of GAM2581 RNA, herein designated GAM RNA, to target binding sites on GAM2581 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2581 target RNA, herein designated GAM TARGET RNA, into GAM2581 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36013] It is appreciated that GAM2581 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2581 target genes. The mRNA of each one of this plurality of GAM2581 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2581 RNA, herein designated GAM RNA, and which when bound by GAM2581 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2581 target proteins.

[36014] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2581 gene, herein designated GAM GENE, on one or more GAM2581 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36015] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2581 correlate with, and may be deduced from, the identity of the target genes which GAM2581 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36016] Nucleotide sequences of the GAM2581 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2581 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2581 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2581 are further described hereinbelow with reference to Table 1.

[36017] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2581 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[36018] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2582 (GAM2582) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[36019] GAM2582 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2582 was detected is described hereinabove with reference to Figs. 2-8.

[36020] GAM2582 gene, herein designated GAM GENE, and GAM2582 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[36021] GAM2582 gene, herein designated GAM GENE, encodes a GAM2582 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2582 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2582 precursor RNA is designated SEQ ID:2559, and is provided hereinbelow with reference to the sequence listing part.

[36022] GAM2582 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2582 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36023] An enzyme complex designated DICER COMPLEX, dices the GAM2582 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2582 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 76%) nucleotide sequence of GAM2582 RNA is designated SEQ ID:5173, and is provided hereinbelow with reference to the sequence listing part.

[36024] GAM2582 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2582 target RNA, herein designated GAM TARGET RNA. GAM2582 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36025] GAM2582 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2582 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2582 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2582 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2582 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36026] The complementary binding of GAM2582 RNA, herein designated GAM RNA, to target binding sites on GAM2582 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2582 target RNA, herein designated GAM TARGET RNA, into GAM2582 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36027] It is appreciated that GAM2582 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2582 target genes. The



mRNA of each one of this plurality of GAM2582 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2582 RNA, herein designated GAM RNA, and which when bound by GAM2582 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2582 target proteins.

[36028] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2582 gene, herein designated GAM GENE, on one or more GAM2582 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36029] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2582 correlate with, and may be deduced from, the identity of the target genes which GAM2582 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36030] Nucleotide sequences of the GAM2582 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2582 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2582 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2582 are further described hereinbelow with reference to Table 1.

[36031] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2582 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[36032] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2583 (GAM2583) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[36033] GAM2583 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2583 was detected is described hereinabove with reference to Figs. 2-8.

[36034] GAM2583 gene, herein designated GAM GENE, and GAM2583 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[36035] GAM2583 gene, herein designated GAM GENE, encodes a GAM2583 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2583 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2583 precursor RNA is designated SEQ ID:2560, and is provided hereinbelow with reference to the sequence listing part.

[36036] GAM2583 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2583 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36037] An enzyme complex designated DICER COMPLEX, dices the GAM2583 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2583 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2583 RNA is designated SEQ ID:5174, and is provided hereinbelow with reference to the sequence listing part.

[36038] GAM2583 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2583 target RNA, herein designated GAM TARGET RNA. GAM2583 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36039] GAM2583 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2583 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2583 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2583 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2583 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36040] The complementary binding of GAM2583 RNA, herein designated GAM RNA, to target binding sites on GAM2583 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2583 target RNA, herein designated GAM TARGET RNA, into GAM2583 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36041] It is appreciated that GAM2583 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2583 target genes. The mRNA of each one of this plurality of GAM2583 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2583 RNA, herein designated GAM RNA, and which when bound by GAM2583 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2583 target proteins.

[36042] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2583 gene, herein designated GAM GENE, on one or more GAM2583 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36043] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2583 correlate with, and may be deduced from, the identity of the target

genes which GAM2583 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36044] Nucleotide sequences of the GAM2583 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2583 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2583 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2583 are further described hereinbelow with reference to Table 1.

[36045] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2583 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[36046] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2584 (GAM2584) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[36047] GAM2584 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2584 was detected is described hereinabove with reference to Figs. 2-8.

[36048] GAM2584 gene, herein designated GAM GENE, and GAM2584 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

[36049] GAM2584 gene, herein designated GAM GENE, encodes a GAM2584 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2584 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2584 precursor RNA is designated SEQ ID:2561, and is provided hereinbelow with reference to the sequence listing part.

[36050] GAM2584 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2584 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36051] An enzyme complex designated DICER COMPLEX, dices the GAM2584 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2584 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of GAM2584 RNA is designated SEQ ID:5175, and is provided

hereinbelow with reference to the sequence listing part.

[36052] GAM2584 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2584 target RNA, herein designated GAM TARGET RNA. GAM2584 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36053] GAM2584 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2584 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2584 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2584 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2584 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.



[36054] The complementary binding of GAM2584 RNA, herein designated GAM RNA, to target binding sites on GAM2584 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2584 target RNA, herein designated GAM TARGET RNA, into GAM2584 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36055] It is appreciated that GAM2584 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2584 target genes. The mRNA of each one of this plurality of GAM2584 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2584 RNA, herein designated GAM RNA, and which when bound by GAM2584 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2584 target proteins.

[36056] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2584 gene, herein designated GAM GENE, on one or more GAM2584 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36057] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2584 correlate with, and may be deduced from, the identity of the target genes which GAM2584 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36058] Nucleotide sequences of the GAM2584 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2584 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2584 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2584 are further described hereinbelow with reference to Table 1.

[36059] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2584 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[36060] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2585 (GAM2585) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[36061] GAM2585 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2585 was detected is described hereinabove with reference to Figs. 2-8.

[36062] GAM2585 gene, herein designated GAM GENE, and GAM2585 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[36063] GAM2585 gene, herein designated GAM GENE, encodes a GAM2585 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2585 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2585 precursor RNA is designated SEQ ID:2562, and is provided hereinbelow with reference to the sequence listing part.

[36064] GAM2585 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2585 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36065] An enzyme complex designated DICER COMPLEX, dices the GAM2585 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2585 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 83%) nucleotide sequence of GAM2585 RNA is designated SEQ ID:5176, and is provided hereinbelow with reference to the sequence listing part.

[36066] GAM2585 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2585 target RNA, herein designated GAM TARGET RNA. GAM2585 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36067] GAM2585 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2585 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2585 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2585 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2585 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36068] The complementary binding of GAM2585 RNA, herein designated GAM RNA, to target binding sites on GAM2585 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2585 target RNA, herein designated GAM TARGET RNA, into GAM2585 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36069] It is appreciated that GAM2585 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2585 target genes. The mRNA of each one of this plurality of GAM2585 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2585 RNA, herein designated GAM RNA, and which when bound by GAM2585 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2585 target proteins.

[36070] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2585 gene, herein designated GAM GENE, on one or more GAM2585 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36071] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2585 correlate with, and may be deduced from, the identity of the target genes which GAM2585 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36072] Nucleotide sequences of the GAM2585 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2585 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2585 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2585 are further described hereinbelow with reference to Table 1.

[36073] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2585 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[36074] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2586 (GAM2586) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[36075] GAM2586 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2586 was detected is described hereinabove with reference to Figs. 2-8.

[36076] GAM2586 gene, herein designated GAM GENE, and GAM2586 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[36077] GAM2586 gene, herein designated GAM GENE, encodes a GAM2586 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2586 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2586 precursor RNA is designated SEQ ID:2563, and is provided hereinbelow with reference to the sequence listing part.

[36078] GAM2586 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2586 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36079] An enzyme complex designated DICER COMPLEX, dices the GAM2586 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2586 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of GAM2586 RNA is designated SEQ ID:5179, and is provided hereinbelow with reference to the sequence listing part.

[36080] GAM2586 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2586 target RNA, herein designated GAM TARGET RNA. GAM2586 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36081] GAM2586 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2586 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2586 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an



illustration only, and is not meant to be limiting GAM2586 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2586 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36082] The complementary binding of GAM2586 RNA, herein designated GAM RNA, to target binding sites on GAM2586 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2586 target RNA, herein designated GAM TARGET RNA, into GAM2586 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36083] It is appreciated that GAM2586 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2586 target genes. The mRNA of each one of this plurality of GAM2586 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2586 RNA, herein designated GAM RNA, and which when bound by GAM2586 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2586 target proteins.

[36084] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2586 gene, herein designated GAM GENE, on one or more GAM2586 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36085] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2586 correlate with, and may be deduced from, the identity of the target genes which GAM2586 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36086] Nucleotide sequences of the GAM2586 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2586 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2586 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2586 are further described hereinbelow with reference to Table 1.

[36087] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2586 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

[36088] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2587 (GAM2587) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[36089] GAM2587 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2587 was detected is described hereinabove with reference to Figs. 2-8.

[36090] GAM2587 gene, herein designated GAM GENE, and GAM2587 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[36091] GAM2587 gene, herein designated GAM GENE, encodes a GAM2587 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2587 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2587 precursor RNA is designated SEQ ID:2564, and is provided hereinbelow with reference to the sequence listing part.

[36092] GAM2587 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2587 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36093] An enzyme complex designated DICER COMPLEX, dices the GAM2587 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2587 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 84%) nucleotide sequence of GAM2587 RNA is designated SEQ ID:5177, and is provided hereinbelow with reference to the sequence listing part.

[36094] GAM2587 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2587 target RNA, herein designated GAM TARGET RNA. GAM2587 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36095] GAM2587 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2587 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2587 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2587 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2587 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36096] The complementary binding of GAM2587 RNA, herein designated GAM RNA, to target binding sites on GAM2587 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2587 target RNA, herein designated GAM TARGET RNA, into GAM2587 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36097] It is appreciated that GAM2587 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2587 target genes. The mRNA of each one of this plurality of GAM2587 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2587 RNA, herein designated GAM RNA, and which when bound by GAM2587 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2587 target proteins.

[36098] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2587 gene, herein designated GAM GENE, on one or more GAM2587 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36099] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2587 correlate with, and may be deduced from, the identity of the target genes which GAM2587 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36100] Nucleotide sequences of the GAM2587 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2587 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2587 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2587 are further described hereinbelow with reference to Table 1.

- [36101] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2587 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.
- [36102] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2588 (GAM2588) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.
- [36103] GAM2588 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2588 was detected is described hereinabove with reference to Figs. 2-8.
- [36104] GAM2588 gene, herein designated GAM GENE, and GAM2588 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.
- [36105] GAM2588 gene, herein designated GAM GENE, encodes a GAM2588 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2588 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2588 precursor RNA is designated SEQ ID:2565, and is provided hereinbelow with reference to the sequence listing part.

[36106] GAM2588 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2588 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36107] An enzyme complex designated DICER COMPLEX, dices the GAM2588 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2588 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 86%) nucleotide sequence of GAM2588 RNA is designated SEQ ID:5178, and is provided hereinbelow with reference to the sequence listing part.

[36108] GAM2588 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2588 target RNA, herein designated GAM TARGET RNA. GAM2588 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.



[36109] GAM2588 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2588 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2588 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2588 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2588 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36110] The complementary binding of GAM2588 RNA, herein designated GAM RNA, to target binding sites on GAM2588 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2588 target RNA, herein designated GAM TARGET RNA, into GAM2588 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36111] It is appreciated that GAM2588 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2588 target genes. The

mRNA of each one of this plurality of GAM2588 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2588 RNA, herein designated GAM RNA, and which when bound by GAM2588 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2588 target proteins.

[36112] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2588 gene, herein designated GAM GENE, on one or more GAM2588 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36113] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2588 correlate with, and may be deduced from, the identity of the target genes which GAM2588 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36114] Nucleotide sequences of the GAM2588 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2588 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2588 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2588 are further described hereinbelow with reference to Table 1.

[36115] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2588 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[36116] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2589 (GAM2589) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[36117] GAM2589 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2589 was detected is described hereinabove with reference to Figs. 2-8.

[36118] GAM2589 gene, herein designated GAM GENE, and GAM2589 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[36119] GAM2589 gene, herein designated GAM GENE, encodes a GAM2589 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2589 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2589 precursor RNA is designated SEQ ID:2566, and is provided hereinbelow with reference to the sequence listing part.

[36120] GAM2589 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2589 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36121] An enzyme complex designated DICER COMPLEX, dices the GAM2589 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2589 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of GAM2589 RNA is designated SEQ ID:5180, and is provided hereinbelow with reference to the sequence listing part.

[36122] GAM2589 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2589 target RNA, herein designated GAM TARGET RNA. GAM2589 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36123] GAM2589 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2589 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2589 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2589 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2589 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36124] The complementary binding of GAM2589 RNA, herein designated GAM RNA, to target binding sites on GAM2589 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2589 target RNA, herein designated GAM TARGET RNA, into GAM2589 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36125] It is appreciated that GAM2589 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2589 target genes. The mRNA of each one of this plurality of GAM2589 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2589 RNA, herein designated GAM RNA, and which when bound by GAM2589 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2589 target proteins.

[36126] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2589 gene, herein designated GAM GENE, on one or more GAM2589 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36127] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2589 correlate with, and may be deduced from, the identity of the target

genes which GAM2589 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36128] Nucleotide sequences of the GAM2589 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2589 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2589 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2589 are further described hereinbelow with reference to Table 1.

[36129] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2589 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[36130] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2590 (GAM2590) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[36131] GAM2590 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2590 was detected is described hereinabove with reference to Figs. 2-8.

[36132] GAM2590 gene, herein designated GAM GENE, and GAM2590 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

[36133] GAM2590 gene, herein designated GAM GENE, encodes a GAM2590 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2590 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2590 precursor RNA is designated SEQ ID:2567, and is provided hereinbelow with reference to the sequence listing part.

[36134] GAM2590 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2590 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36135] An enzyme complex designated DICER COMPLEX, dices the GAM2590 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2590 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of GAM2590 RNA is designated SEQ ID:5181, and is provided



hereinbelow with reference to the sequence listing part.

[36136] GAM2590 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2590 target RNA, herein designated GAM TARGET RNA. GAM2590 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36137] GAM2590 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2590 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2590 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2590 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2590 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36138] The complementary binding of GAM2590 RNA, herein designated GAM RNA, to target binding sites on GAM2590 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2590 target RNA, herein designated GAM TARGET RNA, into GAM2590 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36139] It is appreciated that GAM2590 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2590 target genes. The mRNA of each one of this plurality of GAM2590 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2590 RNA, herein designated GAM RNA, and which when bound by GAM2590 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2590 target proteins.

[36140] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2590 gene, herein designated GAM GENE, on one or more GAM2590 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36141] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2590 correlate with, and may be deduced from, the identity of the target genes which GAM2590 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36142] Nucleotide sequences of the GAM2590 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2590 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2590 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2590 are further described hereinbelow with reference to Table 1.

[36143] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2590 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[36144] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2591 (GAM2591) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[36145] GAM2591 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2591 was detected is described hereinabove with reference to Figs. 2-8.

[36146] GAM2591 gene, herein designated GAM GENE, and GAM2591 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[36147] GAM2591 gene, herein designated GAM GENE, encodes a GAM2591 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2591 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2591 precursor RNA is designated SEQ ID:2568, and is provided hereinbelow with reference to the sequence listing part.

[36148] GAM2591 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2591 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36149] An enzyme complex designated DICER COMPLEX, dices the GAM2591 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2591 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of GAM2591 RNA is designated SEQ ID:5182, and is provided hereinbelow with reference to the sequence listing part.

[36150] GAM2591 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2591 target RNA, herein designated GAM TARGET RNA. GAM2591 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36151] GAM2591 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2591 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2591 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2591 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2591 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36152] The complementary binding of GAM2591 RNA, herein designated GAM RNA, to target binding sites on GAM2591 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2591 target RNA, herein designated GAM TARGET RNA, into GAM2591 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36153] It is appreciated that GAM2591 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2591 target genes. The mRNA of each one of this plurality of GAM2591 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2591 RNA, herein designated GAM RNA, and which when bound by GAM2591 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2591 target proteins.

[36154] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2591 gene, herein designated GAM GENE, on one or more GAM2591 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36155] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2591 correlate with, and may be deduced from, the identity of the target genes which GAM2591 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36156] Nucleotide sequences of the GAM2591 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2591 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2591 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2591 are further described hereinbelow with reference to Table 1.

[36157] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2591 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[36158] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2592 (GAM2592) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

- [36159] GAM2592 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2592 was detected is described hereinabove with reference to Figs. 2-8.
- [36160] GAM2592 gene, herein designated GAM GENE, and GAM2592 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.
- [36161] GAM2592 gene, herein designated GAM GENE, encodes a GAM2592 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2592 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2592 precursor RNA is designated SEQ ID:2569, and is provided hereinbelow with reference to the sequence listing part.
- [36162] GAM2592 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2592 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.



- [36163] An enzyme complex designated DICER COMPLEX, dices the GAM2592 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2592 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 85%) nucleotide sequence of GAM2592 RNA is designated SEQ ID:5183, and is provided hereinbelow with reference to the sequence listing part.
- [36164] GAM2592 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2592 target RNA, herein designated GAM TARGET RNA. GAM2592 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [36165] GAM2592 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2592 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2592 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2592 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2592 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36166] The complementary binding of GAM2592 RNA, herein designated GAM RNA, to target binding sites on GAM2592 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2592 target RNA, herein designated GAM TARGET RNA, into GAM2592 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36167] It is appreciated that GAM2592 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2592 target genes. The mRNA of each one of this plurality of GAM2592 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2592 RNA, herein designated GAM RNA, and which when bound by GAM2592 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2592 target proteins.

[36168] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2592 gene, herein designated GAM GENE, on one or more GAM2592 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36169] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2592 correlate with, and may be deduced from, the identity of the target genes which GAM2592 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36170] Nucleotide sequences of the GAM2592 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2592 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2592 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2592 are further described hereinbelow with reference to Table 1.

[36171] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2592 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

[36172] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2593 (GAM2593) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[36173] GAM2593 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2593 was detected is described hereinabove with reference to Figs. 2-8.

[36174] GAM2593 gene, herein designated GAM GENE, and GAM2593 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[36175] GAM2593 gene, herein designated GAM GENE, encodes a GAM2593 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2593 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2593 precursor RNA is designated SEQ ID:2570, and is provided hereinbelow with reference to the sequence listing part.

[36176] GAM2593 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2593 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36177] An enzyme complex designated DICER COMPLEX, dices the GAM2593 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2593 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2593 RNA is designated SEQ ID:5184, and is provided hereinbelow with reference to the sequence listing part.

[36178] GAM2593 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2593 target RNA, herein designated GAM TARGET RNA. GAM2593 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36179] GAM2593 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2593 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2593 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2593 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2593 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36180] The complementary binding of GAM2593 RNA, herein designated GAM RNA, to target binding sites on GAM2593 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2593 target RNA, herein designated GAM TARGET RNA, into GAM2593 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36181] It is appreciated that GAM2593 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2593 target genes. The mRNA of each one of this plurality of GAM2593 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2593 RNA, herein designated GAM RNA, and which when bound by GAM2593 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2593 target proteins.

[36182] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2593 gene, herein designated GAM GENE, on one or more GAM2593 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36183] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2593 correlate with, and may be deduced from, the identity of the target genes which GAM2593 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36184] Nucleotide sequences of the GAM2593 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2593 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2593 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2593 are further described hereinbelow with reference to Table 1.

- [36185] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2593 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.
- [36186] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2594 (GAM2594) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.
- [36187] GAM2594 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2594 was detected is described hereinabove with reference to Figs. 2-8.
- [36188] GAM2594 gene, herein designated GAM GENE, and GAM2594 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.
- [36189] GAM2594 gene, herein designated GAM GENE, encodes a GAM2594 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2594 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2594 precursor RNA is designated SEQ ID:2571, and is provided hereinbelow with reference to the sequence listing part.



[36190] GAM2594 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2594 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36191] An enzyme complex designated DICER COMPLEX, dices the GAM2594 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2594 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 86%) nucleotide sequence of GAM2594 RNA is designated SEQ ID:5185, and is provided hereinbelow with reference to the sequence listing part.

[36192] GAM2594 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2594 target RNA, herein designated GAM TARGET RNA. GAM2594 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36193] GAM2594 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2594 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2594 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2594 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2594 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36194] The complementary binding of GAM2594 RNA, herein designated GAM RNA, to target binding sites on GAM2594 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2594 target RNA, herein designated GAM TARGET RNA, into GAM2594 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36195] It is appreciated that GAM2594 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2594 target genes. The

mRNA of each one of this plurality of GAM2594 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2594 RNA, herein designated GAM RNA, and which when bound by GAM2594 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2594 target proteins.

[36196] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2594 gene, herein designated GAM GENE, on one or more GAM2594 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36197] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2594 correlate with, and may be deduced from, the identity of the target genes which GAM2594 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36198] Nucleotide sequences of the GAM2594 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2594 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2594 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2594 are further described hereinbelow with reference to Table 1.

[36199] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2594 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[36200] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2595 (GAM2595) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[36201] GAM2595 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2595 was detected is described hereinabove with reference to Figs. 2-8.

[36202] GAM2595 gene, herein designated GAM GENE, and GAM2595 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[36203] GAM2595 gene, herein designated GAM GENE, encodes a GAM2595 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2595 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2595 precursor RNA is designated SEQ ID:2572, and is provided hereinbelow with reference to the sequence listing part.

[36204] GAM2595 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2595 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36205] An enzyme complex designated DICER COMPLEX, dices the GAM2595 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2595 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of GAM2595 RNA is designated SEQ ID:5186, and is provided hereinbelow with reference to the sequence listing part.

[36206] GAM2595 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2595 target RNA, herein designated GAM TARGET RNA. GAM2595 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36207] GAM2595 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2595 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2595 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2595 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2595 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36208] The complementary binding of GAM2595 RNA, herein designated GAM RNA, to target binding sites on GAM2595 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2595 target RNA, herein designated GAM TARGET RNA, into GAM2595 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36209] It is appreciated that GAM2595 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2595 target genes. The mRNA of each one of this plurality of GAM2595 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2595 RNA, herein designated GAM RNA, and which when bound by GAM2595 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2595 target proteins.

[36210] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2595 gene, herein designated GAM GENE, on one or more GAM2595 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36211] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2595 correlate with, and may be deduced from, the identity of the target

genes which GAM2595 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36212] Nucleotide sequences of the GAM2595 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2595 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2595 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2595 are further described hereinbelow with reference to Table 1.

[36213] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2595 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[36214] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2596 (GAM2596) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[36215] GAM2596 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2596 was detected is described hereinabove with reference to Figs. 2-8.

[36216] GAM2596 gene, herein designated GAM GENE, and GAM2596 target gene, herein designated GAM TARGET GENE, are human genes contained in the



human genome.

[36217] GAM2596 gene, herein designated GAM GENE, encodes a GAM2596 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2596 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2596 precursor RNA is designated SEQ ID:2573, and is provided hereinbelow with reference to the sequence listing part.

[36218] GAM2596 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2596 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36219] An enzyme complex designated DICER COMPLEX, dices the GAM2596 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2596 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of GAM2596 RNA is designated SEQ ID:5187, and is provided

hereinbelow with reference to the sequence listing part.

[36220] GAM2596 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2596 target RNA, herein designated GAM TARGET RNA. GAM2596 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36221] GAM2596 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2596 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2596 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2596 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2596 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36222] The complementary binding of GAM2596 RNA, herein designated GAM RNA, to target binding sites on GAM2596 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2596 target RNA, herein designated GAM TARGET RNA, into GAM2596 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36223] It is appreciated that GAM2596 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2596 target genes. The mRNA of each one of this plurality of GAM2596 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2596 RNA, herein designated GAM RNA, and which when bound by GAM2596 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2596 target proteins.

[36224] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2596 gene, herein designated GAM GENE, on one or more GAM2596 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36225] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2596 correlate with, and may be deduced from, the identity of the target genes which GAM2596 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36226] Nucleotide sequences of the GAM2596 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2596 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2596 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2596 are further described hereinbelow with reference to Table 1.

[36227] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2596 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[36228] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2597 (GAM2597) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[36229] GAM2597 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2597 was detected is described hereinabove with reference to Figs. 2-8.

[36230] GAM2597 gene, herein designated GAM GENE, and GAM2597 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[36231] GAM2597 gene, herein designated GAM GENE, encodes a GAM2597 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2597 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2597 precursor RNA is designated SEQ ID:2574, and is provided hereinbelow with reference to the sequence listing part.

[36232] GAM2597 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2597 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36233] An enzyme complex designated DICER COMPLEX, dices the GAM2597 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2597 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 78%) nucleotide sequence of GAM2597 RNA is designated SEQ ID:5188, and is provided hereinbelow with reference to the sequence listing part.

[36234] GAM2597 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2597 target RNA, herein designated GAM TARGET RNA. GAM2597 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36235] GAM2597 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2597 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2597 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2597 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2597 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36236] The complementary binding of GAM2597 RNA, herein designated GAM RNA, to target binding sites on GAM2597 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2597 target RNA, herein designated GAM TARGET RNA, into GAM2597 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36237] It is appreciated that GAM2597 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2597 target genes. The mRNA of each one of this plurality of GAM2597 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2597 RNA, herein designated GAM RNA, and which when bound by GAM2597 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2597 target proteins.

[36238] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2597 gene, herein designated GAM GENE, on one or more GAM2597 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36239] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2597 correlate with, and may be deduced from, the identity of the target genes which GAM2597 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36240] Nucleotide sequences of the GAM2597 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2597 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2597 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2597 are further described hereinbelow with reference to Table 1.

[36241] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2597 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[36242] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2598 (GAM2598) gene, which modulates



expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[36243] GAM2598 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2598 was detected is described hereinabove with reference to Figs. 2-8.

[36244] GAM2598 gene, herein designated GAM GENE, and GAM2598 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[36245] GAM2598 gene, herein designated GAM GENE, encodes a GAM2598 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2598 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2598 precursor RNA is designated SEQ ID:2575, and is provided hereinbelow with reference to the sequence listing part.

[36246] GAM2598 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2598 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

- [36247] An enzyme complex designated DICER COMPLEX, dices the GAM2598 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2598 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 78%) nucleotide sequence of GAM2598 RNA is designated SEQ ID:5189, and is provided hereinbelow with reference to the sequence listing part.
- [36248] GAM2598 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2598 target RNA, herein designated GAM TARGET RNA. GAM2598 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [36249] GAM2598 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2598 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2598 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2598 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2598 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36250] The complementary binding of GAM2598 RNA, herein designated GAM RNA, to target binding sites on GAM2598 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2598 target RNA, herein designated GAM TARGET RNA, into GAM2598 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36251] It is appreciated that GAM2598 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2598 target genes. The mRNA of each one of this plurality of GAM2598 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2598 RNA, herein designated GAM RNA, and which when bound by GAM2598 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2598 target proteins.

[36252] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2598 gene, herein designated GAM GENE, on one or more GAM2598 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36253] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2598 correlate with, and may be deduced from, the identity of the target genes which GAM2598 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36254] Nucleotide sequences of the GAM2598 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2598 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2598 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2598 are further described hereinbelow with reference to Table 1.

[36255] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2598 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

[36256] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2599 (GAM2599) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[36257] GAM2599 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2599 was detected is described hereinabove with reference to Figs. 2-8.

[36258] GAM2599 gene, herein designated GAM GENE, and GAM2599 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[36259] GAM2599 gene, herein designated GAM GENE, encodes a GAM2599 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2599 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2599 precursor RNA is designated SEQ ID:2576, and is provided hereinbelow with reference to the sequence listing part.

[36260] GAM2599 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2599 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36261] An enzyme complex designated DICER COMPLEX, dices the GAM2599 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2599 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of GAM2599 RNA is designated SEQ ID:5190, and is provided hereinbelow with reference to the sequence listing part.

[36262] GAM2599 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2599 target RNA, herein designated GAM TARGET RNA. GAM2599 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36263] GAM2599 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2599 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2599 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2599 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2599 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36264] The complementary binding of GAM2599 RNA, herein designated GAM RNA, to target binding sites on GAM2599 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2599 target RNA, herein designated GAM TARGET RNA, into GAM2599 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36265] It is appreciated that GAM2599 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2599 target genes. The mRNA of each one of this plurality of GAM2599 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2599 RNA, herein designated GAM RNA, and which when bound by GAM2599 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2599 target proteins.

[36266] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2599 gene, herein designated GAM GENE, on one or more GAM2599 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36267] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2599 correlate with, and may be deduced from, the identity of the target genes which GAM2599 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36268] Nucleotide sequences of the GAM2599 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2599 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2599 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2599 are further described hereinbelow with reference to Table 1.



[36269] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2599 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[36270] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2600 (GAM2600) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[36271] GAM2600 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2600 was detected is described hereinabove with reference to Figs. 2-8.

[36272] GAM2600 gene, herein designated GAM GENE, and GAM2600 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[36273] GAM2600 gene, herein designated GAM GENE, encodes a GAM2600 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2600 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2600 precursor RNA is designated SEQ ID:2577, and is provided hereinbelow with reference to the sequence listing part.

[36274] GAM2600 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2600 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36275] An enzyme complex designated DICER COMPLEX, dices the GAM2600 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2600 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of GAM2600 RNA is designated SEQ ID:5191, and is provided hereinbelow with reference to the sequence listing part.

[36276] GAM2600 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2600 target RNA, herein designated GAM TARGET RNA. GAM2600 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36277] GAM2600 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2600 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2600 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2600 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2600 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36278] The complementary binding of GAM2600 RNA, herein designated GAM RNA, to target binding sites on GAM2600 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2600 target RNA, herein designated GAM TARGET RNA, into GAM2600 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36279] It is appreciated that GAM2600 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2600 target genes. The

mRNA of each one of this plurality of GAM2600 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2600 RNA, herein designated GAM RNA, and which when bound by GAM2600 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2600 target proteins.

[36280] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2600 gene, herein designated GAM GENE, on one or more GAM2600 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36281] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2600 correlate with, and may be deduced from, the identity of the target genes which GAM2600 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36282] Nucleotide sequences of the GAM2600 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2600 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2600 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2600 are further described hereinbelow with reference to Table 1.

[36283] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2600 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[36284] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2601 (GAM2601) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[36285] GAM2601 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2601 was detected is described hereinabove with reference to Figs. 2-8.

[36286] GAM2601 gene, herein designated GAM GENE, and GAM2601 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[36287] GAM2601 gene, herein designated GAM GENE, encodes a GAM2601 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2601 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2601 precursor RNA is designated SEQ ID:2578, and is provided hereinbelow with reference to the sequence listing part.

[36288] GAM2601 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2601 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36289] An enzyme complex designated DICER COMPLEX, dices the GAM2601 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2601 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of GAM2601 RNA is designated SEQ ID:5192, and is provided hereinbelow with reference to the sequence listing part.

[36290] GAM2601 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2601 target RNA, herein designated GAM TARGET RNA. GAM2601 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36291] GAM2601 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2601 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2601 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2601 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2601 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36292] The complementary binding of GAM2601 RNA, herein designated GAM RNA, to target binding sites on GAM2601 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2601 target RNA, herein designated GAM TARGET RNA, into GAM2601 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36293] It is appreciated that GAM2601 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2601 target genes. The mRNA of each one of this plurality of GAM2601 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2601 RNA, herein designated GAM RNA, and which when bound by GAM2601 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2601 target proteins.

[36294] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2601 gene, herein designated GAM GENE, on one or more GAM2601 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36295] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2601 correlate with, and may be deduced from, the identity of the target



genes which GAM2601 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36296] Nucleotide sequences of the GAM2601 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2601 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2601 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2601 are further described hereinbelow with reference to Table 1.

[36297] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2601 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[36298] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2602 (GAM2602) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[36299] GAM2602 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2602 was detected is described hereinabove with reference to Figs. 2-8.

[36300] GAM2602 gene, herein designated GAM GENE, and GAM2602 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

[36301] GAM2602 gene, herein designated GAM GENE, encodes a GAM2602 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2602 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2602 precursor RNA is designated SEQ ID:2579, and is provided hereinbelow with reference to the sequence listing part.

[36302] GAM2602 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2602 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36303] An enzyme complex designated DICER COMPLEX, dices the GAM2602 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2602 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 87%) nucleotide sequence of GAM2602 RNA is designated SEQ ID:5193, and is provided

hereinbelow with reference to the sequence listing part.

[36304] GAM2602 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2602 target RNA, herein designated GAM TARGET RNA. GAM2602 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36305] GAM2602 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2602 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2602 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2602 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2602 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36306] The complementary binding of GAM2602 RNA, herein designated GAM RNA, to target binding sites on GAM2602 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2602 target RNA, herein designated GAM TARGET RNA, into GAM2602 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36307] It is appreciated that GAM2602 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2602 target genes. The mRNA of each one of this plurality of GAM2602 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2602 RNA, herein designated GAM RNA, and which when bound by GAM2602 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2602 target proteins.

[36308] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2602 gene, herein designated GAM GENE, on one or more GAM2602 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36309] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2602 correlate with, and may be deduced from, the identity of the target genes which GAM2602 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36310] Nucleotide sequences of the GAM2602 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2602 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2602 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2602 are further described hereinbelow with reference to Table 1.

[36311] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2602 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[36312] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2603 (GAM2603) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[36313] GAM2603 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2603 was detected is described hereinabove with reference to Figs. 2-8.

[36314] GAM2603 gene, herein designated GAM GENE, and GAM2603 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[36315] GAM2603 gene, herein designated GAM GENE, encodes a GAM2603 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2603 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2603 precursor RNA is designated SEQ ID:2580, and is provided hereinbelow with reference to the sequence listing part.

[36316] GAM2603 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2603 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36317] An enzyme complex designated DICER COMPLEX, dices the GAM2603 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2603 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of GAM2603 RNA is designated SEQ ID:5194, and is provided hereinbelow with reference to the sequence listing part.

[36318] GAM2603 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2603 target RNA, herein designated GAM TARGET RNA. GAM2603 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36319] GAM2603 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2603 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2603 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2603 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2603 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36320] The complementary binding of GAM2603 RNA, herein designated GAM RNA, to target binding sites on GAM2603 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2603 target RNA, herein designated GAM TARGET RNA, into GAM2603 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36321] It is appreciated that GAM2603 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2603 target genes. The mRNA of each one of this plurality of GAM2603 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2603 RNA, herein designated GAM RNA, and which when bound by GAM2603 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2603 target proteins.

[36322] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2603 gene, herein designated GAM GENE, on one or more GAM2603 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary



binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36323] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2603 correlate with, and may be deduced from, the identity of the target genes which GAM2603 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36324] Nucleotide sequences of the GAM2603 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2603 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2603 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2603 are further described hereinbelow with reference to Table 1.

[36325] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2603 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[36326] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2604 (GAM2604) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

- [36327] GAM2604 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2604 was detected is described hereinabove with reference to Figs. 2-8.
- [36328] GAM2604 gene, herein designated GAM GENE, and GAM2604 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.
- [36329] GAM2604 gene, herein designated GAM GENE, encodes a GAM2604 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2604 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2604 precursor RNA is designated SEQ ID:2581, and is provided hereinbelow with reference to the sequence listing part.
- [36330] GAM2604 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2604 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

- [36331] An enzyme complex designated DICER COMPLEX, dices the GAM2604 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2604 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 88%) nucleotide sequence of GAM2604 RNA is designated SEQ ID:5195, and is provided hereinbelow with reference to the sequence listing part.
- [36332] GAM2604 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2604 target RNA, herein designated GAM TARGET RNA. GAM2604 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [36333] GAM2604 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2604 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2604 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2604 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2604 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36334] The complementary binding of GAM2604 RNA, herein designated GAM RNA, to target binding sites on GAM2604 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2604 target RNA, herein designated GAM TARGET RNA, into GAM2604 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36335] It is appreciated that GAM2604 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2604 target genes. The mRNA of each one of this plurality of GAM2604 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2604 RNA, herein designated GAM RNA, and which when bound by GAM2604 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2604 target proteins.

[36336] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2604 gene, herein designated GAM GENE, on one or more GAM2604 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36337] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2604 correlate with, and may be deduced from, the identity of the target genes which GAM2604 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36338] Nucleotide sequences of the GAM2604 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2604 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2604 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2604 are further described hereinbelow with reference to Table 1.

[36339] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2604 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

[36340] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2605 (GAM2605) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[36341] GAM2605 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2605 was detected is described hereinabove with reference to Figs. 2-8.

[36342] GAM2605 gene, herein designated GAM GENE, and GAM2605 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[36343] GAM2605 gene, herein designated GAM GENE, encodes a GAM2605 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2605 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2605 precursor RNA is designated SEQ ID:2582, and is provided hereinbelow with reference to the sequence listing part.

[36344] GAM2605 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2605 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36345] An enzyme complex designated DICER COMPLEX, dices the GAM2605 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2605 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of GAM2605 RNA is designated SEQ ID:5196, and is provided hereinbelow with reference to the sequence listing part.

[36346] GAM2605 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2605 target RNA, herein designated GAM TARGET RNA. GAM2605 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36347] GAM2605 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2605 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2605 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2605 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2605 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36348] The complementary binding of GAM2605 RNA, herein designated GAM RNA, to target binding sites on GAM2605 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2605 target RNA, herein designated GAM TARGET RNA, into GAM2605 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36349] It is appreciated that GAM2605 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2605 target genes. The mRNA of each one of this plurality of GAM2605 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2605 RNA, herein designated GAM RNA, and which when bound by GAM2605 RNA, herein designated GAM RNA,



causes inhibition of translation of respective one or more GAM2605 target proteins.

[36350] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2605 gene, herein designated GAM GENE, on one or more GAM2605 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36351] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2605 correlate with, and may be deduced from, the identity of the target genes which GAM2605 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36352] Nucleotide sequences of the GAM2605 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2605 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2605 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2605 are further described hereinbelow with reference to Table 1.

[36353] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2605 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[36354] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2606 (GAM2606) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[36355] GAM2606 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2606 was detected is described hereinabove with reference to Figs. 2-8.

[36356] GAM2606 gene, herein designated GAM GENE, and GAM2606 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[36357] GAM2606 gene, herein designated GAM GENE, encodes a GAM2606 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2606 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2606 precursor RNA is designated SEQ ID:2583, and is provided hereinbelow with reference to the sequence listing part.

[36358] GAM2606 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2606 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36359] An enzyme complex designated DICER COMPLEX, dices the GAM2606 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2606 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 83%) nucleotide sequence of GAM2606 RNA is designated SEQ ID:5197, and is provided hereinbelow with reference to the sequence listing part.

[36360] GAM2606 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2606 target RNA, herein designated GAM TARGET RNA. GAM2606 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36361] GAM2606 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2606 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2606 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2606 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2606 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36362] The complementary binding of GAM2606 RNA, herein designated GAM RNA, to target binding sites on GAM2606 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2606 target RNA, herein designated GAM TARGET RNA, into GAM2606 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36363] It is appreciated that GAM2606 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2606 target genes. The

mRNA of each one of this plurality of GAM2606 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2606 RNA, herein designated GAM RNA, and which when bound by GAM2606 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2606 target proteins.

[36364] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2606 gene, herein designated GAM GENE, on one or more GAM2606 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36365] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2606 correlate with, and may be deduced from, the identity of the target genes which GAM2606 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36366] Nucleotide sequences of the GAM2606 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2606 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2606 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2606 are further described hereinbelow with reference to Table 1.

[36367] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2606 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[36368] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2607 (GAM2607) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[36369] GAM2607 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2607 was detected is described hereinabove with reference to Figs. 2-8.

[36370] GAM2607 gene, herein designated GAM GENE, and GAM2607 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[36371] GAM2607 gene, herein designated GAM GENE, encodes a GAM2607 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2607 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2607 precursor RNA is designated SEQ ID:2584, and is provided hereinbelow with reference to the sequence listing part.

[36372] GAM2607 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2607 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36373] An enzyme complex designated DICER COMPLEX, dices the GAM2607 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2607 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 86%) nucleotide sequence of GAM2607 RNA is designated SEQ ID:5198, and is provided hereinbelow with reference to the sequence listing part.

[36374] GAM2607 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2607 target RNA, herein designated GAM TARGET RNA. GAM2607 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36375] GAM2607 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2607 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2607 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2607 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2607 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36376] The complementary binding of GAM2607 RNA, herein designated GAM RNA, to target binding sites on GAM2607 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2607 target RNA, herein designated GAM TARGET RNA, into GAM2607 target protein, herein



designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36377] It is appreciated that GAM2607 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2607 target genes. The mRNA of each one of this plurality of GAM2607 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2607 RNA, herein designated GAM RNA, and which when bound by GAM2607 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2607 target proteins.

[36378] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2607 gene, herein designated GAM GENE, on one or more GAM2607 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36379] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2607 correlate with, and may be deduced from, the identity of the target

genes which GAM2607 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36380] Nucleotide sequences of the GAM2607 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2607 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2607 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2607 are further described hereinbelow with reference to Table 1.

[36381] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2607 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[36382] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2608 (GAM2608) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[36383] GAM2608 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2608 was detected is described hereinabove with reference to Figs. 2-8.

[36384] GAM2608 gene, herein designated GAM GENE, and GAM2608 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

[36385] GAM2608 gene, herein designated GAM GENE, encodes a GAM2608 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2608 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2608 precursor RNA is designated SEQ ID:2585, and is provided hereinbelow with reference to the sequence listing part.

[36386] GAM2608 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2608 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36387] An enzyme complex designated DICER COMPLEX, dices the GAM2608 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2608 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of GAM2608 RNA is designated SEQ ID:5199, and is provided

hereinbelow with reference to the sequence listing part.

[36388] GAM2608 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2608 target RNA, herein designated GAM TARGET RNA. GAM2608 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36389] GAM2608 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2608 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2608 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2608 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36390] The complementary binding of GAM2608 RNA, herein designated GAM RNA, to target binding sites on GAM2608 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2608 target RNA, herein designated GAM TARGET RNA, into GAM2608 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36391] It is appreciated that GAM2608 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2608 target genes. The mRNA of each one of this plurality of GAM2608 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2608 RNA, herein designated GAM RNA, and which when bound by GAM2608 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2608 target proteins.

[36392] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2608 gene, herein designated GAM GENE, on one or more GAM2608 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36393] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2608 correlate with, and may be deduced from, the identity of the target genes which GAM2608 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36394] Nucleotide sequences of the GAM2608 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2608 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2608 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2608 are further described hereinbelow with reference to Table 1.

[36395] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2608 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[36396] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2609 (GAM2609) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[36397] GAM2609 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2609 was detected is described hereinabove with reference to Figs. 2-8.

[36398] GAM2609 gene, herein designated GAM GENE, and GAM2609 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[36399] GAM2609 gene, herein designated GAM GENE, encodes a GAM2609 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2609 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2609 precursor RNA is designated SEQ ID:2586, and is provided hereinbelow with reference to the sequence listing part.

[36400] GAM2609 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2609 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36401] An enzyme complex designated DICER COMPLEX, dices the GAM2609 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2609 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 83%) nucleotide sequence of GAM2609 RNA is designated SEQ ID:5200, and is provided hereinbelow with reference to the sequence listing part.

[36402] GAM2609 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2609 target RNA, herein designated GAM TARGET RNA. GAM2609 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36403] GAM2609 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2609 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2609 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2609 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2609 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target



binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36404] The complementary binding of GAM2609 RNA, herein designated GAM RNA, to target binding sites on GAM2609 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2609 target RNA, herein designated GAM TARGET RNA, into GAM2609 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36405] It is appreciated that GAM2609 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2609 target genes. The mRNA of each one of this plurality of GAM2609 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2609 RNA, herein designated GAM RNA, and which when bound by GAM2609 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2609 target proteins.

[36406] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2609 gene, herein designated GAM GENE, on one or more GAM2609 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36407] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2609 correlate with, and may be deduced from, the identity of the target genes which GAM2609 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36408] Nucleotide sequences of the GAM2609 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2609 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2609 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2609 are further described hereinbelow with reference to Table 1.

[36409] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2609 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[36410] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2610 (GAM2610) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

- [36411] GAM2610 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2610 was detected is described hereinabove with reference to Figs. 2-8.
- [36412] GAM2610 gene, herein designated GAM GENE, and GAM2610 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.
- [36413] GAM2610 gene, herein designated GAM GENE, encodes a GAM2610 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2610 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2610 precursor RNA is designated SEQ ID:2587, and is provided hereinbelow with reference to the sequence listing part.
- [36414] GAM2610 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2610 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

- [36415] An enzyme complex designated DICER COMPLEX, dices the GAM2610 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2610 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2610 RNA is designated SEQ ID:5201, and is provided hereinbelow with reference to the sequence listing part.
- [36416] GAM2610 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2610 target RNA, herein designated GAM TARGET RNA. GAM2610 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [36417] GAM2610 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2610 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2610 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2610 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2610 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36418] The complementary binding of GAM2610 RNA, herein designated GAM RNA, to target binding sites on GAM2610 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2610 target RNA, herein designated GAM TARGET RNA, into GAM2610 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36419] It is appreciated that GAM2610 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2610 target genes. The mRNA of each one of this plurality of GAM2610 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2610 RNA, herein designated GAM RNA, and which when bound by GAM2610 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2610 target proteins.

[36420] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2610 gene, herein designated GAM GENE, on one or more GAM2610 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36421] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2610 correlate with, and may be deduced from, the identity of the target genes which GAM2610 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36422] Nucleotide sequences of the GAM2610 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2610 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2610 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2610 are further described hereinbelow with reference to Table 1.

[36423] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2610 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

- [36424] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2611 (GAM2611) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.
- [36425] GAM2611 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2611 was detected is described hereinabove with reference to Figs. 2-8.
- [36426] GAM2611 gene, herein designated GAM GENE, and GAM2611 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.
- [36427] GAM2611 gene, herein designated GAM GENE, encodes a GAM2611 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2611 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2611 precursor RNA is designated SEQ ID:2588, and is provided hereinbelow with reference to the sequence listing part.
- [36428] GAM2611 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2611 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36429] An enzyme complex designated DICER COMPLEX, dices the GAM2611 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2611 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2611 RNA is designated SEQ ID:5202, and is provided hereinbelow with reference to the sequence listing part.

[36430] GAM2611 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2611 target RNA, herein designated GAM TARGET RNA. GAM2611 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36431] GAM2611 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2611 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2611 RNA,



herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2611 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2611 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36432] The complementary binding of GAM2611 RNA, herein designated GAM RNA, to target binding sites on GAM2611 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2611 target RNA, herein designated GAM TARGET RNA, into GAM2611 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36433] It is appreciated that GAM2611 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2611 target genes. The mRNA of each one of this plurality of GAM2611 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2611 RNA, herein designated GAM RNA, and which when bound by GAM2611 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2611 target proteins.

[36434] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2611 gene, herein designated GAM GENE, on one or more GAM2611 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36435] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2611 correlate with, and may be deduced from, the identity of the target genes which GAM2611 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36436] Nucleotide sequences of the GAM2611 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2611 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2611 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2611 are further described hereinbelow with reference to Table 1.

- [36437] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2611 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.
- [36438] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2612 (GAM2612) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.
- [36439] GAM2612 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2612 was detected is described hereinabove with reference to Figs. 2-8.
- [36440] GAM2612 gene, herein designated GAM GENE, and GAM2612 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.
- [36441] GAM2612 gene, herein designated GAM GENE, encodes a GAM2612 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2612 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2612 precursor RNA is designated SEQ ID:2589, and is provided hereinbelow with reference to the sequence listing part.

[36442] GAM2612 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2612 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36443] An enzyme complex designated DICER COMPLEX, dices the GAM2612 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2612 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of GAM2612 RNA is designated SEQ ID:5203, and is provided hereinbelow with reference to the sequence listing part.

[36444] GAM2612 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2612 target RNA, herein designated GAM TARGET RNA. GAM2612 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36445] GAM2612 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2612 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2612 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2612 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2612 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36446] The complementary binding of GAM2612 RNA, herein designated GAM RNA, to target binding sites on GAM2612 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2612 target RNA, herein designated GAM TARGET RNA, into GAM2612 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36447] It is appreciated that GAM2612 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2612 target genes. The

mRNA of each one of this plurality of GAM2612 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2612 RNA, herein designated GAM RNA, and which when bound by GAM2612 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2612 target proteins.

[36448] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2612 gene, herein designated GAM GENE, on one or more GAM2612 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36449] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2612 correlate with, and may be deduced from, the identity of the target genes which GAM2612 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36450] Nucleotide sequences of the GAM2612 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2612 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2612 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2612 are further described hereinbelow with reference to Table 1.

[36451] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2612 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[36452] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2613 (GAM2613) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[36453] GAM2613 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2613 was detected is described hereinabove with reference to Figs. 2-8.

[36454] GAM2613 gene, herein designated GAM GENE, and GAM2613 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[36455] GAM2613 gene, herein designated GAM GENE, encodes a GAM2613 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2613 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2613 precursor RNA is designated SEQ ID:2590, and is provided hereinbelow with reference to the sequence listing part.

[36456] GAM2613 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2613 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36457] An enzyme complex designated DICER COMPLEX, dices the GAM2613 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2613 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of GAM2613 RNA is designated SEQ ID:5204, and is provided hereinbelow with reference to the sequence listing part.

[36458] GAM2613 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2613 target RNA, herein designated GAM TARGET RNA. GAM2613 target RNA, herein designated GAM



TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36459] GAM2613 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2613 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2613 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2613 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2613 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36460] The complementary binding of GAM2613 RNA, herein designated GAM RNA, to target binding sites on GAM2613 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2613 target RNA, herein designated GAM TARGET RNA, into GAM2613 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36461] It is appreciated that GAM2613 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2613 target genes. The mRNA of each one of this plurality of GAM2613 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2613 RNA, herein designated GAM RNA, and which when bound by GAM2613 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2613 target proteins.

[36462] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2613 gene, herein designated GAM GENE, on one or more GAM2613 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36463] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2613 correlate with, and may be deduced from, the identity of the target

genes which GAM2613 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36464] Nucleotide sequences of the GAM2613 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2613 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2613 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2613 are further described hereinbelow with reference to Table 1.

[36465] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2613 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[36466] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2614 (GAM2614) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[36467] GAM2614 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2614 was detected is described hereinabove with reference to Figs. 2-8.

[36468] GAM2614 gene, herein designated GAM GENE, and GAM2614 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

[36469] GAM2614 gene, herein designated GAM GENE, encodes a GAM2614 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2614 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2614 precursor RNA is designated SEQ ID:2591, and is provided hereinbelow with reference to the sequence listing part.

[36470] GAM2614 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2614 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36471] An enzyme complex designated DICER COMPLEX, dices the GAM2614 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2614 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of GAM2614 RNA is designated SEQ ID:5205, and is provided

hereinbelow with reference to the sequence listing part.

[36472] GAM2614 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2614 target RNA, herein designated GAM TARGET RNA. GAM2614 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36473] GAM2614 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2614 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2614 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2614 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2614 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36474] The complementary binding of GAM2614 RNA, herein designated GAM RNA, to target binding sites on GAM2614 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2614 target RNA, herein designated GAM TARGET RNA, into GAM2614 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36475] It is appreciated that GAM2614 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2614 target genes. The mRNA of each one of this plurality of GAM2614 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2614 RNA, herein designated GAM RNA, and which when bound by GAM2614 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2614 target proteins.

[36476] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2614 gene, herein designated GAM GENE, on one or more GAM2614 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36477] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2614 correlate with, and may be deduced from, the identity of the target genes which GAM2614 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36478] Nucleotide sequences of the GAM2614 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2614 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2614 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2614 are further described hereinbelow with reference to Table 1.

[36479] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2614 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[36480] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2615 (GAM2615) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[36481] GAM2615 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2615 was detected is described hereinabove with reference to Figs. 2-8.

[36482] GAM2615 gene, herein designated GAM GENE, and GAM2615 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[36483] GAM2615 gene, herein designated GAM GENE, encodes a GAM2615 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2615 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2615 precursor RNA is designated SEQ ID:2592, and is provided hereinbelow with reference to the sequence listing part.

[36484] GAM2615 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2615 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36485] An enzyme complex designated DICER COMPLEX, dices the GAM2615 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2615 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin



structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of GAM2615 RNA is designated SEQ ID:5206, and is provided hereinbelow with reference to the sequence listing part.

[36486] GAM2615 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2615 target RNA, herein designated GAM TARGET RNA. GAM2615 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36487] GAM2615 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2615 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2615 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2615 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2615 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36488] The complementary binding of GAM2615 RNA, herein designated GAM RNA, to target binding sites on GAM2615 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2615 target RNA, herein designated GAM TARGET RNA, into GAM2615 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36489] It is appreciated that GAM2615 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2615 target genes. The mRNA of each one of this plurality of GAM2615 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2615 RNA, herein designated GAM RNA, and which when bound by GAM2615 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2615 target proteins.

[36490] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2615 gene, herein designated GAM GENE, on one or more GAM2615 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36491] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2615 correlate with, and may be deduced from, the identity of the target genes which GAM2615 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36492] Nucleotide sequences of the GAM2615 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2615 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2615 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2615 are further described hereinbelow with reference to Table 1.

[36493] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2615 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[36494] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2616 (GAM2616) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[36495] GAM2616 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2616 was detected is described hereinabove with reference to Figs. 2-8.

[36496] GAM2616 gene, herein designated GAM GENE, and GAM2616 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[36497] GAM2616 gene, herein designated GAM GENE, encodes a GAM2616 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2616 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2616 precursor RNA is designated SEQ ID:2593, and is provided hereinbelow with reference to the sequence listing part.

[36498] GAM2616 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2616 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36499] An enzyme complex designated DICER COMPLEX, dices the GAM2616 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2616 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 83%) nucleotide sequence of GAM2616 RNA is designated SEQ ID:5207, and is provided hereinbelow with reference to the sequence listing part.

[36500] GAM2616 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2616 target RNA, herein designated GAM TARGET RNA. GAM2616 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36501] GAM2616 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2616 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2616 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2616 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2616 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36502] The complementary binding of GAM2616 RNA, herein designated GAM RNA, to target binding sites on GAM2616 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2616 target RNA, herein designated GAM TARGET RNA, into GAM2616 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36503] It is appreciated that GAM2616 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2616 target genes. The mRNA of each one of this plurality of GAM2616 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2616 RNA, herein designated GAM RNA, and which when bound by GAM2616 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2616 target proteins.

[36504] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2616 gene, herein designated GAM GENE, on one or more GAM2616 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36505] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2616 correlate with, and may be deduced from, the identity of the target genes which GAM2616 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36506] Nucleotide sequences of the GAM2616 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2616 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2616 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2616 are further described hereinbelow with reference to Table 1.

[36507] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2616 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

[36508] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2617 (GAM2617) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[36509] GAM2617 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2617 was detected is described hereinabove with reference to Figs. 2-8.

[36510] GAM2617 gene, herein designated GAM GENE, and GAM2617 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[36511] GAM2617 gene, herein designated GAM GENE, encodes a GAM2617 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2617 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2617 precursor RNA is designated SEQ ID:2594, and is provided hereinbelow with reference to the sequence listing part.

[36512] GAM2617 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2617 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA



encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36513] An enzyme complex designated DICER COMPLEX, dices the GAM2617 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2617 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2617 RNA is designated SEQ ID:5208, and is provided hereinbelow with reference to the sequence listing part.

[36514] GAM2617 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2617 target RNA, herein designated GAM TARGET RNA. GAM2617 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36515] GAM2617 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2617 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2617 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2617 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2617 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36516] The complementary binding of GAM2617 RNA, herein designated GAM RNA, to target binding sites on GAM2617 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2617 target RNA, herein designated GAM TARGET RNA, into GAM2617 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36517] It is appreciated that GAM2617 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2617 target genes. The mRNA of each one of this plurality of GAM2617 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2617 RNA, herein designated GAM RNA, and which when bound by GAM2617 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2617 target proteins.

[36518] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2617 gene, herein designated GAM GENE, on one or more GAM2617 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36519] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2617 correlate with, and may be deduced from, the identity of the target genes which GAM2617 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36520] Nucleotide sequences of the GAM2617 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2617 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2617 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2617 are further described hereinbelow with reference to Table 1.

[36521] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2617 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[36522] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2618 (GAM2618) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[36523] GAM2618 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2618 was detected is described hereinabove with reference to Figs. 2-8.

[36524] GAM2618 gene, herein designated GAM GENE, and GAM2618 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[36525] GAM2618 gene, herein designated GAM GENE, encodes a GAM2618 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2618 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2618 precursor RNA is designated SEQ ID:2595, and is provided hereinbelow with reference to the sequence listing part.

[36526] GAM2618 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2618 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36527] An enzyme complex designated DICER COMPLEX, dices the GAM2618 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2618 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of GAM2618 RNA is designated SEQ ID:5209, and is provided hereinbelow with reference to the sequence listing part.

[36528] GAM2618 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2618 target RNA, herein designated GAM TARGET RNA. GAM2618 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36529] GAM2618 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2618 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2618 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2618 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2618 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36530] The complementary binding of GAM2618 RNA, herein designated GAM RNA, to target binding sites on GAM2618 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2618 target RNA, herein designated GAM TARGET RNA, into GAM2618 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36531] It is appreciated that GAM2618 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2618 target genes. The

mRNA of each one of this plurality of GAM2618 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2618 RNA, herein designated GAM RNA, and which when bound by GAM2618 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2618 target proteins.

[36532] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2618 gene, herein designated GAM GENE, on one or more GAM2618 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36533] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2618 correlate with, and may be deduced from, the identity of the target genes which GAM2618 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36534] Nucleotide sequences of the GAM2618 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2618 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2618 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2618 are further described hereinbelow with reference to Table 1.

[36535] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2618 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[36536] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2619 (GAM2619) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[36537] GAM2619 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2619 was detected is described hereinabove with reference to Figs. 2-8.

[36538] GAM2619 gene, herein designated GAM GENE, and GAM2619 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[36539] GAM2619 gene, herein designated GAM GENE, encodes a GAM2619 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2619 precursor RNA,



herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2619 precursor RNA is designated SEQ ID:2596, and is provided hereinbelow with reference to the sequence listing part.

[36540] GAM2619 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2619 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36541] An enzyme complex designated DICER COMPLEX, dices the GAM2619 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2619 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 84%) nucleotide sequence of GAM2619 RNA is designated SEQ ID:5210, and is provided hereinbelow with reference to the sequence listing part.

[36542] GAM2619 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2619 target RNA, herein designated GAM TARGET RNA. GAM2619 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36543] GAM2619 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2619 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2619 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2619 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2619 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36544] The complementary binding of GAM2619 RNA, herein designated GAM RNA, to target binding sites on GAM2619 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2619 target RNA, herein designated GAM TARGET RNA, into GAM2619 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36545] It is appreciated that GAM2619 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2619 target genes. The mRNA of each one of this plurality of GAM2619 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2619 RNA, herein designated GAM RNA, and which when bound by GAM2619 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2619 target proteins.

[36546] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2619 gene, herein designated GAM GENE, on one or more GAM2619 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36547] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2619 correlate with, and may be deduced from, the identity of the target

genes which GAM2619 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36548] Nucleotide sequences of the GAM2619 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2619 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2619 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2619 are further described hereinbelow with reference to Table 1.

[36549] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2619 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[36550] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2620 (GAM2620) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[36551] GAM2620 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2620 was detected is described hereinabove with reference to Figs. 2-8.

[36552] GAM2620 gene, herein designated GAM GENE, and GAM2620 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

[36553] GAM2620 gene, herein designated GAM GENE, encodes a GAM2620 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2620 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2620 precursor RNA is designated SEQ ID:2597, and is provided hereinbelow with reference to the sequence listing part.

[36554] GAM2620 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2620 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36555] An enzyme complex designated DICER COMPLEX, dices the GAM2620 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2620 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of GAM2620 RNA is designated SEQ ID:5211, and is provided

hereinbelow with reference to the sequence listing part.

[36556] GAM2620 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2620 target RNA, herein designated GAM TARGET RNA. GAM2620 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36557] GAM2620 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2620 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2620 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2620 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2620 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36558] The complementary binding of GAM2620 RNA, herein designated GAM RNA, to target binding sites on GAM2620 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2620 target RNA, herein designated GAM TARGET RNA, into GAM2620 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36559] It is appreciated that GAM2620 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2620 target genes. The mRNA of each one of this plurality of GAM2620 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2620 RNA, herein designated GAM RNA, and which when bound by GAM2620 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2620 target proteins.

[36560] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2620 gene, herein designated GAM GENE, on one or more GAM2620 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36561] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2620 correlate with, and may be deduced from, the identity of the target genes which GAM2620 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36562] Nucleotide sequences of the GAM2620 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2620 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2620 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2620 are further described hereinbelow with reference to Table 1.

[36563] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2620 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[36564] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2621 (GAM2621) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[36565] GAM2621 is a novel bioinformatically detected regulatory, non protein



coding, micro RNA (miRNA) gene. The method by which GAM2621 was detected is described hereinabove with reference to Figs. 2-8.

[36566] GAM2621 gene, herein designated GAM GENE, and GAM2621 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[36567] GAM2621 gene, herein designated GAM GENE, encodes a GAM2621 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2621 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2621 precursor RNA is designated SEQ ID:2598, and is provided hereinbelow with reference to the sequence listing part.

[36568] GAM2621 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2621 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36569] An enzyme complex designated DICER COMPLEX, dices the GAM2621 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2621 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2621 RNA is designated SEQ ID:5212, and is provided hereinbelow with reference to the sequence listing part.

[36570] GAM2621 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2621 target RNA, herein designated GAM TARGET RNA. GAM2621 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36571] GAM2621 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2621 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2621 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2621 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2621 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36572] The complementary binding of GAM2621 RNA, herein designated GAM RNA, to target binding sites on GAM2621 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2621 target RNA, herein designated GAM TARGET RNA, into GAM2621 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36573] It is appreciated that GAM2621 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2621 target genes. The mRNA of each one of this plurality of GAM2621 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2621 RNA, herein designated GAM RNA, and which when bound by GAM2621 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2621 target proteins.

[36574] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2621 gene, herein designated GAM GENE, on one or more GAM2621 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36575] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2621 correlate with, and may be deduced from, the identity of the target genes which GAM2621 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36576] Nucleotide sequences of the GAM2621 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2621 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2621 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2621 are further described hereinbelow with reference to Table 1.

[36577] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2621 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[36578] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2622 (GAM2622) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[36579] GAM2622 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2622 was detected is described hereinabove with reference to Figs. 2-8.

[36580] GAM2622 gene, herein designated GAM GENE, and GAM2622 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[36581] GAM2622 gene, herein designated GAM GENE, encodes a GAM2622 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2622 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2622 precursor RNA is designated SEQ ID:2599, and is provided hereinbelow with reference to the sequence listing part.

[36582] GAM2622 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2622 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

- [36583] An enzyme complex designated DICER COMPLEX, dices the GAM2622 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2622 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of GAM2622 RNA is designated SEQ ID:5213, and is provided hereinbelow with reference to the sequence listing part.
- [36584] GAM2622 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2622 target RNA, herein designated GAM TARGET RNA. GAM2622 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [36585] GAM2622 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2622 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2622 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2622 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2622 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36586] The complementary binding of GAM2622 RNA, herein designated GAM RNA, to target binding sites on GAM2622 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2622 target RNA, herein designated GAM TARGET RNA, into GAM2622 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36587] It is appreciated that GAM2622 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2622 target genes. The mRNA of each one of this plurality of GAM2622 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2622 RNA, herein designated GAM RNA, and which when bound by GAM2622 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2622 target proteins.

[36588] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2622 gene, herein designated GAM GENE, on one or more GAM2622 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36589] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2622 correlate with, and may be deduced from, the identity of the target genes which GAM2622 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36590] Nucleotide sequences of the GAM2622 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2622 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2622 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2622 are further described hereinbelow with reference to Table 1.

[36591] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2622 RNA, herein designated GAM RNA, are described hereinbelow



with reference to Table 2.

[36592] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2623 (GAM2623) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[36593] GAM2623 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2623 was detected is described hereinabove with reference to Figs. 2-8.

[36594] GAM2623 gene, herein designated GAM GENE, and GAM2623 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[36595] GAM2623 gene, herein designated GAM GENE, encodes a GAM2623 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2623 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2623 precursor RNA is designated SEQ ID:2600, and is provided hereinbelow with reference to the sequence listing part.

[36596] GAM2623 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2623 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36597] An enzyme complex designated DICER COMPLEX, dices the GAM2623 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2623 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of GAM2623 RNA is designated SEQ ID:5214, and is provided hereinbelow with reference to the sequence listing part.

[36598] GAM2623 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2623 target RNA, herein designated GAM TARGET RNA. GAM2623 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36599] GAM2623 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2623 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2623 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2623 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2623 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36600] The complementary binding of GAM2623 RNA, herein designated GAM RNA, to target binding sites on GAM2623 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2623 target RNA, herein designated GAM TARGET RNA, into GAM2623 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36601] It is appreciated that GAM2623 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2623 target genes. The mRNA of each one of this plurality of GAM2623 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2623 RNA, herein designated GAM RNA, and which when bound by GAM2623 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2623 target proteins.

[36602] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2623 gene, herein designated GAM GENE, on one or more GAM2623 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36603] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2623 correlate with, and may be deduced from, the identity of the target genes which GAM2623 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36604] Nucleotide sequences of the GAM2623 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2623 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2623 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2623 are further described hereinbelow with reference to Table 1.

- [36605] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2623 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.
- [36606] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2624 (GAM2624) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.
- [36607] GAM2624 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2624 was detected is described hereinabove with reference to Figs. 2-8.
- [36608] GAM2624 gene, herein designated GAM GENE, and GAM2624 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.
- [36609] GAM2624 gene, herein designated GAM GENE, encodes a GAM2624 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2624 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2624 precursor RNA is designated SEQ ID:2601, and is provided hereinbelow with reference to the sequence listing part.

[36610] GAM2624 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2624 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36611] An enzyme complex designated DICER COMPLEX, dices the GAM2624 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2624 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 84%) nucleotide sequence of GAM2624 RNA is designated SEQ ID:5215, and is provided hereinbelow with reference to the sequence listing part.

[36612] GAM2624 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2624 target RNA, herein designated GAM TARGET RNA. GAM2624 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36613] GAM2624 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2624 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2624 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2624 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2624 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36614] The complementary binding of GAM2624 RNA, herein designated GAM RNA, to target binding sites on GAM2624 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2624 target RNA, herein designated GAM TARGET RNA, into GAM2624 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36615] It is appreciated that GAM2624 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2624 target genes. The

mRNA of each one of this plurality of GAM2624 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2624 RNA, herein designated GAM RNA, and which when bound by GAM2624 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2624 target proteins.

[36616] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2624 gene, herein designated GAM GENE, on one or more GAM2624 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36617] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2624 correlate with, and may be deduced from, the identity of the target genes which GAM2624 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36618] Nucleotide sequences of the GAM2624 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2624 RNA, herein



designated GAM RNA, and a schematic representation of the secondary folding of GAM2624 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2624 are further described hereinbelow with reference to Table 1.

[36619] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2624 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[36620] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2625 (GAM2625) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[36621] GAM2625 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2625 was detected is described hereinabove with reference to Figs. 2-8.

[36622] GAM2625 gene, herein designated GAM GENE, and GAM2625 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[36623] GAM2625 gene, herein designated GAM GENE, encodes a GAM2625 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2625 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2625 precursor RNA is designated SEQ ID:2602, and is provided hereinbelow with reference to the sequence listing part.

[36624] GAM2625 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2625 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36625] An enzyme complex designated DICER COMPLEX, dices the GAM2625 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2625 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 84%) nucleotide sequence of GAM2625 RNA is designated SEQ ID:5216, and is provided hereinbelow with reference to the sequence listing part.

[36626] GAM2625 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2625 target RNA, herein designated GAM TARGET RNA. GAM2625 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36627] GAM2625 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2625 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2625 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2625 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2625 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36628] The complementary binding of GAM2625 RNA, herein designated GAM RNA, to target binding sites on GAM2625 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2625 target RNA, herein designated GAM TARGET RNA, into GAM2625 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36629] It is appreciated that GAM2625 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2625 target genes. The mRNA of each one of this plurality of GAM2625 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2625 RNA, herein designated GAM RNA, and which when bound by GAM2625 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2625 target proteins.

[36630] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2625 gene, herein designated GAM GENE, on one or more GAM2625 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36631] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2625 correlate with, and may be deduced from, the identity of the target

genes which GAM2625 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36632] Nucleotide sequences of the GAM2625 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2625 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2625 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2625 are further described hereinbelow with reference to Table 1.

[36633] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2625 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[36634] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2626 (GAM2626) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[36635] GAM2626 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2626 was detected is described hereinabove with reference to Figs. 2-8.

[36636] GAM2626 gene, herein designated GAM GENE, and GAM2626 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

[36637] GAM2626 gene, herein designated GAM GENE, encodes a GAM2626 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2626 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2626 precursor RNA is designated SEQ ID:2603, and is provided hereinbelow with reference to the sequence listing part.

[36638] GAM2626 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2626 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36639] An enzyme complex designated DICER COMPLEX, dices the GAM2626 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2626 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of GAM2626 RNA is designated SEQ ID:5217, and is provided

hereinbelow with reference to the sequence listing part.

[36640] GAM2626 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2626 target RNA, herein designated GAM TARGET RNA. GAM2626 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36641] GAM2626 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2626 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2626 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2626 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2626 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36642] The complementary binding of GAM2626 RNA, herein designated GAM RNA, to target binding sites on GAM2626 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2626 target RNA, herein designated GAM TARGET RNA, into GAM2626 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36643] It is appreciated that GAM2626 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2626 target genes. The mRNA of each one of this plurality of GAM2626 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2626 RNA, herein designated GAM RNA, and which when bound by GAM2626 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2626 target proteins.

[36644] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2626 gene, herein designated GAM GENE, on one or more GAM2626 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding



sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36645] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2626 correlate with, and may be deduced from, the identity of the target genes which GAM2626 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36646] Nucleotide sequences of the GAM2626 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2626 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2626 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2626 are further described hereinbelow with reference to Table 1.

[36647] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2626 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[36648] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2627 (GAM2627) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[36649] GAM2627 is a novel bioinformatically detected regulatory, non protein

coding, micro RNA (miRNA) gene. The method by which GAM2627 was detected is described hereinabove with reference to Figs. 2-8.

[36650] GAM2627 gene, herein designated GAM GENE, and GAM2627 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[36651] GAM2627 gene, herein designated GAM GENE, encodes a GAM2627 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2627 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2627 precursor RNA is designated SEQ ID:2604, and is provided hereinbelow with reference to the sequence listing part.

[36652] GAM2627 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2627 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36653] An enzyme complex designated DICER COMPLEX, dices the GAM2627 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2627 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin

structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 84%) nucleotide sequence of GAM2627 RNA is designated SEQ ID:5218, and is provided hereinbelow with reference to the sequence listing part.

[36654] GAM2627 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2627 target RNA, herein designated GAM TARGET RNA. GAM2627 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36655] GAM2627 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2627 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2627 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2627 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2627 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target

binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36656] The complementary binding of GAM2627 RNA, herein designated GAM RNA, to target binding sites on GAM2627 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2627 target RNA, herein designated GAM TARGET RNA, into GAM2627 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36657] It is appreciated that GAM2627 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2627 target genes. The mRNA of each one of this plurality of GAM2627 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2627 RNA, herein designated GAM RNA, and which when bound by GAM2627 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2627 target proteins.

[36658] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2627 gene, herein designated GAM GENE, on one or more GAM2627 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36659] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2627 correlate with, and may be deduced from, the identity of the target genes which GAM2627 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36660] Nucleotide sequences of the GAM2627 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2627 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2627 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2627 are further described hereinbelow with reference to Table 1.

[36661] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2627 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[36662] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2628 (GAM2628) gene, which modulates

expression of respective target genes thereof, the function and utility of which target genes is known in the art.

- [36663] GAM2628 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2628 was detected is described hereinabove with reference to Figs. 2-8.
- [36664] GAM2628 gene, herein designated GAM GENE, and GAM2628 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.
- [36665] GAM2628 gene, herein designated GAM GENE, encodes a GAM2628 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2628 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2628 precursor RNA is designated SEQ ID:2605, and is provided hereinbelow with reference to the sequence listing part.
- [36666] GAM2628 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2628 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

- [36667] An enzyme complex designated DICER COMPLEX, dices the GAM2628 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2628 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of GAM2628 RNA is designated SEQ ID:5219, and is provided hereinbelow with reference to the sequence listing part.
- [36668] GAM2628 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2628 target RNA, herein designated GAM TARGET RNA. GAM2628 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [36669] GAM2628 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2628 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2628 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an

illustration only, and is not meant to be limiting GAM2628 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2628 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36670] The complementary binding of GAM2628 RNA, herein designated GAM RNA, to target binding sites on GAM2628 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2628 target RNA, herein designated GAM TARGET RNA, into GAM2628 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36671] It is appreciated that GAM2628 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2628 target genes. The mRNA of each one of this plurality of GAM2628 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2628 RNA, herein designated GAM RNA, and which when bound by GAM2628 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2628 target proteins.

[36672] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition



exerted by GAM2628 gene, herein designated GAM GENE, on one or more GAM2628 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36673] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2628 correlate with, and may be deduced from, the identity of the target genes which GAM2628 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36674] Nucleotide sequences of the GAM2628 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2628 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2628 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2628 are further described hereinbelow with reference to Table 1.

[36675] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2628 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

- [36676] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2629 (GAM2629) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.
- [36677] GAM2629 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2629 was detected is described hereinabove with reference to Figs. 2-8.
- [36678] GAM2629 gene, herein designated GAM GENE, and GAM2629 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.
- [36679] GAM2629 gene, herein designated GAM GENE, encodes a GAM2629 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2629 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2629 precursor RNA is designated SEQ ID:2606, and is provided hereinbelow with reference to the sequence listing part.
- [36680] GAM2629 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2629 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36681] An enzyme complex designated DICER COMPLEX, dices the GAM2629 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2629 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 84%) nucleotide sequence of GAM2629 RNA is designated SEQ ID:5220, and is provided hereinbelow with reference to the sequence listing part.

[36682] GAM2629 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2629 target RNA, herein designated GAM TARGET RNA. GAM2629 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36683] GAM2629 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2629 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2629 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2629 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2629 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36684] The complementary binding of GAM2629 RNA, herein designated GAM RNA, to target binding sites on GAM2629 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2629 target RNA, herein designated GAM TARGET RNA, into GAM2629 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36685] It is appreciated that GAM2629 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2629 target genes. The mRNA of each one of this plurality of GAM2629 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2629 RNA, herein designated GAM RNA, and which when bound by GAM2629 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2629 target proteins.

[36686] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2629 gene, herein designated GAM GENE, on one or more GAM2629 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36687] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2629 correlate with, and may be deduced from, the identity of the target genes which GAM2629 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36688] Nucleotide sequences of the GAM2629 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2629 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2629 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2629 are further described hereinbelow with reference to Table 1.

[36689] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2629 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[36690] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2630 (GAM2630) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[36691] GAM2630 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2630 was detected is described hereinabove with reference to Figs. 2-8.

[36692] GAM2630 gene, herein designated GAM GENE, and GAM2630 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[36693] GAM2630 gene, herein designated GAM GENE, encodes a GAM2630 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2630 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2630 precursor RNA is designated SEQ ID:2607, and is provided hereinbelow with reference to the sequence listing part.

[36694] GAM2630 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2630 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36695] An enzyme complex designated DICER COMPLEX, dices the GAM2630 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2630 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 93%) nucleotide sequence of GAM2630 RNA is designated SEQ ID:5221, and is provided hereinbelow with reference to the sequence listing part.

[36696] GAM2630 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2630 target RNA, herein designated GAM TARGET RNA. GAM2630 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36697] GAM2630 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2630 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2630 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2630 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2630 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36698] The complementary binding of GAM2630 RNA, herein designated GAM RNA, to target binding sites on GAM2630 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2630 target RNA, herein designated GAM TARGET RNA, into GAM2630 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36699] It is appreciated that GAM2630 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2630 target genes. The



mRNA of each one of this plurality of GAM2630 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2630 RNA, herein designated GAM RNA, and which when bound by GAM2630 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2630 target proteins.

[36700] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2630 gene, herein designated GAM GENE, on one or more GAM2630 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36701] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2630 correlate with, and may be deduced from, the identity of the target genes which GAM2630 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36702] Nucleotide sequences of the GAM2630 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2630 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2630 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2630 are further described hereinbelow with reference to Table 1.

[36703] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2630 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[36704] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2631 (GAM2631) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[36705] GAM2631 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2631 was detected is described hereinabove with reference to Figs. 2-8.

[36706] GAM2631 gene, herein designated GAM GENE, and GAM2631 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[36707] GAM2631 gene, herein designated GAM GENE, encodes a GAM2631 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2631 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2631 precursor RNA is designated SEQ ID:2608, and is provided hereinbelow with reference to the sequence listing part.

[36708] GAM2631 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2631 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36709] An enzyme complex designated DICER COMPLEX, dices the GAM2631 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2631 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 91%) nucleotide sequence of GAM2631 RNA is designated SEQ ID:5222, and is provided hereinbelow with reference to the sequence listing part.

[36710] GAM2631 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2631 target RNA, herein designated GAM TARGET RNA. GAM2631 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36711] GAM2631 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2631 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2631 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2631 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2631 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36712] The complementary binding of GAM2631 RNA, herein designated GAM RNA, to target binding sites on GAM2631 target RNA, herein designated

GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2631 target RNA, herein designated GAM TARGET RNA, into GAM2631 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36713] It is appreciated that GAM2631 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2631 target genes. The mRNA of each one of this plurality of GAM2631 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2631 RNA, herein designated GAM RNA, and which when bound by GAM2631 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2631 target proteins.

[36714] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2631 gene, herein designated GAM GENE, on one or more GAM2631 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36715] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2631 correlate with, and may be deduced from, the identity of the target genes which GAM2631 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36716] Nucleotide sequences of the GAM2631 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2631 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2631 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2631 are further described hereinbelow with reference to Table 1.

[36717] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2631 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[36718] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2632 (GAM2632) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[36719] GAM2632 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2632 was detected is described hereinabove with reference to Figs. 2-8.

[36720] GAM2632 gene, herein designated GAM GENE, and GAM2632 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[36721] GAM2632 gene, herein designated GAM GENE, encodes a GAM2632 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2632 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2632 precursor RNA is designated SEQ ID:2609, and is provided hereinbelow with reference to the sequence listing part.

[36722] GAM2632 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2632 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36723] An enzyme complex designated DICER COMPLEX, dices the GAM2632 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2632 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer

together with other necessary proteins. A probable (over 84%) nucleotide sequence of GAM2632 RNA is designated SEQ ID:5223, and is provided hereinbelow with reference to the sequence listing part.

[36724] GAM2632 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2632 target RNA, herein designated GAM TARGET RNA. GAM2632 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36725] GAM2632 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2632 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2632 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2632 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2632 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or



in both 3UTR and 5UTR regions.

[36726] The complementary binding of GAM2632 RNA, herein designated GAM RNA, to target binding sites on GAM2632 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2632 target RNA, herein designated GAM TARGET RNA, into GAM2632 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36727] It is appreciated that GAM2632 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2632 target genes. The mRNA of each one of this plurality of GAM2632 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2632 RNA, herein designated GAM RNA, and which when bound by GAM2632 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2632 target proteins.

[36728] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2632 gene, herein designated GAM GENE, on one or more GAM2632 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes

are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36729] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2632 correlate with, and may be deduced from, the identity of the target genes which GAM2632 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36730] Nucleotide sequences of the GAM2632 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2632 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2632 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2632 are further described hereinbelow with reference to Table 1.

[36731] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2632 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[36732] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2633 (GAM2633) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

- [36733] GAM2633 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2633 was detected is described hereinabove with reference to Figs. 2-8.
- [36734] GAM2633 gene, herein designated GAM GENE, and GAM2633 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.
- [36735] GAM2633 gene, herein designated GAM GENE, encodes a GAM2633 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2633 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2633 precursor RNA is designated SEQ ID:2610, and is provided hereinbelow with reference to the sequence listing part.
- [36736] GAM2633 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2633 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.
- [36737] An enzyme complex designated DICER COMPLEX, dices the GAM2633 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2633 RNA, herein designated GAM RNA, a single stranded

~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 83%) nucleotide sequence of GAM2633 RNA is designated SEQ ID:5225, and is provided hereinbelow with reference to the sequence listing part.

[36738] GAM2633 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2633 target RNA, herein designated GAM TARGET RNA. GAM2633 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36739] GAM2633 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2633 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2633 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2633 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2633 target RNA, herein designated GAM

TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36740] The complementary binding of GAM2633 RNA, herein designated GAM RNA, to target binding sites on GAM2633 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2633 target RNA, herein designated GAM TARGET RNA, into GAM2633 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36741] It is appreciated that GAM2633 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2633 target genes. The mRNA of each one of this plurality of GAM2633 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2633 RNA, herein designated GAM RNA, and which when bound by GAM2633 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2633 target proteins.

[36742] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2633 gene, herein designated GAM GENE, on one or more GAM2633 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with

reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36743] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2633 correlate with, and may be deduced from, the identity of the target genes which GAM2633 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36744] Nucleotide sequences of the GAM2633 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2633 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2633 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2633 are further described hereinbelow with reference to Table 1.

[36745] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2633 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[36746] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as

Genomic Address Messenger 2634 (GAM2634) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[36747] GAM2634 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2634 was detected is described hereinabove with reference to Figs. 2-8.

[36748] GAM2634 gene, herein designated GAM GENE, and GAM2634 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[36749] GAM2634 gene, herein designated GAM GENE, encodes a GAM2634 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2634 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2634 precursor RNA is designated SEQ ID:2611, and is provided hereinbelow with reference to the sequence listing part.

[36750] GAM2634 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2634 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

- [36751] An enzyme complex designated DICER COMPLEX, dices the GAM2634 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2634 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of GAM2634 RNA is designated SEQ ID:5226, and is provided hereinbelow with reference to the sequence listing part.
- [36752] GAM2634 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2634 target RNA, herein designated GAM TARGET RNA. GAM2634 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.
- [36753] GAM2634 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2634 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2634 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an



illustration only, and is not meant to be limiting GAM2634 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2634 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36754] The complementary binding of GAM2634 RNA, herein designated GAM RNA, to target binding sites on GAM2634 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2634 target RNA, herein designated GAM TARGET RNA, into GAM2634 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36755] It is appreciated that GAM2634 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2634 target genes. The mRNA of each one of this plurality of GAM2634 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2634 RNA, herein designated GAM RNA, and which when bound by GAM2634 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2634 target proteins.

[36756] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition

exerted by GAM2634 gene, herein designated GAM GENE, on one or more GAM2634 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36757] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2634 correlate with, and may be deduced from, the identity of the target genes which GAM2634 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36758] Nucleotide sequences of the GAM2634 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2634 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2634 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2634 are further described hereinbelow with reference to Table 1.

[36759] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2634 RNA, herein designated GAM RNA, are described hereinbelow

with reference to Table 2.

- [36760] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2635 (GAM2635) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.
- [36761] GAM2635 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2635 was detected is described hereinabove with reference to Figs. 2-8.
- [36762] GAM2635 gene, herein designated GAM GENE, and GAM2635 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.
- [36763] GAM2635 gene, herein designated GAM GENE, encodes a GAM2635 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2635 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2635 precursor RNA is designated SEQ ID:2612, and is provided hereinbelow with reference to the sequence listing part.
- [36764] GAM2635 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2635 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA

encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36765] An enzyme complex designated DICER COMPLEX, dices the GAM2635 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2635 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 87%) nucleotide sequence of GAM2635 RNA is designated SEQ ID:5224, and is provided hereinbelow with reference to the sequence listing part.

[36766] GAM2635 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2635 target RNA, herein designated GAM TARGET RNA. GAM2635 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36767] GAM2635 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2635 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2635 RNA,

herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2635 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2635 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36768] The complementary binding of GAM2635 RNA, herein designated GAM RNA, to target binding sites on GAM2635 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2635 target RNA, herein designated GAM TARGET RNA, into GAM2635 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36769] It is appreciated that GAM2635 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2635 target genes. The mRNA of each one of this plurality of GAM2635 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2635 RNA, herein designated GAM RNA, and which when bound by GAM2635 RNA, herein designated GAM RNA,

causes inhibition of translation of respective one or more GAM2635 target proteins.

[36770] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2635 gene, herein designated GAM GENE, on one or more GAM2635 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36771] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2635 correlate with, and may be deduced from, the identity of the target genes which GAM2635 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36772] Nucleotide sequences of the GAM2635 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2635 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2635 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2635 are further described hereinbelow with reference to Table 1.

[36773] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2635 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[36774] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2636 (GAM2636) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[36775] GAM2636 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2636 was detected is described hereinabove with reference to Figs. 2-8.

[36776] GAM2636 gene, herein designated GAM GENE, and GAM2636 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[36777] GAM2636 gene, herein designated GAM GENE, encodes a GAM2636 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2636 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2636 precursor RNA is designated SEQ ID:2613, and is provided hereinbelow with reference to the sequence listing part.

[36778] GAM2636 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2636 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36779] An enzyme complex designated DICER COMPLEX, dices the GAM2636 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2636 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2636 RNA is designated SEQ ID:5227, and is provided hereinbelow with reference to the sequence listing part.

[36780] GAM2636 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2636 target RNA, herein designated GAM TARGET RNA. GAM2636 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.



[36781] GAM2636 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2636 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2636 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2636 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2636 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36782] The complementary binding of GAM2636 RNA, herein designated GAM RNA, to target binding sites on GAM2636 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2636 target RNA, herein designated GAM TARGET RNA, into GAM2636 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36783] It is appreciated that GAM2636 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2636 target genes. The

mRNA of each one of this plurality of GAM2636 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2636 RNA, herein designated GAM RNA, and which when bound by GAM2636 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2636 target proteins.

[36784] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2636 gene, herein designated GAM GENE, on one or more GAM2636 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36785] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2636 correlate with, and may be deduced from, the identity of the target genes which GAM2636 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36786] Nucleotide sequences of the GAM2636 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2636 RNA, herein

designated GAM RNA, and a schematic representation of the secondary folding of GAM2636 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2636 are further described hereinbelow with reference to Table 1.

[36787] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2636 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[36788] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2637 (GAM2637) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[36789] GAM2637 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2637 was detected is described hereinabove with reference to Figs. 2-8.

[36790] GAM2637 gene, herein designated GAM GENE, and GAM2637 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[36791] GAM2637 gene, herein designated GAM GENE, encodes a GAM2637 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2637 precursor RNA,

herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2637 precursor RNA is designated SEQ ID:2614, and is provided hereinbelow with reference to the sequence listing part.

[36792] GAM2637 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2637 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36793] An enzyme complex designated DICER COMPLEX, dices the GAM2637 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2637 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 87%) nucleotide sequence of GAM2637 RNA is designated SEQ ID:5228, and is provided hereinbelow with reference to the sequence listing part.

[36794] GAM2637 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2637 target RNA, herein designated GAM TARGET RNA. GAM2637 target RNA, herein designated GAM

TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36795] GAM2637 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2637 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2637 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2637 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2637 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36796] The complementary binding of GAM2637 RNA, herein designated GAM RNA, to target binding sites on GAM2637 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2637 target RNA, herein designated GAM TARGET RNA, into GAM2637 target protein, herein

designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36797] It is appreciated that GAM2637 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2637 target genes. The mRNA of each one of this plurality of GAM2637 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2637 RNA, herein designated GAM RNA, and which when bound by GAM2637 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2637 target proteins.

[36798] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2637 gene, herein designated GAM GENE, on one or more GAM2637 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36799] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2637 correlate with, and may be deduced from, the identity of the target

genes which GAM2637 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36800] Nucleotide sequences of the GAM2637 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2637 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2637 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2637 are further described hereinbelow with reference to Table 1.

[36801] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2637 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[36802] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 2638 (GAM2638) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[36803] GAM2638 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2638 was detected is described hereinabove with reference to Figs. 2-8.

[36804] GAM2638 gene, herein designated GAM GENE, and GAM2638 target gene, herein designated GAM TARGET GENE, are human genes contained in the

human genome.

[36805] GAM2638 gene, herein designated GAM GENE, encodes a GAM2638 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2638 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2638 precursor RNA is designated SEQ ID:2615, and is provided hereinbelow with reference to the sequence listing part.

[36806] GAM2638 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM2638 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36807] An enzyme complex designated DICER COMPLEX, dices the GAM2638 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM2638 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of GAM2638 RNA is designated SEQ ID:5229, and is provided



hereinbelow with reference to the sequence listing part.

[36808] GAM2638 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM2638 target RNA, herein designated GAM TARGET RNA. GAM2638 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[36809] GAM2638 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2638 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2638 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2638 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM2638 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[36810] The complementary binding of GAM2638 RNA, herein designated GAM RNA, to target binding sites on GAM2638 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2638 target RNA, herein designated GAM TARGET RNA, into GAM2638 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36811] It is appreciated that GAM2638 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM2638 target genes. The mRNA of each one of this plurality of GAM2638 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2638 RNA, herein designated GAM RNA, and which when bound by GAM2638 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM2638 target proteins.

[36812] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2638 gene, herein designated GAM GENE, on one or more GAM2638 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding

sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36813] It is yet further appreciated that specific functions, and accordingly utilities, of GAM2638 correlate with, and may be deduced from, the identity of the target genes which GAM2638 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36814] Nucleotide sequences of the GAM2638 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM2638 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM2638 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM2638 are further described hereinbelow with reference to Table 1.

[36815] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM2638 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table 2.

[36816] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2639 (GR2639) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

- [36817] GR2639 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2639 gene was detected is described hereinabove with reference to Figs. 6-15.
- [36818] GR2639 gene encodes GR2639 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [36819] GR2639 precursor RNA folds spatially, forming GR2639 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2639 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2639 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.
- [36820] GR2639 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM24 precursor RNA, GAM25 precursor RNA and GAM26 precursor RNA, herein schematically represented by GAM1 PRECURSOR, GAM2 PRECURSOR and GAM3 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[36821] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM24 RNA, GAM25 RNA and GAM26 RNA respectively, herein schematically represented by GAM1 RNA, GAM2 RNA and GAM3 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[36822] GAM24 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM24 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM24 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM24 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[36823] GAM25 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM25 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM25 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM25 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[36824] GAM26 RNA, herein schematically represented by GAM3 binds complementarily to a target binding site located in an untranslated region of

GAM26 target RNA, herein schematically represented by GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM26 target RNA, herein schematically represented by GAM3 TARGET RNA into GAM26 target protein, herein schematically represented by GAM3 TARGET PROTEIN, both of Fig. 8.

[36825] It is appreciated that specific functions, and accordingly utilities, of GR2639 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2639 gene: GAM24 target protein, GAM25 target protein and GAM26 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM24, GAM25 and GAM26

[36826] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2640(GR2640) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[36827] GR2640 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2640 gene was detected is described hereinabove with reference to Figs. 6-15.

[36828] GR2640 gene encodes GR2640 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[36829] GR2640 precursor RNA folds spatially, forming GR2640 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2640 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2640 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[36830] GR2640 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM27 precursor RNA, GAM28 precursor RNA and GAM29 precursor RNA, herein schematically represented by GAM1 PRECURSOR, GAM2 PRECURSOR and GAM3 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[36831] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM27 RNA, GAM28 RNA and GAM29 RNA respectively, herein schematically represented by GAM1 RNA, GAM2 RNA and GAM3 RNA

respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[36832] GAM27 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM27 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM27 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM27 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[36833] GAM28 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM28 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM28 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM28 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[36834] GAM29 RNA, herein schematically represented by GAM3 binds complementarily to a target binding site located in an untranslated region of GAM29 target RNA, herein schematically represented by GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM29 target RNA, herein schematically



represented by GAM3 TARGET RNA into GAM29 target protein, herein schematically represented by GAM3 TARGET PROTEIN, both of Fig. 8.

[36835] It is appreciated that specific functions, and accordingly utilities, of GR2640 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2640 gene: GAM27 target protein, GAM28 target protein and GAM29 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM27, GAM28 and GAM29

[36836] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2641 (GR2641) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[36837] GR2641 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2641 gene was detected is described hereinabove with reference to Figs. 6-15.

[36838] GR2641 gene encodes GR2641 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[36839] GR2641 precursor RNA folds spatially, forming GR2641 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2641 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2641 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[36840] GR2641 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM30 precursor RNA, GAM31 precursor RNA and GAM32 precursor RNA, herein schematically represented by GAM1 PRECURSOR, GAM2 PRECURSOR and GAM3 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[36841] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM30 RNA, GAM31 RNA and GAM32 RNA respectively, herein schematically represented by GAM1 RNA, GAM2 RNA and GAM3 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[36842] GAM30 RNA, herein schematically represented by GAM1 binds

complimentarily to a target binding site located in an untranslated region of GAM30 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM30 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM30 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[36843] GAM31 RNA, herein schematically represented by GAM2 binds complimentarily to a target binding site located in an untranslated region of GAM31 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM31 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM31 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[36844] GAM32 RNA, herein schematically represented by GAM3 binds complimentarily to a target binding site located in an untranslated region of GAM32 target RNA, herein schematically represented by GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM32 target RNA, herein schematically represented by GAM3 TARGET RNA into GAM32 target protein, herein schematically represented by GAM3 TARGET PROTEIN, both of Fig. 8.

[36845] It is appreciated that specific functions, and accordingly utilities, of GR2641

gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2641 gene: GAM30 target protein, GAM31 target protein and GAM32 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM30, GAM31 and GAM32

[36846] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2642(GR2642) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[36847] GR2642 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2642 gene was detected is described hereinabove with reference to Figs. 6-15.

[36848] GR2642 gene encodes GR2642 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[36849] GR2642 precursor RNA folds spatially, forming GR2642 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2642 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as

hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2642 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[36850] GR2642 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM33 precursor RNA, GAM34 precursor RNA and GAM35 precursor RNA, herein schematically represented by GAM1 PRECURSOR, GAM2 PRECURSOR and GAM3 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[36851] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM33 RNA, GAM34 RNA and GAM35 RNA respectively, herein schematically represented by GAM1 RNA, GAM2 RNA and GAM3 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[36852] GAM33 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM33 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby

inhibiting translation of GAM33 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM33 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[36853] GAM34 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM34 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM34 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM34 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[36854] GAM35 RNA, herein schematically represented by GAM3 binds complementarily to a target binding site located in an untranslated region of GAM35 target RNA, herein schematically represented by GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM35 target RNA, herein schematically represented by GAM3 TARGET RNA into GAM35 target protein, herein schematically represented by GAM3 TARGET PROTEIN, both of Fig. 8.

[36855] It is appreciated that specific functions, and accordingly utilities, of GR2642 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2642 gene: GAM33 target protein, GAM34 target protein and GAM35 target protein, herein schematically

represented by GAM1 TARGET PROTEIN through GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM33, GAM34 and GAM35

- [36856] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2643(GR2643) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [36857] GR2643 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2643 gene was detected is described hereinabove with reference to Figs. 6-15.
- [36858] GR2643 gene encodes GR2643 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [36859] GR2643 precursor RNA folds spatially, forming GR2643 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2643 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2643 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

[36860] GR2643 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM36 precursor RNA, GAM37 precursor RNA and GAM38 precursor RNA, herein schematically represented by GAM1 PRECURSOR, GAM2 PRECURSOR and GAM3 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[36861] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM36 RNA, GAM37 RNA and GAM38 RNA respectively, herein schematically represented by GAM1 RNA, GAM2 RNA and GAM3 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[36862] GAM36 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM36 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM36 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM36 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[36863] GAM37 RNA, herein schematically represented by GAM2 binds



complimentarily to a target binding site located in an untranslated region of GAM37 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM37 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM37 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[36864] GAM38 RNA, herein schematically represented by GAM3 binds complimentarily to a target binding site located in an untranslated region of GAM38 target RNA, herein schematically represented by GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM38 target RNA, herein schematically represented by GAM3 TARGET RNA into GAM38 target protein, herein schematically represented by GAM3 TARGET PROTEIN, both of Fig. 8.

[36865] It is appreciated that specific functions, and accordingly utilities, of GR2643 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2643 gene: GAM36 target protein, GAM37 target protein and GAM38 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM36, GAM37 and GAM38

[36866] Fig. 16 further provides a conceptual description of novel bioinformatically

detected regulatory gene, referred to here as Genomic Record 2644(GR2644) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[36867] GR2644 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2644 gene was detected is described hereinabove with reference to Figs. 6-15.

[36868] GR2644 gene encodes GR2644 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[36869] GR2644 precursor RNA folds spatially, forming GR2644 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2644 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2644 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[36870] GR2644 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM39 precursor RNA, GAM40

precursor RNA, GAM41 precursor RNA and GAM1300 precursor RNA, herein schematically represented by GAM1 PRECURSOR, GAM2 PRECURSOR, GAM3 PRECURSOR and GAM4 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[36871] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM39 RNA, GAM40 RNA, GAM41 RNA and GAM1300 RNA respectively, herein schematically represented by GAM1 RNA, GAM2 RNA, GAM3 RNA and GAM4 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[36872] GAM39 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM39 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM39 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM39 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[36873] GAM40 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM40 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby

inhibiting translation of GAM40 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM40 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[36874] GAM41 RNA, herein schematically represented by GAM3 binds complementarily to a target binding site located in an untranslated region of GAM41 target RNA, herein schematically represented by GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM41 target RNA, herein schematically represented by GAM3 TARGET RNA into GAM41 target protein, herein schematically represented by GAM3 TARGET PROTEIN, both of Fig. 8.

[36875] GAM1300 RNA, herein schematically represented by GAM4 binds complementarily to a target binding site located in an untranslated region of GAM1300 target RNA, herein schematically represented by GAM4 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1300 target RNA, herein schematically represented by GAM4 TARGET RNA into GAM1300 target protein, herein schematically represented by GAM4 TARGET PROTEIN, both of Fig. 8.

[36876] It is appreciated that specific functions, and accordingly utilities, of GR2644 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2644 gene: GAM39 target protein, GAM40 target protein, GAM41 target protein and GAM1300 target protein,

herein schematically represented by GAM1 TARGET PROTEIN through GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM39, GAM40, GAM41 and GAM1300

- [36877] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2645(GR2645) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [36878] GR2645 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2645 gene was detected is described hereinabove with reference to Figs. 6-15.
- [36879] GR2645 gene encodes GR2645 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [36880] GR2645 precursor RNA folds spatially, forming GR2645 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2645 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2645 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[36881] GR2645 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM42 precursor RNA, GAM43 precursor RNA and GAM44 precursor RNA, herein schematically represented by GAM1 PRECURSOR, GAM2 PRECURSOR and GAM3 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[36882] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM42 RNA, GAM43 RNA and GAM44 RNA respectively, herein schematically represented by GAM1 RNA, GAM2 RNA and GAM3 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[36883] GAM42 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM42 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM42 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM42 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

- [36884] GAM43 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM43 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM43 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM43 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.
- [36885] GAM44 RNA, herein schematically represented by GAM3 binds complementarily to a target binding site located in an untranslated region of GAM44 target RNA, herein schematically represented by GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM44 target RNA, herein schematically represented by GAM3 TARGET RNA into GAM44 target protein, herein schematically represented by GAM3 TARGET PROTEIN, both of Fig. 8.
- [36886] It is appreciated that specific functions, and accordingly utilities, of GR2645 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2645 gene: GAM42 target protein, GAM43 target protein and GAM44 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM42, GAM43 and GAM44

- [36887] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2646(GR2646) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [36888] GR2646 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2646 gene was detected is described hereinabove with reference to Figs. 6-15.
- [36889] GR2646 gene encodes GR2646 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [36890] GR2646 precursor RNA folds spatially, forming GR2646 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2646 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2646 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.
- [36891] GR2646 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into



at least 2 separate GAM precursor RNAs, GAM45 precursor RNA and GAM46 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[36892] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM45 RNA and GAM46 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[36893] GAM45 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM45 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM45 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM45 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[36894] GAM46 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM46 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM46 target RNA, herein schematically

represented by GAM2 TARGET RNA into GAM46 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[36895] It is appreciated that specific functions, and accordingly utilities, of GR2646 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2646 gene: GAM45 target protein and GAM46 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM45 and GAM46

[36896] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2647 (GR2647) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[36897] GR2647 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2647 gene was detected is described hereinabove with reference to Figs. 6-15.

[36898] GR2647 gene encodes GR2647 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[36899] GR2647 precursor RNA folds spatially, forming GR2647 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2647 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2647 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[36900] GR2647 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM50 precursor RNA, GAM51 precursor RNA and GAM52 precursor RNA, herein schematically represented by GAM1 PRECURSOR, GAM2 PRECURSOR and GAM3 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[36901] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM50 RNA, GAM51 RNA and GAM52 RNA respectively, herein schematically represented by GAM1 RNA, GAM2 RNA and GAM3 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[36902] GAM50 RNA, herein schematically represented by GAM1 binds

complimentarily to a target binding site located in an untranslated region of GAM50 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM50 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM50 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[36903] GAM51 RNA, herein schematically represented by GAM2 binds complimentarily to a target binding site located in an untranslated region of GAM51 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM51 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM51 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[36904] GAM52 RNA, herein schematically represented by GAM3 binds complimentarily to a target binding site located in an untranslated region of GAM52 target RNA, herein schematically represented by GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM52 target RNA, herein schematically represented by GAM3 TARGET RNA into GAM52 target protein, herein schematically represented by GAM3 TARGET PROTEIN, both of Fig. 8.

[36905] It is appreciated that specific functions, and accordingly utilities, of GR2647

gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2647 gene: GAM50 target protein, GAM51 target protein and GAM52 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM50, GAM51 and GAM52

[36906] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2648(GR2648) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[36907] GR2648 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2648 gene was detected is described hereinabove with reference to Figs. 6-15.

[36908] GR2648 gene encodes GR2648 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[36909] GR2648 precursor RNA folds spatially, forming GR2648 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2648 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as

hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2648 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[36910] GR2648 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM58 precursor RNA and GAM59 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[36911] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM58 RNA and GAM59 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[36912] GAM58 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM58 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM58 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM58 target protein, herein

schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[36913] GAM59 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM59 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM59 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM59 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[36914] It is appreciated that specific functions, and accordingly utilities, of GR2648 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2648 gene: GAM58 target protein and GAM59 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM58 and GAM59

[36915] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2649 (GR2649) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[36916] GR2649 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR2649 gene was detected is described hereinabove with reference to Figs. 6-15.

[36917] GR2649 gene encodes GR2649 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[36918] GR2649 precursor RNA folds spatially, forming GR2649 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2649 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2649 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[36919] GR2649 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM65 precursor RNA and GAM66 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[36920] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in



length, GAM65 RNA and GAM66 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[36921] GAM65 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM65 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM65 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM65 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[36922] GAM66 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM66 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM66 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM66 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[36923] It is appreciated that specific functions, and accordingly utilities, of GR2649 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2649 gene: GAM65 target protein and GAM66 target protein, herein schematically represented by GAM1

TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM65 and GAM66

- [36924] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2650 (GR2650) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [36925] GR2650 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2650 gene was detected is described hereinabove with reference to Figs. 6-15.
- [36926] GR2650 gene encodes GR2650 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [36927] GR2650 precursor RNA folds spatially, forming GR2650 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2650 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2650 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

- [36928] GR2650 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM69 precursor RNA and GAM70 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [36929] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM69 RNA and GAM70 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.
- [36930] GAM69 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM69 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM69 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM69 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.
- [36931] GAM70 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM70 target RNA, herein schematically represented by GAM2 TARGET

RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM70 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM70 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[36932] It is appreciated that specific functions, and accordingly utilities, of GR2650 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2650 gene: GAM69 target protein and GAM70 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM69 and GAM70

[36933] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2651 (GR2651) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[36934] GR2651 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2651 gene was detected is described hereinabove with reference to Figs. 6-15.

[36935] GR2651 gene encodes GR2651 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[36936] GR2651 precursor RNA folds spatially, forming GR2651 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2651 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2651 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[36937] GR2651 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM71 precursor RNA and GAM72 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[36938] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM71 RNA and GAM72 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[36939] GAM71 RNA, herein schematically represented by GAM1 binds

complimentarily to a target binding site located in an untranslated region of GAM71 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM71 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM71 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[36940] GAM72 RNA, herein schematically represented by GAM2 binds complimentarily to a target binding site located in an untranslated region of GAM72 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM72 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM72 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[36941] It is appreciated that specific functions, and accordingly utilities, of GR2651 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2651 gene: GAM71 target protein and GAM72 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM71 and GAM72

[36942] Fig. 16 further provides a conceptual description of novel bioinformatically

detected regulatory gene, referred to here as Genomic Record

2652(GR2652) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[36943] GR2652 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2652 gene was detected is described hereinabove with reference to Figs. 6-15.

[36944] GR2652 gene encodes GR2652 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[36945] GR2652 precursor RNA folds spatially, forming GR2652 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2652 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2652 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[36946] GR2652 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM79 precursor RNA and

GAM80 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[36947] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM79 RNA and GAM80 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[36948] GAM79 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM79 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM79 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM79 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[36949] GAM80 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM80 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM80 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM80 target protein, herein



schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[36950] It is appreciated that specific functions, and accordingly utilities, of GR2652 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2652 gene: GAM79 target protein and GAM80 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM79 and GAM80

[36951] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2653 (GR2653) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[36952] GR2653 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2653 gene was detected is described hereinabove with reference to Figs. 6-15.

[36953] GR2653 gene encodes GR2653 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[36954] GR2653 precursor RNA folds spatially, forming GR2653 folded precursor

RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2653 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2653 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[36955] GR2653 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM82 precursor RNA and GAM83 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[36956] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM82 RNA and GAM83 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[36957] GAM82 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM82 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM82 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM82 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[36958] GAM83 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM83 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM83 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM83 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[36959] It is appreciated that specific functions, and accordingly utilities, of GR2653 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2653 gene: GAM82 target protein and GAM83 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM82 and GAM83

[36960] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2654(GR2654) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

[36961] GR2654 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2654 gene was detected is described hereinabove with reference to Figs. 6-15.

[36962] GR2654 gene encodes GR2654 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[36963] GR2654 precursor RNA folds spatially, forming GR2654 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2654 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2654 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[36964] GR2654 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM87 precursor RNA and GAM88 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to

## GAM PRECURSOR RNA of Fig. 8.

[36965] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM87 RNA and GAM88 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[36966] GAM87 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM87 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM87 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM87 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[36967] GAM88 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM88 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM88 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM88 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[36968] It is appreciated that specific functions, and accordingly utilities, of GR2654 gene, herein designated GR GENE, correlate with, and may be deduced

from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2654 gene: GAM87 target protein and GAM88 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM87 and GAM88

[36969] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2655 (GR2655) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[36970] GR2655 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2655 gene was detected is described hereinabove with reference to Figs. 6-15.

[36971] GR2655 gene encodes GR2655 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[36972] GR2655 precursor RNA folds spatially, forming GR2655 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2655 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the

nucleotide sequence of GR2655 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[36973] GR2655 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM89 precursor RNA and GAM90 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[36974] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM89 RNA and GAM90 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[36975] GAM89 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM89 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM89 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM89 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[36976] GAM90 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM90 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM90 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM90 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[36977] It is appreciated that specific functions, and accordingly utilities, of GR2655 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2655 gene: GAM89 target protein and GAM90 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM89 and GAM90

[36978] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2656 (GR2656) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[36979] GR2656 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which



GR2656 gene was detected is described hereinabove with reference to Figs. 6-15.

[36980] GR2656 gene encodes GR2656 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[36981] GR2656 precursor RNA folds spatially, forming GR2656 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2656 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2656 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[36982] GR2656 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM91 precursor RNA and GAM92 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[36983] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM91 RNA and GAM92 RNA respectively, herein schematically

represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[36984] GAM91 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM91 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM91 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM91 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[36985] GAM92 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM92 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM92 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM92 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[36986] It is appreciated that specific functions, and accordingly utilities, of GR2656 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2656 gene: GAM91 target protein and GAM92 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function

of these target genes is elaborated hereinabove with reference to GAM91 and GAM92

- [36987] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2657(GR2657) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [36988] GR2657 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2657 gene was detected is described hereinabove with reference to Figs. 6-15.
- [36989] GR2657 gene encodes GR2657 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [36990] GR2657 precursor RNA folds spatially, forming GR2657 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2657 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2657 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

- [36991] GR2657 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM96 precursor RNA, GAM97 precursor RNA and GAM98 precursor RNA, herein schematically represented by GAM1 PRECURSOR, GAM2 PRECURSOR and GAM3 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [36992] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM96 RNA, GAM97 RNA and GAM98 RNA respectively, herein schematically represented by GAM1 RNA, GAM2 RNA and GAM3 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.
- [36993] GAM96 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM96 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM96 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM96 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.
- [36994] GAM97 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of

GAM97 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM97 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM97 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[36995] GAM98 RNA, herein schematically represented by GAM3 binds complementarily to a target binding site located in an untranslated region of GAM98 target RNA, herein schematically represented by GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM98 target RNA, herein schematically represented by GAM3 TARGET RNA into GAM98 target protein, herein schematically represented by GAM3 TARGET PROTEIN, both of Fig. 8.

[36996] It is appreciated that specific functions, and accordingly utilities, of GR2657 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2657 gene: GAM96 target protein, GAM97 target protein and GAM98 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM96, GAM97 and GAM98

[36997] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record

2658(GR2658) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[36998] GR2658 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2658 gene was detected is described hereinabove with reference to Figs. 6-15.

[36999] GR2658 gene encodes GR2658 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37000] GR2658 precursor RNA folds spatially, forming GR2658 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2658 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2658 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37001] GR2658 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM106 precursor RNA and GAM107 precursor RNA, herein schematically represented by GAM1

PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37002] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM106 RNA and GAM107 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37003] GAM106 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM106 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM106 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM106 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37004] GAM107 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM107 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM107 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM107 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37005] It is appreciated that specific functions, and accordingly utilities, of GR2658 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2658 gene: GAM106 target protein and GAM107 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM106 and GAM107

[37006] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2659 (GR2659) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37007] GR2659 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2659 gene was detected is described hereinabove with reference to Figs. 6-15.

[37008] GR2659 gene encodes GR2659 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37009] GR2659 precursor RNA folds spatially, forming GR2659 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2659 folded precursor RNA, herein designated GR FOLDED



PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2659 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37010] GR2659 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM111 precursor RNA and GAM112 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37011] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM111 RNA and GAM112 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37012] GAM111 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM111 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM111 target RNA, herein schematically

represented by GAM1 TARGET RNA into GAM111 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37013] GAM112 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM112 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM112 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM112 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37014] It is appreciated that specific functions, and accordingly utilities, of GR2659 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2659 gene: GAM111 target protein and GAM112 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM111 and GAM112

[37015] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2660 (GR2660) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

- [37016] GR2660 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2660 gene was detected is described hereinabove with reference to Figs. 6-15.
- [37017] GR2660 gene encodes GR2660 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [37018] GR2660 precursor RNA folds spatially, forming GR2660 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2660 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2660 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.
- [37019] GR2660 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM113 precursor RNA and GAM114 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [37020] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX

of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM113 RNA and GAM114 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37021] GAM113 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM113 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM113 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM113 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37022] GAM114 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM114 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM114 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM114 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37023] It is appreciated that specific functions, and accordingly utilities, of GR2660 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2660 gene: GAM113 target

protein and GAM114 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM113 and GAM114

[37024] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2661 (GR2661) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37025] GR2661 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2661 gene was detected is described hereinabove with reference to Figs. 6-15.

[37026] GR2661 gene encodes GR2661 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37027] GR2661 precursor RNA folds spatially, forming GR2661 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2661 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2661 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37028] GR2661 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM122 precursor RNA and GAM123 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37029] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM122 RNA and GAM123 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37030] GAM122 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM122 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM122 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM122 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37031] GAM123 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of

GAM123 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM123 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM123 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37032] It is appreciated that specific functions, and accordingly utilities, of GR2661 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2661 gene: GAM122 target protein and GAM123 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM122 and GAM123

[37033] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2662 (GR2662) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37034] GR2662 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2662 gene was detected is described hereinabove with reference to Figs. 6-15.

[37035] GR2662 gene encodes GR2662 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37036] GR2662 precursor RNA folds spatially, forming GR2662 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2662 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2662 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37037] GR2662 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM128 precursor RNA and GAM129 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37038] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM128 RNA and GAM129 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.



[37039] GAM128 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM128 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM128 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM128 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37040] GAM129 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM129 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM129 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM129 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37041] It is appreciated that specific functions, and accordingly utilities, of GR2662 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2662 gene: GAM128 target protein and GAM129 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM128 and GAM129

- [37042] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2663(GR2663) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [37043] GR2663 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2663 gene was detected is described hereinabove with reference to Figs. 6-15.
- [37044] GR2663 gene encodes GR2663 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [37045] GR2663 precursor RNA folds spatially, forming GR2663 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2663 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2663 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.
- [37046] GR2663 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into

at least 2 separate GAM precursor RNAs, GAM131 precursor RNA and GAM132 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37047] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM131 RNA and GAM132 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37048] GAM131 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM131 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM131 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM131 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37049] GAM132 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM132 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM132 target RNA, herein schematically

represented by GAM2 TARGET RNA into GAM132 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37050] It is appreciated that specific functions, and accordingly utilities, of GR2663 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2663 gene: GAM131 target protein and GAM132 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM131 and GAM132

[37051] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2664 (GR2664) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37052] GR2664 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2664 gene was detected is described hereinabove with reference to Figs. 6-15.

[37053] GR2664 gene encodes GR2664 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37054] GR2664 precursor RNA folds spatially, forming GR2664 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2664 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2664 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37055] GR2664 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM133 precursor RNA and GAM134 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37056] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM133 RNA and GAM134 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37057] GAM133 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM133 target RNA, herein schematically represented by GAM1 TARGET

RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM133 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM133 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37058] GAM134 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM134 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM134 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM134 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37059] It is appreciated that specific functions, and accordingly utilities, of GR2664 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2664 gene: GAM133 target protein and GAM134 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM133 and GAM134

[37060] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2665(GR2665) gene, which encodes an operon-like cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37061] GR2665 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2665 gene was detected is described hereinabove with reference to Figs. 6-15.

[37062] GR2665 gene encodes GR2665 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37063] GR2665 precursor RNA folds spatially, forming GR2665 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2665 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2665 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37064] GR2665 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM142 precursor RNA and GAM143 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM

precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37065] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM142 RNA and GAM143 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37066] GAM142 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM142 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM142 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM142 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37067] GAM143 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM143 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM143 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM143 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37068] It is appreciated that specific functions, and accordingly utilities, of GR2665



gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2665 gene: GAM142 target protein and GAM143 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM142 and GAM143

[37069] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2666 (GR2666) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37070] GR2666 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2666 gene was detected is described hereinabove with reference to Figs. 6-15.

[37071] GR2666 gene encodes GR2666 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37072] GR2666 precursor RNA folds spatially, forming GR2666 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2666 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as

hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2666 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37073] GR2666 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM148 precursor RNA and GAM149 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37074] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM148 RNA and GAM149 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37075] GAM148 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM148 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM148 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM148 target protein, herein

schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37076] GAM149 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM149 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM149 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM149 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37077] It is appreciated that specific functions, and accordingly utilities, of GR2666 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2666 gene: GAM148 target protein and GAM149 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM148 and GAM149

[37078] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2667 (GR2667) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37079] GR2667 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR2667 gene was detected is described hereinabove with reference to Figs. 6-15.

[37080] GR2667 gene encodes GR2667 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37081] GR2667 precursor RNA folds spatially, forming GR2667 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2667 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2667 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37082] GR2667 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM152 precursor RNA and GAM153 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37083] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in

length, GAM152 RNA and GAM153 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37084] GAM152 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM152 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM152 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM152 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37085] GAM153 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM153 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM153 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM153 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37086] It is appreciated that specific functions, and accordingly utilities, of GR2667 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2667 gene: GAM152 target protein and GAM153 target protein, herein schematically represented by

GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM152 and GAM153

[37087] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2668 (GR2668) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37088] GR2668 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2668 gene was detected is described hereinabove with reference to Figs. 6-15.

[37089] GR2668 gene encodes GR2668 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37090] GR2668 precursor RNA folds spatially, forming GR2668 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2668 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2668 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

- [37091] GR2668 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM159 precursor RNA and GAM160 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [37092] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM159 RNA and GAM160 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.
- [37093] GAM159 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM159 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM159 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM159 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.
- [37094] GAM160 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM160 target RNA, herein schematically represented by GAM2 TARGET

RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM160 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM160 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37095] It is appreciated that specific functions, and accordingly utilities, of GR2668 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2668 gene: GAM159 target protein and GAM160 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM159 and GAM160

[37096] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2669 (GR2669) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37097] GR2669 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2669 gene was detected is described hereinabove with reference to Figs. 6-15.

[37098] GR2669 gene encodes GR2669 precursor RNA, herein designated GR



PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37099] GR2669 precursor RNA folds spatially, forming GR2669 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2669 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2669 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37100] GR2669 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM163 precursor RNA and GAM164 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37101] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM163 RNA and GAM164 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37102] GAM163 RNA, herein schematically represented by GAM1 binds

complimentarily to a target binding site located in an untranslated region of GAM163 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM163 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM163 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37103] GAM164 RNA, herein schematically represented by GAM2 binds complimentarily to a target binding site located in an untranslated region of GAM164 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM164 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM164 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37104] It is appreciated that specific functions, and accordingly utilities, of GR2669 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2669 gene: GAM163 target protein and GAM164 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM163 and GAM164

[37105] Fig. 16 further provides a conceptual description of novel bioinformatically

detected regulatory gene, referred to here as Genomic Record 2670 (GR2670) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37106] GR2670 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2670 gene was detected is described hereinabove with reference to Figs. 6-15.

[37107] GR2670 gene encodes GR2670 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37108] GR2670 precursor RNA folds spatially, forming GR2670 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2670 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2670 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37109] GR2670 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM170 precursor RNA and

GAM171 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37110] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM170 RNA and GAM171 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37111] GAM170 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM170 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM170 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM170 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37112] GAM171 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM171 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM171 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM171 target protein, herein

schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37113] It is appreciated that specific functions, and accordingly utilities, of GR2670 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2670 gene: GAM170 target protein and GAM171 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM170 and GAM171

[37114] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2671 (GR2671) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37115] GR2671 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2671 gene was detected is described hereinabove with reference to Figs. 6-15.

[37116] GR2671 gene encodes GR2671 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37117] GR2671 precursor RNA folds spatially, forming GR2671 folded precursor

RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2671 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2671 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37118] GR2671 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM174 precursor RNA, GAM175 precursor RNA and GAM176 precursor RNA, herein schematically represented by GAM1 PRECURSOR, GAM2 PRECURSOR and GAM3 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37119] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM174 RNA, GAM175 RNA and GAM176 RNA respectively, herein schematically represented by GAM1 RNA, GAM2 RNA and GAM3 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37120] GAM174 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of

GAM174 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM174 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM174 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37121] GAM175 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM175 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM175 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM175 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37122] GAM176 RNA, herein schematically represented by GAM3 binds complementarily to a target binding site located in an untranslated region of GAM176 target RNA, herein schematically represented by GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM176 target RNA, herein schematically represented by GAM3 TARGET RNA into GAM176 target protein, herein schematically represented by GAM3 TARGET PROTEIN, both of Fig. 8.

[37123] It is appreciated that specific functions, and accordingly utilities, of GR2671 gene, herein designated GR GENE, correlate with, and may be deduced

from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2671 gene: GAM174 target protein, GAM175 target protein and GAM176 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM174, GAM175 and GAM176

[37124] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2672 (GR2672) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37125] GR2672 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2672 gene was detected is described hereinabove with reference to Figs. 6-15.

[37126] GR2672 gene encodes GR2672 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37127] GR2672 precursor RNA folds spatially, forming GR2672 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2672 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the



nucleotide sequence of GR2672 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37128] GR2672 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM178 precursor RNA and GAM179 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37129] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM178 RNA and GAM179 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37130] GAM178 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM178 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM178 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM178 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37131] GAM179 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM179 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM179 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM179 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37132] It is appreciated that specific functions, and accordingly utilities, of GR2672 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2672 gene: GAM178 target protein and GAM179 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM178 and GAM179

[37133] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2673 (GR2673) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37134] GR2673 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which

GR2673 gene was detected is described hereinabove with reference to Figs. 6-15.

[37135] GR2673 gene encodes GR2673 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37136] GR2673 precursor RNA folds spatially, forming GR2673 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2673 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2673 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37137] GR2673 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM181 precursor RNA and GAM182 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37138] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM181 RNA and GAM182 RNA respectively, herein schematically

represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37139] GAM181 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM181 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM181 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM181 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37140] GAM182 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM182 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM182 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM182 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37141] It is appreciated that specific functions, and accordingly utilities, of GR2673 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2673 gene: GAM181 target protein and GAM182 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The

function of these target genes is elaborated hereinabove with reference to GAM181 and GAM182

[37142] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2674 (GR2674) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37143] GR2674 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2674 gene was detected is described hereinabove with reference to Figs. 6-15.

[37144] GR2674 gene encodes GR2674 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37145] GR2674 precursor RNA folds spatially, forming GR2674 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2674 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2674 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37146] GR2674 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM186 precursor RNA and GAM187 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37147] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM186 RNA and GAM187 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37148] GAM186 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM186 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM186 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM186 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37149] GAM187 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM187 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM187 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM187 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37150] It is appreciated that specific functions, and accordingly utilities, of GR2674 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2674 gene: GAM186 target protein and GAM187 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM186 and GAM187

[37151] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2675 (GR2675) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37152] GR2675 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2675 gene was detected is described hereinabove with reference to Figs. 6-15.

[37153] GR2675 gene encodes GR2675 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides

long.

[37154] GR2675 precursor RNA folds spatially, forming GR2675 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2675 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2675 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37155] GR2675 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM200 precursor RNA and GAM201 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37156] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM200 RNA and GAM201 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37157] GAM200 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of



GAM200 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM200 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM200 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37158] GAM201 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM201 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM201 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM201 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37159] It is appreciated that specific functions, and accordingly utilities, of GR2675 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2675 gene: GAM200 target protein and GAM201 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM200 and GAM201

[37160] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record

2676(GR2676) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37161] GR2676 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2676 gene was detected is described hereinabove with reference to Figs. 6-15.

[37162] GR2676 gene encodes GR2676 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37163] GR2676 precursor RNA folds spatially, forming GR2676 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2676 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2676 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37164] GR2676 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM203 precursor RNA and GAM204 precursor RNA, herein schematically represented by GAM1

PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37165] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM203 RNA and GAM204 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37166] GAM203 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM203 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM203 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM203 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37167] GAM204 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM204 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM204 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM204 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37168] It is appreciated that specific functions, and accordingly utilities, of GR2676 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2676 gene: GAM203 target protein and GAM204 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM203 and GAM204

[37169] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2677 (GR2677) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37170] GR2677 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2677 gene was detected is described hereinabove with reference to Figs. 6-15.

[37171] GR2677 gene encodes GR2677 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37172] GR2677 precursor RNA folds spatially, forming GR2677 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2677 folded precursor RNA, herein designated GR FOLDED

PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2677 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37173] GR2677 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM206 precursor RNA, GAM207 precursor RNA, GAM208 precursor RNA and GAM209 precursor RNA, herein schematically represented by GAM1 PRECURSOR, GAM2 PRECURSOR, GAM3 PRECURSOR and GAM4 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37174] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM206 RNA, GAM207 RNA, GAM208 RNA and GAM209 RNA respectively, herein schematically represented by GAM1 RNA, GAM2 RNA, GAM3 RNA and GAM4 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37175] GAM206 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM206 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM206 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM206 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37176] GAM207 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM207 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM207 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM207 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37177] GAM208 RNA, herein schematically represented by GAM3 binds complementarily to a target binding site located in an untranslated region of GAM208 target RNA, herein schematically represented by GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM208 target RNA, herein schematically represented by GAM3 TARGET RNA into GAM208 target protein, herein schematically represented by GAM3 TARGET PROTEIN, both of Fig. 8.

[37178] GAM209 RNA, herein schematically represented by GAM4 binds complementarily to a target binding site located in an untranslated region of GAM209 target RNA, herein schematically represented by GAM4 TARGET RNA, which target binding site corresponds to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM209 target RNA, herein schematically represented by GAM4 TARGET RNA into GAM209 target protein, herein schematically represented by GAM4 TARGET PROTEIN, both of Fig. 8.

[37179] It is appreciated that specific functions, and accordingly utilities, of GR2677 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2677 gene: GAM206 target protein, GAM207 target protein, GAM208 target protein and GAM209 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM206, GAM207, GAM208 and GAM209

[37180] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2678 (GR2678) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37181] GR2678 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2678 gene was detected is described hereinabove with reference to Figs. 6-15.

[37182] GR2678 gene encodes GR2678 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37183] GR2678 precursor RNA folds spatially, forming GR2678 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2678 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2678 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37184] GR2678 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM211 precursor RNA and GAM212 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37185] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM211 RNA and GAM212 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37186] GAM211 RNA, herein schematically represented by GAM1 binds



complimentarily to a target binding site located in an untranslated region of GAM211 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM211 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM211 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37187] GAM212 RNA, herein schematically represented by GAM2 binds complimentarily to a target binding site located in an untranslated region of GAM212 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM212 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM212 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37188] It is appreciated that specific functions, and accordingly utilities, of GR2678 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2678 gene: GAM211 target protein and GAM212 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM211 and GAM212

[37189] Fig. 16 further provides a conceptual description of novel bioinformatically

detected regulatory gene, referred to here as Genomic Record 2679(GR2679) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37190] GR2679 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2679 gene was detected is described hereinabove with reference to Figs. 6-15.

[37191] GR2679 gene encodes GR2679 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37192] GR2679 precursor RNA folds spatially, forming GR2679 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2679 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2679 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37193] GR2679 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM214 precursor RNA and

GAM215 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37194] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM214 RNA and GAM215 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37195] GAM214 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM214 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM214 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM214 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37196] GAM215 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM215 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM215 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM215 target protein, herein

schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37197] It is appreciated that specific functions, and accordingly utilities, of GR2679 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2679 gene: GAM214 target protein and GAM215 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM214 and GAM215

[37198] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2680 (GR2680) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37199] GR2680 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2680 gene was detected is described hereinabove with reference to Figs. 6-15.

[37200] GR2680 gene encodes GR2680 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37201] GR2680 precursor RNA folds spatially, forming GR2680 folded precursor

RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2680 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2680 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37202] GR2680 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM221 precursor RNA, GAM222 precursor RNA and GAM223 precursor RNA, herein schematically represented by GAM1 PRECURSOR, GAM2 PRECURSOR and GAM3 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37203] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM221 RNA, GAM222 RNA and GAM223 RNA respectively, herein schematically represented by GAM1 RNA, GAM2 RNA and GAM3 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37204] GAM221 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of

GAM221 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM221 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM221 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37205] GAM222 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM222 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM222 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM222 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37206] GAM223 RNA, herein schematically represented by GAM3 binds complementarily to a target binding site located in an untranslated region of GAM223 target RNA, herein schematically represented by GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM223 target RNA, herein schematically represented by GAM3 TARGET RNA into GAM223 target protein, herein schematically represented by GAM3 TARGET PROTEIN, both of Fig. 8.

[37207] It is appreciated that specific functions, and accordingly utilities, of GR2680 gene, herein designated GR GENE, correlate with, and may be deduced

from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2680 gene: GAM221 target protein, GAM222 target protein and GAM223 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM221, GAM222 and GAM223

[37208] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2681 (GR2681) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37209] GR2681 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2681 gene was detected is described hereinabove with reference to Figs. 6-15.

[37210] GR2681 gene encodes GR2681 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37211] GR2681 precursor RNA folds spatially, forming GR2681 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2681 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the

nucleotide sequence of GR2681 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

- [37212] GR2681 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM226 precursor RNA and GAM227 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [37213] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM226 RNA and GAM227 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.
- [37214] GAM226 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM226 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM226 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM226 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.



[37215] GAM227 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM227 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM227 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM227 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37216] It is appreciated that specific functions, and accordingly utilities, of GR2681 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2681 gene: GAM226 target protein and GAM227 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM226 and GAM227

[37217] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2682 (GR2682) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37218] GR2682 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which

GR2682 gene was detected is described hereinabove with reference to Figs. 6-15.

[37219] GR2682 gene encodes GR2682 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37220] GR2682 precursor RNA folds spatially, forming GR2682 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2682 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2682 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37221] GR2682 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM234 precursor RNA and GAM235 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37222] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM234 RNA and GAM235 RNA respectively, herein schematically

represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37223] GAM234 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM234 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM234 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM234 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37224] GAM235 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM235 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM235 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM235 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37225] It is appreciated that specific functions, and accordingly utilities, of GR2682 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2682 gene: GAM234 target protein and GAM235 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The

function of these target genes is elaborated hereinabove with reference to GAM234 and GAM235

- [37226] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2683 (GR2683) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [37227] GR2683 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2683 gene was detected is described hereinabove with reference to Figs. 6-15.
- [37228] GR2683 gene encodes GR2683 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [37229] GR2683 precursor RNA folds spatially, forming GR2683 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2683 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2683 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

- [37230] GR2683 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM236 precursor RNA and GAM237 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [37231] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM236 RNA and GAM237 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.
- [37232] GAM236 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM236 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM236 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM236 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.
- [37233] GAM237 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM237 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM237 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM237 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37234] It is appreciated that specific functions, and accordingly utilities, of GR2683 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2683 gene: GAM236 target protein and GAM237 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM236 and GAM237

[37235] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2684 (GR2684) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37236] GR2684 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2684 gene was detected is described hereinabove with reference to Figs. 6-15.

[37237] GR2684 gene encodes GR2684 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides

long.

[37238] GR2684 precursor RNA folds spatially, forming GR2684 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2684 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2684 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37239] GR2684 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM244 precursor RNA, GAM245 precursor RNA and GAM246 precursor RNA, herein schematically represented by GAM1 PRECURSOR, GAM2 PRECURSOR and GAM3 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37240] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM244 RNA, GAM245 RNA and GAM246 RNA respectively, herein schematically represented by GAM1 RNA, GAM2 RNA and GAM3 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37241] GAM244 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM244 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM244 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM244 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37242] GAM245 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM245 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM245 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM245 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37243] GAM246 RNA, herein schematically represented by GAM3 binds complementarily to a target binding site located in an untranslated region of GAM246 target RNA, herein schematically represented by GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM246 target RNA, herein schematically represented by GAM3 TARGET RNA into GAM246 target protein, herein schematically represented by GAM3 TARGET PROTEIN, both of Fig. 8.



[37244] It is appreciated that specific functions, and accordingly utilities, of GR2684 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2684 gene: GAM244 target protein, GAM245 target protein and GAM246 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM244, GAM245 and GAM246

[37245] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2685 (GR2685) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37246] GR2685 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2685 gene was detected is described hereinabove with reference to Figs. 6-15.

[37247] GR2685 gene encodes GR2685 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37248] GR2685 precursor RNA folds spatially, forming GR2685 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2685 folded precursor RNA, herein designated GR FOLDED

PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2685 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37249] GR2685 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM250 precursor RNA and GAM251 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37250] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM250 RNA and GAM251 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37251] GAM250 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM250 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM250 target RNA, herein schematically

represented by GAM1 TARGET RNA into GAM250 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37252] GAM251 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM251 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM251 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM251 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37253] It is appreciated that specific functions, and accordingly utilities, of GR2685 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2685 gene: GAM250 target protein and GAM251 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM250 and GAM251

[37254] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2686 (GR2686) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37255] GR2686 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2686 gene was detected is described hereinabove with reference to Figs. 6-15.

[37256] GR2686 gene encodes GR2686 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37257] GR2686 precursor RNA folds spatially, forming GR2686 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2686 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2686 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37258] GR2686 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM252 precursor RNA and GAM253 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37259] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX

of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM252 RNA and GAM253 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37260] GAM252 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM252 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM252 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM252 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37261] GAM253 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM253 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM253 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM253 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37262] It is appreciated that specific functions, and accordingly utilities, of GR2686 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2686 gene: GAM252 target

protein and GAM253 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM252 and GAM253

[37263] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2687 (GR2687) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37264] GR2687 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2687 gene was detected is described hereinabove with reference to Figs. 6-15.

[37265] GR2687 gene encodes GR2687 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37266] GR2687 precursor RNA folds spatially, forming GR2687 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2687 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2687 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37267] GR2687 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM257 precursor RNA and GAM258 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37268] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM257 RNA and GAM258 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37269] GAM257 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM257 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM257 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM257 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37270] GAM258 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of

GAM258 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM258 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM258 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37271] It is appreciated that specific functions, and accordingly utilities, of GR2687 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2687 gene: GAM257 target protein and GAM258 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM257 and GAM258

[37272] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2688 (GR2688) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37273] GR2688 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2688 gene was detected is described hereinabove with reference to Figs. 6-15.



[37274] GR2688 gene encodes GR2688 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37275] GR2688 precursor RNA folds spatially, forming GR2688 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2688 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2688 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37276] GR2688 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM261 precursor RNA and GAM262 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37277] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM261 RNA and GAM262 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37278] GAM261 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM261 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM261 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM261 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37279] GAM262 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM262 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM262 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM262 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37280] It is appreciated that specific functions, and accordingly utilities, of GR2688 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2688 gene: GAM261 target protein and GAM262 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM261 and GAM262

- [37281] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2689 (GR2689) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [37282] GR2689 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2689 gene was detected is described hereinabove with reference to Figs. 6-15.
- [37283] GR2689 gene encodes GR2689 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [37284] GR2689 precursor RNA folds spatially, forming GR2689 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2689 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2689 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.
- [37285] GR2689 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into

at least 2 separate GAM precursor RNAs, GAM263 precursor RNA and GAM264 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37286] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM263 RNA and GAM264 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37287] GAM263 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM263 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM263 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM263 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37288] GAM264 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM264 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM264 target RNA, herein schematically

represented by GAM2 TARGET RNA into GAM264 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37289] It is appreciated that specific functions, and accordingly utilities, of GR2689 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2689 gene: GAM263 target protein and GAM264 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM263 and GAM264

[37290] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2690 (GR2690) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37291] GR2690 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2690 gene was detected is described hereinabove with reference to Figs. 6-15.

[37292] GR2690 gene encodes GR2690 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37293] GR2690 precursor RNA folds spatially, forming GR2690 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2690 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2690 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37294] GR2690 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM265 precursor RNA and GAM266 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37295] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM265 RNA and GAM266 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37296] GAM265 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM265 target RNA, herein schematically represented by GAM1 TARGET

RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM265 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM265 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37297] GAM266 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM266 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM266 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM266 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37298] It is appreciated that specific functions, and accordingly utilities, of GR2690 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2690 gene: GAM265 target protein and GAM266 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM265 and GAM266

[37299] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2691 (GR2691) gene, which encodes an operon-like cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37300] GR2691 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2691 gene was detected is described hereinabove with reference to Figs. 6-15.

[37301] GR2691 gene encodes GR2691 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37302] GR2691 precursor RNA folds spatially, forming GR2691 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2691 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2691 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37303] GR2691 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM271 precursor RNA and GAM272 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM



precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37304] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM271 RNA and GAM272 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37305] GAM271 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM271 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM271 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM271 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37306] GAM272 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM272 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM272 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM272 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37307] It is appreciated that specific functions, and accordingly utilities, of GR2691

gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2691 gene: GAM271 target protein and GAM272 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM271 and GAM272

[37308] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2692 (GR2692) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37309] GR2692 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2692 gene was detected is described hereinabove with reference to Figs. 6-15.

[37310] GR2692 gene encodes GR2692 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37311] GR2692 precursor RNA folds spatially, forming GR2692 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2692 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as

hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2692 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37312] GR2692 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM276 precursor RNA and GAM277 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37313] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM276 RNA and GAM277 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37314] GAM276 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM276 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM276 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM276 target protein, herein

schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37315] GAM277 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM277 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM277 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM277 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37316] It is appreciated that specific functions, and accordingly utilities, of GR2692 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2692 gene: GAM276 target protein and GAM277 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM276 and GAM277

[37317] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2693 (GR2693) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37318] GR2693 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR2693 gene was detected is described hereinabove with reference to Figs. 6-15.

[37319] GR2693 gene encodes GR2693 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37320] GR2693 precursor RNA folds spatially, forming GR2693 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2693 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2693 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37321] GR2693 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM282 precursor RNA and GAM283 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37322] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in

length, GAM282 RNA and GAM283 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37323] GAM282 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM282 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM282 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM282 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37324] GAM283 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM283 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM283 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM283 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37325] It is appreciated that specific functions, and accordingly utilities, of GR2693 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2693 gene: GAM282 target protein and GAM283 target protein, herein schematically represented by

GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM282 and GAM283

[37326] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2694 (GR2694) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37327] GR2694 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2694 gene was detected is described hereinabove with reference to Figs. 6-15.

[37328] GR2694 gene encodes GR2694 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37329] GR2694 precursor RNA folds spatially, forming GR2694 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2694 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2694 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

- [37330] GR2694 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM287 precursor RNA and GAM288 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [37331] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM287 RNA and GAM288 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.
- [37332] GAM287 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM287 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM287 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM287 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.
- [37333] GAM288 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM288 target RNA, herein schematically represented by GAM2 TARGET



RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM288 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM288 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37334] It is appreciated that specific functions, and accordingly utilities, of GR2694 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2694 gene: GAM287 target protein and GAM288 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM287 and GAM288

[37335] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2695 (GR2695) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37336] GR2695 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2695 gene was detected is described hereinabove with reference to Figs. 6-15.

[37337] GR2695 gene encodes GR2695 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37338] GR2695 precursor RNA folds spatially, forming GR2695 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2695 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2695 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37339] GR2695 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM292 precursor RNA and GAM293 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37340] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM292 RNA and GAM293 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37341] GAM292 RNA, herein schematically represented by GAM1 binds

complimentarily to a target binding site located in an untranslated region of GAM292 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM292 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM292 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37342] GAM293 RNA, herein schematically represented by GAM2 binds complimentarily to a target binding site located in an untranslated region of GAM293 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM293 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM293 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37343] It is appreciated that specific functions, and accordingly utilities, of GR2695 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2695 gene: GAM292 target protein and GAM293 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM292 and GAM293

[37344] Fig. 16 further provides a conceptual description of novel bioinformatically

detected regulatory gene, referred to here as Genomic Record 2696(GR2696) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37345] GR2696 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2696 gene was detected is described hereinabove with reference to Figs. 6-15.

[37346] GR2696 gene encodes GR2696 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37347] GR2696 precursor RNA folds spatially, forming GR2696 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2696 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2696 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37348] GR2696 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM299 precursor RNA and

GAM300 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37349] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM299 RNA and GAM300 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37350] GAM299 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM299 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM299 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM299 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37351] GAM300 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM300 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM300 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM300 target protein, herein

schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37352] It is appreciated that specific functions, and accordingly utilities, of GR2696 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2696 gene: GAM299 target protein and GAM300 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM299 and GAM300

[37353] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2697 (GR2697) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37354] GR2697 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2697 gene was detected is described hereinabove with reference to Figs. 6-15.

[37355] GR2697 gene encodes GR2697 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37356] GR2697 precursor RNA folds spatially, forming GR2697 folded precursor

RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2697 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2697 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37357] GR2697 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM303 precursor RNA and GAM304 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37358] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM303 RNA and GAM304 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37359] GAM303 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM303 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM303 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM303 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37360] GAM304 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM304 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM304 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM304 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37361] It is appreciated that specific functions, and accordingly utilities, of GR2697 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2697 gene: GAM303 target protein and GAM304 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM303 and GAM304

[37362] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2698 (GR2698) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one



target gene, the function and utility of which at least one target gene is known in the art.

[37363] GR2698 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2698 gene was detected is described hereinabove with reference to Figs. 6-15.

[37364] GR2698 gene encodes GR2698 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37365] GR2698 precursor RNA folds spatially, forming GR2698 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2698 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2698 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37366] GR2698 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM305 precursor RNA and GAM306 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to

GAM PRECURSOR RNA of Fig. 8.

[37367] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM305 RNA and GAM306 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37368] GAM305 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM305 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM305 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM305 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37369] GAM306 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM306 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM306 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM306 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37370] It is appreciated that specific functions, and accordingly utilities, of GR2698 gene, herein designated GR GENE, correlate with, and may be deduced

from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2698 gene: GAM305 target protein and GAM306 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM305 and GAM306

[37371] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2699 (GR2699) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37372] GR2699 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2699 gene was detected is described hereinabove with reference to Figs. 6-15.

[37373] GR2699 gene encodes GR2699 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37374] GR2699 precursor RNA folds spatially, forming GR2699 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2699 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the

nucleotide sequence of GR2699 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

- [37375] GR2699 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM319 precursor RNA and GAM320 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [37376] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM319 RNA and GAM320 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.
- [37377] GAM319 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM319 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM319 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM319 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37378] GAM320 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM320 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM320 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM320 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37379] It is appreciated that specific functions, and accordingly utilities, of GR2699 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2699 gene: GAM319 target protein and GAM320 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM319 and GAM320

[37380] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2700 (GR2700) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37381] GR2700 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which

GR2700 gene was detected is described hereinabove with reference to Figs. 6-15.

[37382] GR2700 gene encodes GR2700 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37383] GR2700 precursor RNA folds spatially, forming GR2700 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2700 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2700 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37384] GR2700 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM321 precursor RNA and GAM322 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37385] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM321 RNA and GAM322 RNA respectively, herein schematically

represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37386] GAM321 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM321 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM321 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM321 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37387] GAM322 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM322 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM322 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM322 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37388] It is appreciated that specific functions, and accordingly utilities, of GR2700 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2700 gene: GAM321 target protein and GAM322 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The

function of these target genes is elaborated hereinabove with reference to GAM321 and GAM322

- [37389] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2701 (GR2701) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [37390] GR2701 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2701 gene was detected is described hereinabove with reference to Figs. 6-15.
- [37391] GR2701 gene encodes GR2701 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [37392] GR2701 precursor RNA folds spatially, forming GR2701 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2701 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2701 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.



- [37393] GR2701 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM324 precursor RNA and GAM325 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [37394] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM324 RNA and GAM325 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.
- [37395] GAM324 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM324 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM324 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM324 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.
- [37396] GAM325 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM325 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM325 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM325 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37397] It is appreciated that specific functions, and accordingly utilities, of GR2701 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2701 gene: GAM324 target protein and GAM325 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM324 and GAM325

[37398] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2702 (GR2702) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37399] GR2702 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2702 gene was detected is described hereinabove with reference to Figs. 6-15.

[37400] GR2702 gene encodes GR2702 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides

long.

[37401] GR2702 precursor RNA folds spatially, forming GR2702 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2702 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2702 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37402] GR2702 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM342 precursor RNA and GAM343 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37403] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM342 RNA and GAM343 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37404] GAM342 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of

GAM342 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM342 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM342 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37405] GAM343 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM343 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM343 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM343 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37406] It is appreciated that specific functions, and accordingly utilities, of GR2702 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2702 gene: GAM342 target protein and GAM343 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM342 and GAM343

[37407] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record

2703(GR2703) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37408] GR2703 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2703 gene was detected is described hereinabove with reference to Figs. 6-15.

[37409] GR2703 gene encodes GR2703 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37410] GR2703 precursor RNA folds spatially, forming GR2703 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2703 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2703 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37411] GR2703 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM352 precursor RNA and GAM353 precursor RNA, herein schematically represented by GAM1

PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37412] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM352 RNA and GAM353 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37413] GAM352 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM352 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM352 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM352 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37414] GAM353 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM353 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM353 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM353 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37415] It is appreciated that specific functions, and accordingly utilities, of GR2703 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2703 gene: GAM352 target protein and GAM353 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM352 and GAM353

[37416] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2704 (GR2704) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37417] GR2704 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2704 gene was detected is described hereinabove with reference to Figs. 6-15.

[37418] GR2704 gene encodes GR2704 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37419] GR2704 precursor RNA folds spatially, forming GR2704 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2704 folded precursor RNA, herein designated GR FOLDED

PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2704 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37420] GR2704 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM354 precursor RNA and GAM355 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37421] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM354 RNA and GAM355 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37422] GAM354 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM354 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM354 target RNA, herein schematically



represented by GAM1 TARGET RNA into GAM354 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37423] GAM355 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM355 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM355 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM355 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37424] It is appreciated that specific functions, and accordingly utilities, of GR2704 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2704 gene: GAM354 target protein and GAM355 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM354 and GAM355

[37425] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2705 (GR2705) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

- [37426] GR2705 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2705 gene was detected is described hereinabove with reference to Figs. 6-15.
- [37427] GR2705 gene encodes GR2705 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [37428] GR2705 precursor RNA folds spatially, forming GR2705 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2705 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2705 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.
- [37429] GR2705 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM368 precursor RNA and GAM369 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [37430] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX

of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM368 RNA and GAM369 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37431] GAM368 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM368 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM368 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM368 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37432] GAM369 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM369 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM369 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM369 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37433] It is appreciated that specific functions, and accordingly utilities, of GR2705 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2705 gene: GAM368 target

protein and GAM369 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM368 and GAM369

[37434] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2706 (GR2706) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37435] GR2706 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2706 gene was detected is described hereinabove with reference to Figs. 6-15.

[37436] GR2706 gene encodes GR2706 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37437] GR2706 precursor RNA folds spatially, forming GR2706 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2706 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2706 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37438] GR2706 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM372 precursor RNA and GAM373 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37439] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM372 RNA and GAM373 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37440] GAM372 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM372 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM372 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM372 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37441] GAM373 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of

GAM373 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM373 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM373 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37442] It is appreciated that specific functions, and accordingly utilities, of GR2706 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2706 gene: GAM372 target protein and GAM373 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM372 and GAM373

[37443] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2707 (GR2707) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37444] GR2707 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2707 gene was detected is described hereinabove with reference to Figs. 6-15.

[37445] GR2707 gene encodes GR2707 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37446] GR2707 precursor RNA folds spatially, forming GR2707 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2707 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2707 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37447] GR2707 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM401 precursor RNA and GAM402 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37448] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM401 RNA and GAM402 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37449] GAM401 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM401 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM401 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM401 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37450] GAM402 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM402 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM402 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM402 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37451] It is appreciated that specific functions, and accordingly utilities, of GR2707 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2707 gene: GAM401 target protein and GAM402 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM401 and GAM402



- [37452] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2708(GR2708) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [37453] GR2708 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2708 gene was detected is described hereinabove with reference to Figs. 6-15.
- [37454] GR2708 gene encodes GR2708 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [37455] GR2708 precursor RNA folds spatially, forming GR2708 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2708 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2708 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.
- [37456] GR2708 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into

at least 2 separate GAM precursor RNAs, GAM407 precursor RNA and GAM408 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37457] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM407 RNA and GAM408 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37458] GAM407 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM407 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM407 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM407 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37459] GAM408 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM408 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM408 target RNA, herein schematically

represented by GAM2 TARGET RNA into GAM408 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37460] It is appreciated that specific functions, and accordingly utilities, of GR2708 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2708 gene: GAM407 target protein and GAM408 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM407 and GAM408

[37461] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2709 (GR2709) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37462] GR2709 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2709 gene was detected is described hereinabove with reference to Figs. 6-15.

[37463] GR2709 gene encodes GR2709 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37464] GR2709 precursor RNA folds spatially, forming GR2709 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2709 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2709 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37465] GR2709 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM413 precursor RNA and GAM414 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37466] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM413 RNA and GAM414 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37467] GAM413 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM413 target RNA, herein schematically represented by GAM1 TARGET

RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM413 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM413 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37468] GAM414 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM414 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM414 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM414 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37469] It is appreciated that specific functions, and accordingly utilities, of GR2709 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2709 gene: GAM413 target protein and GAM414 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM413 and GAM414

[37470] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2710(GR2710) gene, which encodes an operon-like cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37471] GR2710 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2710 gene was detected is described hereinabove with reference to Figs. 6-15.

[37472] GR2710 gene encodes GR2710 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37473] GR2710 precursor RNA folds spatially, forming GR2710 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2710 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2710 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37474] GR2710 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM416 precursor RNA and GAM417 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM

precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37475] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM416 RNA and GAM417 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37476] GAM416 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM416 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM416 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM416 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37477] GAM417 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM417 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM417 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM417 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37478] It is appreciated that specific functions, and accordingly utilities, of GR2710

gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2710 gene: GAM416 target protein and GAM417 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM416 and GAM417

[37479] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2711 (GR2711) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37480] GR2711 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2711 gene was detected is described hereinabove with reference to Figs. 6-15.

[37481] GR2711 gene encodes GR2711 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37482] GR2711 precursor RNA folds spatially, forming GR2711 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2711 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as



hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2711 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37483] GR2711 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM428 precursor RNA and GAM429 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37484] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM428 RNA and GAM429 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37485] GAM428 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM428 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM428 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM428 target protein, herein

schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37486] GAM429 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM429 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM429 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM429 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37487] It is appreciated that specific functions, and accordingly utilities, of GR2711 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2711 gene: GAM428 target protein and GAM429 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM428 and GAM429

[37488] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2712(GR2712) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37489] GR2712 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR2712 gene was detected is described hereinabove with reference to Figs. 6-15.

[37490] GR2712 gene encodes GR2712 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37491] GR2712 precursor RNA folds spatially, forming GR2712 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2712 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2712 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37492] GR2712 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM431 precursor RNA and GAM432 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37493] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in

length, GAM431 RNA and GAM432 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37494] GAM431 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM431 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM431 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM431 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37495] GAM432 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM432 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM432 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM432 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37496] It is appreciated that specific functions, and accordingly utilities, of GR2712 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2712 gene: GAM431 target protein and GAM432 target protein, herein schematically represented by

GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM431 and GAM432

[37497] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2713 (GR2713) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37498] GR2713 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2713 gene was detected is described hereinabove with reference to Figs. 6-15.

[37499] GR2713 gene encodes GR2713 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37500] GR2713 precursor RNA folds spatially, forming GR2713 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2713 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2713 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

- [37501] GR2713 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM433 precursor RNA and GAM434 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [37502] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM433 RNA and GAM434 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.
- [37503] GAM433 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM433 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM433 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM433 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.
- [37504] GAM434 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM434 target RNA, herein schematically represented by GAM2 TARGET

RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM434 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM434 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37505] It is appreciated that specific functions, and accordingly utilities, of GR2713 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2713 gene: GAM433 target protein and GAM434 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM433 and GAM434

[37506] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2714 (GR2714) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37507] GR2714 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2714 gene was detected is described hereinabove with reference to Figs. 6-15.

[37508] GR2714 gene encodes GR2714 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37509] GR2714 precursor RNA folds spatially, forming GR2714 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2714 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2714 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37510] GR2714 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM440 precursor RNA and GAM441 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37511] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM440 RNA and GAM441 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37512] GAM440 RNA, herein schematically represented by GAM1 binds



complimentarily to a target binding site located in an untranslated region of GAM440 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM440 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM440 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37513] GAM441 RNA, herein schematically represented by GAM2 binds complimentarily to a target binding site located in an untranslated region of GAM441 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM441 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM441 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37514] It is appreciated that specific functions, and accordingly utilities, of GR2714 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2714 gene: GAM440 target protein and GAM441 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM440 and GAM441

[37515] Fig. 16 further provides a conceptual description of novel bioinformatically

detected regulatory gene, referred to here as Genomic Record 2715(GR2715) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37516] GR2715 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2715 gene was detected is described hereinabove with reference to Figs. 6-15.

[37517] GR2715 gene encodes GR2715 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37518] GR2715 precursor RNA folds spatially, forming GR2715 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2715 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2715 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37519] GR2715 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM444 precursor RNA and

GAM445 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37520] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM444 RNA and GAM445 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37521] GAM444 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM444 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM444 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM444 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37522] GAM445 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM445 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM445 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM445 target protein, herein

schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37523] It is appreciated that specific functions, and accordingly utilities, of GR2715 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2715 gene: GAM444 target protein and GAM445 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM444 and GAM445

[37524] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2716 (GR2716) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37525] GR2716 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2716 gene was detected is described hereinabove with reference to Figs. 6-15.

[37526] GR2716 gene encodes GR2716 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37527] GR2716 precursor RNA folds spatially, forming GR2716 folded precursor

RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2716 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2716 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37528] GR2716 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM454 precursor RNA and GAM455 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37529] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM454 RNA and GAM455 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37530] GAM454 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM454 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM454 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM454 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37531] GAM455 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM455 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM455 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM455 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37532] It is appreciated that specific functions, and accordingly utilities, of GR2716 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2716 gene: GAM454 target protein and GAM455 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM454 and GAM455

[37533] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2717 (GR2717) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

[37534] GR2717 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2717 gene was detected is described hereinabove with reference to Figs. 6-15.

[37535] GR2717 gene encodes GR2717 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37536] GR2717 precursor RNA folds spatially, forming GR2717 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2717 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2717 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37537] GR2717 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM461 precursor RNA and GAM462 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to

GAM PRECURSOR RNA of Fig. 8.

[37538] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM461 RNA and GAM462 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37539] GAM461 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM461 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM461 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM461 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37540] GAM462 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM462 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM462 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM462 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37541] It is appreciated that specific functions, and accordingly utilities, of GR2717 gene, herein designated GR GENE, correlate with, and may be deduced



from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2717 gene: GAM461 target protein and GAM462 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM461 and GAM462

[37542] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2718 (GR2718) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37543] GR2718 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2718 gene was detected is described hereinabove with reference to Figs. 6-15.

[37544] GR2718 gene encodes GR2718 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37545] GR2718 precursor RNA folds spatially, forming GR2718 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2718 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the

nucleotide sequence of GR2718 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

- [37546] GR2718 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM467 precursor RNA and GAM468 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [37547] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM467 RNA and GAM468 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.
- [37548] GAM467 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM467 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM467 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM467 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37549] GAM468 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM468 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM468 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM468 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37550] It is appreciated that specific functions, and accordingly utilities, of GR2718 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2718 gene: GAM467 target protein and GAM468 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM467 and GAM468

[37551] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2719 (GR2719) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37552] GR2719 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which

GR2719 gene was detected is described hereinabove with reference to Figs. 6-15.

[37553] GR2719 gene encodes GR2719 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37554] GR2719 precursor RNA folds spatially, forming GR2719 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2719 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2719 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37555] GR2719 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM471 precursor RNA and GAM472 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37556] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM471 RNA and GAM472 RNA respectively, herein schematically

represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37557] GAM471 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM471 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM471 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM471 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37558] GAM472 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM472 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM472 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM472 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37559] It is appreciated that specific functions, and accordingly utilities, of GR2719 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2719 gene: GAM471 target protein and GAM472 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The

function of these target genes is elaborated hereinabove with reference to GAM471 and GAM472

- [37560] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2720(GR2720) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [37561] GR2720 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2720 gene was detected is described hereinabove with reference to Figs. 6-15.
- [37562] GR2720 gene encodes GR2720 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [37563] GR2720 precursor RNA folds spatially, forming GR2720 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2720 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2720 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37564] GR2720 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM473 precursor RNA and GAM474 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37565] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM473 RNA and GAM474 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37566] GAM473 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM473 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM473 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM473 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37567] GAM474 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM474 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM474 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM474 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37568] It is appreciated that specific functions, and accordingly utilities, of GR2720 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2720 gene: GAM473 target protein and GAM474 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM473 and GAM474

[37569] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2721 (GR2721) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37570] GR2721 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2721 gene was detected is described hereinabove with reference to Figs. 6-15.

[37571] GR2721 gene encodes GR2721 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides



long.

[37572] GR2721 precursor RNA folds spatially, forming GR2721 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2721 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2721 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37573] GR2721 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM477 precursor RNA and GAM478 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37574] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM477 RNA and GAM478 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37575] GAM477 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of

GAM477 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM477 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM477 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37576] GAM478 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM478 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM478 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM478 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37577] It is appreciated that specific functions, and accordingly utilities, of GR2721 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2721 gene: GAM477 target protein and GAM478 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM477 and GAM478

[37578] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record

2722(GR2722) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37579] GR2722 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2722 gene was detected is described hereinabove with reference to Figs. 6-15.

[37580] GR2722 gene encodes GR2722 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37581] GR2722 precursor RNA folds spatially, forming GR2722 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2722 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2722 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37582] GR2722 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM483 precursor RNA and GAM484 precursor RNA, herein schematically represented by GAM1

PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37583] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM483 RNA and GAM484 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37584] GAM483 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM483 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM483 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM483 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37585] GAM484 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM484 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM484 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM484 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37586] It is appreciated that specific functions, and accordingly utilities, of GR2722 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2722 gene: GAM483 target protein and GAM484 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM483 and GAM484

[37587] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2723 (GR2723) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37588] GR2723 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2723 gene was detected is described hereinabove with reference to Figs. 6-15.

[37589] GR2723 gene encodes GR2723 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37590] GR2723 precursor RNA folds spatially, forming GR2723 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2723 folded precursor RNA, herein designated GR FOLDED

PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2723 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37591] GR2723 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM485 precursor RNA and GAM486 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37592] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM485 RNA and GAM486 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37593] GAM485 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM485 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM485 target RNA, herein schematically

represented by GAM1 TARGET RNA into GAM485 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37594] GAM486 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM486 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM486 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM486 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37595] It is appreciated that specific functions, and accordingly utilities, of GR2723 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2723 gene: GAM485 target protein and GAM486 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM485 and GAM486

[37596] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2724 (GR2724) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37597] GR2724 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2724 gene was detected is described hereinabove with reference to Figs. 6-15.

[37598] GR2724 gene encodes GR2724 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37599] GR2724 precursor RNA folds spatially, forming GR2724 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2724 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2724 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37600] GR2724 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM488 precursor RNA and GAM489 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37601] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX



of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM488 RNA and GAM489 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37602] GAM488 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM488 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM488 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM488 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37603] GAM489 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM489 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM489 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM489 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37604] It is appreciated that specific functions, and accordingly utilities, of GR2724 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2724 gene: GAM488 target

protein and GAM489 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM488 and GAM489

[37605] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2725 (GR2725) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37606] GR2725 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2725 gene was detected is described hereinabove with reference to Figs. 6-15.

[37607] GR2725 gene encodes GR2725 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37608] GR2725 precursor RNA folds spatially, forming GR2725 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2725 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2725 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37609] GR2725 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM495 precursor RNA and GAM496 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37610] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM495 RNA and GAM496 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37611] GAM495 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM495 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM495 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM495 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37612] GAM496 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of

GAM496 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM496 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM496 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37613] It is appreciated that specific functions, and accordingly utilities, of GR2725 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2725 gene: GAM495 target protein and GAM496 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM495 and GAM496

[37614] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2726 (GR2726) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37615] GR2726 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2726 gene was detected is described hereinabove with reference to Figs. 6-15.

[37616] GR2726 gene encodes GR2726 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37617] GR2726 precursor RNA folds spatially, forming GR2726 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2726 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2726 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37618] GR2726 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM505 precursor RNA and GAM506 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37619] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM505 RNA and GAM506 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37620] GAM505 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM505 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM505 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM505 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37621] GAM506 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM506 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM506 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM506 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37622] It is appreciated that specific functions, and accordingly utilities, of GR2726 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2726 gene: GAM505 target protein and GAM506 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM505 and GAM506

- [37623] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2727(GR2727) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [37624] GR2727 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2727 gene was detected is described hereinabove with reference to Figs. 6-15.
- [37625] GR2727 gene encodes GR2727 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [37626] GR2727 precursor RNA folds spatially, forming GR2727 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2727 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2727 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.
- [37627] GR2727 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into

at least 2 separate GAM precursor RNAs, GAM508 precursor RNA and GAM509 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37628] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM508 RNA and GAM509 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37629] GAM508 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM508 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM508 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM508 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37630] GAM509 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM509 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM509 target RNA, herein schematically



represented by GAM2 TARGET RNA into GAM509 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37631] It is appreciated that specific functions, and accordingly utilities, of GR2727 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2727 gene: GAM508 target protein and GAM509 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM508 and GAM509

[37632] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2728 (GR2728) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37633] GR2728 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2728 gene was detected is described hereinabove with reference to Figs. 6-15.

[37634] GR2728 gene encodes GR2728 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37635] GR2728 precursor RNA folds spatially, forming GR2728 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2728 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2728 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37636] GR2728 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM520 precursor RNA and GAM521 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37637] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM520 RNA and GAM521 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37638] GAM520 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM520 target RNA, herein schematically represented by GAM1 TARGET

RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM520 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM520 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37639] GAM521 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM521 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM521 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM521 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37640] It is appreciated that specific functions, and accordingly utilities, of GR2728 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2728 gene: GAM520 target protein and GAM521 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM520 and GAM521

[37641] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2729(GR2729) gene, which encodes an operon-like cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37642] GR2729 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2729 gene was detected is described hereinabove with reference to Figs. 6-15.

[37643] GR2729 gene encodes GR2729 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37644] GR2729 precursor RNA folds spatially, forming GR2729 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2729 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2729 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37645] GR2729 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM527 precursor RNA and GAM528 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM

precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37646] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM527 RNA and GAM528 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37647] GAM527 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM527 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM527 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM527 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37648] GAM528 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM528 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM528 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM528 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37649] It is appreciated that specific functions, and accordingly utilities, of GR2729

gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2729 gene: GAM527 target protein and GAM528 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM527 and GAM528

[37650] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2730 (GR2730) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37651] GR2730 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2730 gene was detected is described hereinabove with reference to Figs. 6-15.

[37652] GR2730 gene encodes GR2730 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37653] GR2730 precursor RNA folds spatially, forming GR2730 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2730 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as

hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2730 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37654] GR2730 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM530 precursor RNA and GAM531 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37655] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM530 RNA and GAM531 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37656] GAM530 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM530 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM530 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM530 target protein, herein

schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37657] GAM531 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM531 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM531 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM531 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37658] It is appreciated that specific functions, and accordingly utilities, of GR2730 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2730 gene: GAM530 target protein and GAM531 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM530 and GAM531

[37659] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2731 (GR2731) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37660] GR2731 gene, herein designated GR GENE, is a novel bioinformatically



detected regulatory, non protein coding, RNA gene. The method by which GR2731 gene was detected is described hereinabove with reference to Figs. 6-15.

[37661] GR2731 gene encodes GR2731 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37662] GR2731 precursor RNA folds spatially, forming GR2731 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2731 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2731 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37663] GR2731 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM532 precursor RNA and GAM533 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37664] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in

length, GAM532 RNA and GAM533 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37665] GAM532 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM532 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM532 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM532 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37666] GAM533 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM533 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM533 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM533 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37667] It is appreciated that specific functions, and accordingly utilities, of GR2731 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2731 gene: GAM532 target protein and GAM533 target protein, herein schematically represented by

GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM532 and GAM533

[37668] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2732 (GR2732) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37669] GR2732 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2732 gene was detected is described hereinabove with reference to Figs. 6-15.

[37670] GR2732 gene encodes GR2732 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37671] GR2732 precursor RNA folds spatially, forming GR2732 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2732 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2732 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

- [37672] GR2732 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM539 precursor RNA and GAM540 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [37673] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM539 RNA and GAM540 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.
- [37674] GAM539 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM539 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM539 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM539 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.
- [37675] GAM540 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM540 target RNA, herein schematically represented by GAM2 TARGET

RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM540 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM540 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37676] It is appreciated that specific functions, and accordingly utilities, of GR2732 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2732 gene: GAM539 target protein and GAM540 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM539 and GAM540

[37677] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2733 (GR2733) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37678] GR2733 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2733 gene was detected is described hereinabove with reference to Figs. 6-15.

[37679] GR2733 gene encodes GR2733 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37680] GR2733 precursor RNA folds spatially, forming GR2733 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2733 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2733 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37681] GR2733 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM541 precursor RNA and GAM542 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37682] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM541 RNA and GAM542 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37683] GAM541 RNA, herein schematically represented by GAM1 binds

complimentarily to a target binding site located in an untranslated region of GAM541 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM541 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM541 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37684] GAM542 RNA, herein schematically represented by GAM2 binds complimentarily to a target binding site located in an untranslated region of GAM542 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM542 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM542 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37685] It is appreciated that specific functions, and accordingly utilities, of GR2733 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2733 gene: GAM541 target protein and GAM542 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM541 and GAM542

[37686] Fig. 16 further provides a conceptual description of novel bioinformatically

detected regulatory gene, referred to here as Genomic Record 2734(GR2734) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37687] GR2734 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2734 gene was detected is described hereinabove with reference to Figs. 6-15.

[37688] GR2734 gene encodes GR2734 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37689] GR2734 precursor RNA folds spatially, forming GR2734 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2734 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2734 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37690] GR2734 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM548 precursor RNA and



GAM549 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37691] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM548 RNA and GAM549 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37692] GAM548 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM548 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM548 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM548 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37693] GAM549 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM549 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM549 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM549 target protein, herein

schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37694] It is appreciated that specific functions, and accordingly utilities, of GR2734 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2734 gene: GAM548 target protein and GAM549 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM548 and GAM549

[37695] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2735 (GR2735) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37696] GR2735 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2735 gene was detected is described hereinabove with reference to Figs. 6-15.

[37697] GR2735 gene encodes GR2735 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37698] GR2735 precursor RNA folds spatially, forming GR2735 folded precursor

RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2735 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2735 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37699] GR2735 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM552 precursor RNA, GAM553 precursor RNA and GAM554 precursor RNA, herein schematically represented by GAM1 PRECURSOR, GAM2 PRECURSOR and GAM3 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37700] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM552 RNA, GAM553 RNA and GAM554 RNA respectively, herein schematically represented by GAM1 RNA, GAM2 RNA and GAM3 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37701] GAM552 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of

GAM552 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM552 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM552 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37702] GAM553 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM553 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM553 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM553 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37703] GAM554 RNA, herein schematically represented by GAM3 binds complementarily to a target binding site located in an untranslated region of GAM554 target RNA, herein schematically represented by GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM554 target RNA, herein schematically represented by GAM3 TARGET RNA into GAM554 target protein, herein schematically represented by GAM3 TARGET PROTEIN, both of Fig. 8.

[37704] It is appreciated that specific functions, and accordingly utilities, of GR2735 gene, herein designated GR GENE, correlate with, and may be deduced

from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2735 gene: GAM552 target protein, GAM553 target protein and GAM554 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM552, GAM553 and GAM554

[37705] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2736(GR2736) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37706] GR2736 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2736 gene was detected is described hereinabove with reference to Figs. 6-15.

[37707] GR2736 gene encodes GR2736 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37708] GR2736 precursor RNA folds spatially, forming GR2736 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2736 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the

nucleotide sequence of GR2736 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37709] GR2736 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM557 precursor RNA and GAM558 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37710] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM557 RNA and GAM558 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37711] GAM557 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM557 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM557 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM557 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37712] GAM558 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM558 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM558 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM558 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37713] It is appreciated that specific functions, and accordingly utilities, of GR2736 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2736 gene: GAM557 target protein and GAM558 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM557 and GAM558

[37714] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2737 (GR2737) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37715] GR2737 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which

GR2737 gene was detected is described hereinabove with reference to Figs. 6-15.

[37716] GR2737 gene encodes GR2737 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37717] GR2737 precursor RNA folds spatially, forming GR2737 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2737 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2737 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37718] GR2737 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM561 precursor RNA and GAM562 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37719] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM561 RNA and GAM562 RNA respectively, herein schematically



represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37720] GAM561 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM561 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM561 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM561 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37721] GAM562 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM562 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM562 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM562 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37722] It is appreciated that specific functions, and accordingly utilities, of GR2737 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2737 gene: GAM561 target protein and GAM562 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The

function of these target genes is elaborated hereinabove with reference to GAM561 and GAM562

- [37723] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2738 (GR2738) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [37724] GR2738 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2738 gene was detected is described hereinabove with reference to Figs. 6-15.
- [37725] GR2738 gene encodes GR2738 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [37726] GR2738 precursor RNA folds spatially, forming GR2738 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2738 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2738 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37727] GR2738 folded precursor RNA, herein designated GR FOLDED

PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM564 precursor RNA, GAM565 precursor RNA, GAM566 precursor RNA and GAM567 precursor RNA, herein schematically represented by GAM1 PRECURSOR, GAM2 PRECURSOR, GAM3 PRECURSOR and GAM4 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37728] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM564 RNA, GAM565 RNA, GAM566 RNA and GAM567 RNA respectively, herein schematically represented by GAM1 RNA, GAM2 RNA, GAM3 RNA and GAM4 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37729] GAM564 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM564 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM564 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM564 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37730] GAM565 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM565 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM565 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM565 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37731] GAM566 RNA, herein schematically represented by GAM3 binds complementarily to a target binding site located in an untranslated region of GAM566 target RNA, herein schematically represented by GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM566 target RNA, herein schematically represented by GAM3 TARGET RNA into GAM566 target protein, herein schematically represented by GAM3 TARGET PROTEIN, both of Fig. 8.

[37732] GAM567 RNA, herein schematically represented by GAM4 binds complementarily to a target binding site located in an untranslated region of GAM567 target RNA, herein schematically represented by GAM4 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM567 target RNA, herein schematically represented by GAM4 TARGET RNA into GAM567 target protein, herein schematically represented by GAM4 TARGET PROTEIN, both of Fig. 8.

[37733] It is appreciated that specific functions, and accordingly utilities, of GR2738 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2738 gene: GAM564 target protein, GAM565 target protein, GAM566 target protein and GAM567 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM564, GAM565, GAM566 and GAM567

[37734] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2739(GR2739) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37735] GR2739 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR2739 gene was detected is described hereinabove with reference to Figs. 6-15.

[37736] GR2739 gene encodes GR2739 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37737] GR2739 precursor RNA folds spatially, forming GR2739 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2739 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2739 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37738] GR2739 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM571 precursor RNA and GAM572 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37739] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in

length, GAM571 RNA and GAM572 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37740] GAM571 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM571 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM571 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM571 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37741] GAM572 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM572 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM572 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM572 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37742] It is appreciated that specific functions, and accordingly utilities, of GR2739 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2739 gene: GAM571 target protein and GAM572 target protein, herein schematically represented by

GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM571 and GAM572

[37743] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2740 (GR2740) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37744] GR2740 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2740 gene was detected is described hereinabove with reference to Figs. 6-15.

[37745] GR2740 gene encodes GR2740 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37746] GR2740 precursor RNA folds spatially, forming GR2740 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2740 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2740 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half



thereof, as is well known in the art.

- [37747] GR2740 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM573 precursor RNA and GAM574 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [37748] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM573 RNA and GAM574 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.
- [37749] GAM573 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM573 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM573 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM573 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.
- [37750] GAM574 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM574 target RNA, herein schematically represented by GAM2 TARGET

RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM574 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM574 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37751] It is appreciated that specific functions, and accordingly utilities, of GR2740 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2740 gene: GAM573 target protein and GAM574 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM573 and GAM574

[37752] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2741 (GR2741) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37753] GR2741 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2741 gene was detected is described hereinabove with reference to Figs. 6-15.

[37754] GR2741 gene encodes GR2741 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37755] GR2741 precursor RNA folds spatially, forming GR2741 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2741 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2741 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37756] GR2741 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM579 precursor RNA and GAM580 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37757] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM579 RNA and GAM580 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37758] GAM579 RNA, herein schematically represented by GAM1 binds

complimentarily to a target binding site located in an untranslated region of GAM579 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM579 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM579 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37759] GAM580 RNA, herein schematically represented by GAM2 binds complimentarily to a target binding site located in an untranslated region of GAM580 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM580 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM580 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37760] It is appreciated that specific functions, and accordingly utilities, of GR2741 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2741 gene: GAM579 target protein and GAM580 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM579 and GAM580

[37761] Fig. 16 further provides a conceptual description of novel bioinformatically

detected regulatory gene, referred to here as Genomic Record 2742(GR2742) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37762] GR2742 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2742 gene was detected is described hereinabove with reference to Figs. 6-15.

[37763] GR2742 gene encodes GR2742 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37764] GR2742 precursor RNA folds spatially, forming GR2742 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2742 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2742 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37765] GR2742 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM582 precursor RNA and

GAM583 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37766] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM582 RNA and GAM583 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37767] GAM582 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM582 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM582 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM582 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37768] GAM583 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM583 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM583 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM583 target protein, herein

schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37769] It is appreciated that specific functions, and accordingly utilities, of GR2742 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2742 gene: GAM582 target protein and GAM583 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM582 and GAM583

[37770] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2743 (GR2743) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37771] GR2743 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2743 gene was detected is described hereinabove with reference to Figs. 6-15.

[37772] GR2743 gene encodes GR2743 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37773] GR2743 precursor RNA folds spatially, forming GR2743 folded precursor

RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2743 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2743 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37774] GR2743 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM592 precursor RNA and GAM593 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37775] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM592 RNA and GAM593 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37776] GAM592 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM592 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as



BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM592 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM592 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37777] GAM593 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM593 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM593 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM593 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37778] It is appreciated that specific functions, and accordingly utilities, of GR2743 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2743 gene: GAM592 target protein and GAM593 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM592 and GAM593

[37779] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2744(GR2744) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

[37780] GR2744 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2744 gene was detected is described hereinabove with reference to Figs. 6-15.

[37781] GR2744 gene encodes GR2744 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37782] GR2744 precursor RNA folds spatially, forming GR2744 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2744 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2744 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37783] GR2744 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM594 precursor RNA and GAM595 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to

GAM PRECURSOR RNA of Fig. 8.

[37784] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM594 RNA and GAM595 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37785] GAM594 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM594 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM594 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM594 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37786] GAM595 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM595 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM595 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM595 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37787] It is appreciated that specific functions, and accordingly utilities, of GR2744 gene, herein designated GR GENE, correlate with, and may be deduced

from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2744 gene: GAM594 target protein and GAM595 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM594 and GAM595

[37788] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2745 (GR2745) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37789] GR2745 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2745 gene was detected is described hereinabove with reference to Figs. 6-15.

[37790] GR2745 gene encodes GR2745 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37791] GR2745 precursor RNA folds spatially, forming GR2745 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2745 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the

nucleotide sequence of GR2745 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37792] GR2745 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM604 precursor RNA and GAM605 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37793] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM604 RNA and GAM605 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37794] GAM604 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM604 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM604 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM604 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37795] GAM605 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM605 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM605 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM605 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37796] It is appreciated that specific functions, and accordingly utilities, of GR2745 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2745 gene: GAM604 target protein and GAM605 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM604 and GAM605

[37797] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2746 (GR2746) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37798] GR2746 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which

GR2746 gene was detected is described hereinabove with reference to Figs. 6-15.

[37799] GR2746 gene encodes GR2746 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37800] GR2746 precursor RNA folds spatially, forming GR2746 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2746 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2746 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37801] GR2746 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM608 precursor RNA and GAM609 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37802] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM608 RNA and GAM609 RNA respectively, herein schematically

represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37803] GAM608 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM608 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM608 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM608 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37804] GAM609 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM609 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM609 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM609 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37805] It is appreciated that specific functions, and accordingly utilities, of GR2746 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2746 gene: GAM608 target protein and GAM609 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The



function of these target genes is elaborated hereinabove with reference to GAM608 and GAM609

- [37806] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2747(GR2747) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [37807] GR2747 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2747 gene was detected is described hereinabove with reference to Figs. 6-15.
- [37808] GR2747 gene encodes GR2747 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [37809] GR2747 precursor RNA folds spatially, forming GR2747 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2747 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2747 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

- [37810] GR2747 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM610 precursor RNA and GAM611 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [37811] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM610 RNA and GAM611 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.
- [37812] GAM610 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM610 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM610 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM610 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.
- [37813] GAM611 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM611 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM611 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM611 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37814] It is appreciated that specific functions, and accordingly utilities, of GR2747 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2747 gene: GAM610 target protein and GAM611 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM610 and GAM611

[37815] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2748 (GR2748) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37816] GR2748 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2748 gene was detected is described hereinabove with reference to Figs. 6-15.

[37817] GR2748 gene encodes GR2748 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides

long.

[37818] GR2748 precursor RNA folds spatially, forming GR2748 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2748 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2748 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37819] GR2748 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM612 precursor RNA and GAM613 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37820] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM612 RNA and GAM613 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37821] GAM612 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of

GAM612 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM612 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM612 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37822] GAM613 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM613 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM613 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM613 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37823] It is appreciated that specific functions, and accordingly utilities, of GR2748 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2748 gene: GAM612 target protein and GAM613 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM612 and GAM613

[37824] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record

2749(GR2749) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37825] GR2749 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2749 gene was detected is described hereinabove with reference to Figs. 6-15.

[37826] GR2749 gene encodes GR2749 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37827] GR2749 precursor RNA folds spatially, forming GR2749 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2749 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2749 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37828] GR2749 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM623 precursor RNA, GAM624 precursor RNA and GAM625 precursor RNA, herein schematically

represented by GAM1 PRECURSOR, GAM2 PRECURSOR and GAM3 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37829] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM623 RNA, GAM624 RNA and GAM625 RNA respectively, herein schematically represented by GAM1 RNA, GAM2 RNA and GAM3 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37830] GAM623 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM623 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM623 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM623 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37831] GAM624 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM624 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM624 target RNA, herein schematically

represented by GAM2 TARGET RNA into GAM624 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37832] GAM625 RNA, herein schematically represented by GAM3 binds complementarily to a target binding site located in an untranslated region of GAM625 target RNA, herein schematically represented by GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM625 target RNA, herein schematically represented by GAM3 TARGET RNA into GAM625 target protein, herein schematically represented by GAM3 TARGET PROTEIN, both of Fig. 8.

[37833] It is appreciated that specific functions, and accordingly utilities, of GR2749 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2749 gene: GAM623 target protein, GAM624 target protein and GAM625 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM623, GAM624 and GAM625

[37834] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2750(GR2750) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.



- [37835] GR2750 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2750 gene was detected is described hereinabove with reference to Figs. 6-15.
- [37836] GR2750 gene encodes GR2750 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [37837] GR2750 precursor RNA folds spatially, forming GR2750 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2750 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2750 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.
- [37838] GR2750 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM627 precursor RNA and GAM628 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [37839] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX

of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM627 RNA and GAM628 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37840] GAM627 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM627 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM627 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM627 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37841] GAM628 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM628 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM628 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM628 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37842] It is appreciated that specific functions, and accordingly utilities, of GR2750 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2750 gene: GAM627 target

protein and GAM628 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM627 and GAM628

[37843] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2751 (GR2751) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37844] GR2751 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2751 gene was detected is described hereinabove with reference to Figs. 6-15.

[37845] GR2751 gene encodes GR2751 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37846] GR2751 precursor RNA folds spatially, forming GR2751 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2751 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2751 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37847] GR2751 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM635 precursor RNA and GAM636 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37848] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM635 RNA and GAM636 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37849] GAM635 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM635 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM635 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM635 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37850] GAM636 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of

GAM636 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM636 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM636 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37851] It is appreciated that specific functions, and accordingly utilities, of GR2751 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2751 gene: GAM635 target protein and GAM636 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM635 and GAM636

[37852] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2752 (GR2752) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37853] GR2752 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2752 gene was detected is described hereinabove with reference to Figs. 6-15.

[37854] GR2752 gene encodes GR2752 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37855] GR2752 precursor RNA folds spatially, forming GR2752 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2752 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2752 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37856] GR2752 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM655 precursor RNA and GAM656 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37857] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM655 RNA and GAM656 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37858] GAM655 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM655 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM655 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM655 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37859] GAM656 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM656 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM656 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM656 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37860] It is appreciated that specific functions, and accordingly utilities, of GR2752 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2752 gene: GAM655 target protein and GAM656 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM655 and GAM656

- [37861] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2753(GR2753) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [37862] GR2753 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2753 gene was detected is described hereinabove with reference to Figs. 6-15.
- [37863] GR2753 gene encodes GR2753 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [37864] GR2753 precursor RNA folds spatially, forming GR2753 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2753 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2753 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.
- [37865] GR2753 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into



at least 2 separate GAM precursor RNAs, GAM657 precursor RNA and GAM658 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37866] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM657 RNA and GAM658 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37867] GAM657 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM657 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM657 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM657 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37868] GAM658 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM658 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM658 target RNA, herein schematically

represented by GAM2 TARGET RNA into GAM658 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37869] It is appreciated that specific functions, and accordingly utilities, of GR2753 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2753 gene: GAM657 target protein and GAM658 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM657 and GAM658

[37870] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2754 (GR2754) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37871] GR2754 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2754 gene was detected is described hereinabove with reference to Figs. 6-15.

[37872] GR2754 gene encodes GR2754 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37873] GR2754 precursor RNA folds spatially, forming GR2754 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2754 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2754 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37874] GR2754 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM659 precursor RNA, GAM660 precursor RNA and GAM661 precursor RNA, herein schematically represented by GAM1 PRECURSOR, GAM2 PRECURSOR and GAM3 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37875] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM659 RNA, GAM660 RNA and GAM661 RNA respectively, herein schematically represented by GAM1 RNA, GAM2 RNA and GAM3 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37876] GAM659 RNA, herein schematically represented by GAM1 binds

complimentarily to a target binding site located in an untranslated region of GAM659 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM659 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM659 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37877] GAM660 RNA, herein schematically represented by GAM2 binds complimentarily to a target binding site located in an untranslated region of GAM660 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM660 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM660 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37878] GAM661 RNA, herein schematically represented by GAM3 binds complimentarily to a target binding site located in an untranslated region of GAM661 target RNA, herein schematically represented by GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM661 target RNA, herein schematically represented by GAM3 TARGET RNA into GAM661 target protein, herein schematically represented by GAM3 TARGET PROTEIN, both of Fig. 8.

[37879] It is appreciated that specific functions, and accordingly utilities, of GR2754

gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2754 gene: GAM659 target protein, GAM660 target protein and GAM661 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM659, GAM660 and GAM661

[37880] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2755(GR2755) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37881] GR2755 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2755 gene was detected is described hereinabove with reference to Figs. 6-15.

[37882] GR2755 gene encodes GR2755 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37883] GR2755 precursor RNA folds spatially, forming GR2755 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2755 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as

hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2755 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37884] GR2755 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM662 precursor RNA and GAM663 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37885] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM662 RNA and GAM663 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37886] GAM662 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM662 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM662 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM662 target protein, herein

schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37887] GAM663 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM663 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM663 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM663 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37888] It is appreciated that specific functions, and accordingly utilities, of GR2755 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2755 gene: GAM662 target protein and GAM663 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM662 and GAM663

[37889] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2756 (GR2756) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37890] GR2756 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR2756 gene was detected is described hereinabove with reference to Figs. 6-15.

[37891] GR2756 gene encodes GR2756 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37892] GR2756 precursor RNA folds spatially, forming GR2756 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2756 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2756 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37893] GR2756 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM665 precursor RNA and GAM666 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37894] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in



length, GAM665 RNA and GAM666 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37895] GAM665 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM665 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM665 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM665 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37896] GAM666 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM666 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM666 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM666 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37897] It is appreciated that specific functions, and accordingly utilities, of GR2756 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2756 gene: GAM665 target protein and GAM666 target protein, herein schematically represented by

GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM665 and GAM666

[37898] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2757 (GR2757) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37899] GR2757 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2757 gene was detected is described hereinabove with reference to Figs. 6-15.

[37900] GR2757 gene encodes GR2757 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37901] GR2757 precursor RNA folds spatially, forming GR2757 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2757 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2757 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

- [37902] GR2757 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM667 precursor RNA and GAM668 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [37903] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM667 RNA and GAM668 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.
- [37904] GAM667 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM667 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM667 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM667 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.
- [37905] GAM668 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM668 target RNA, herein schematically represented by GAM2 TARGET

RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM668 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM668 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37906] It is appreciated that specific functions, and accordingly utilities, of GR2757 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2757 gene: GAM667 target protein and GAM668 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM667 and GAM668

[37907] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2758 (GR2758) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37908] GR2758 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2758 gene was detected is described hereinabove with reference to Figs. 6-15.

[37909] GR2758 gene encodes GR2758 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37910] GR2758 precursor RNA folds spatially, forming GR2758 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2758 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2758 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37911] GR2758 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM669 precursor RNA and GAM670 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37912] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM669 RNA and GAM670 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37913] GAM669 RNA, herein schematically represented by GAM1 binds

complimentarily to a target binding site located in an untranslated region of GAM669 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM669 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM669 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37914] GAM670 RNA, herein schematically represented by GAM2 binds complimentarily to a target binding site located in an untranslated region of GAM670 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM670 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM670 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37915] It is appreciated that specific functions, and accordingly utilities, of GR2758 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2758 gene: GAM669 target protein and GAM670 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM669 and GAM670

[37916] Fig. 16 further provides a conceptual description of novel bioinformatically

detected regulatory gene, referred to here as Genomic Record 2759(GR2759) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37917] GR2759 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2759 gene was detected is described hereinabove with reference to Figs. 6-15.

[37918] GR2759 gene encodes GR2759 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37919] GR2759 precursor RNA folds spatially, forming GR2759 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2759 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2759 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37920] GR2759 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM673 precursor RNA and

GAM674 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37921] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM673 RNA and GAM674 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37922] GAM673 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM673 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM673 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM673 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37923] GAM674 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM674 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM674 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM674 target protein, herein



schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37924] It is appreciated that specific functions, and accordingly utilities, of GR2759 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2759 gene: GAM673 target protein and GAM674 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM673 and GAM674

[37925] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2760 (GR2760) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37926] GR2760 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2760 gene was detected is described hereinabove with reference to Figs. 6-15.

[37927] GR2760 gene encodes GR2760 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37928] GR2760 precursor RNA folds spatially, forming GR2760 folded precursor

RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2760 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2760 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37929] GR2760 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM675 precursor RNA and GAM676 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37930] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM675 RNA and GAM676 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37931] GAM675 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM675 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM675 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM675 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37932] GAM676 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM676 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM676 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM676 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37933] It is appreciated that specific functions, and accordingly utilities, of GR2760 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2760 gene: GAM675 target protein and GAM676 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM675 and GAM676

[37934] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2761 (GR2761) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

[37935] GR2761 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2761 gene was detected is described hereinabove with reference to Figs. 6-15.

[37936] GR2761 gene encodes GR2761 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37937] GR2761 precursor RNA folds spatially, forming GR2761 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2761 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2761 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37938] GR2761 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM679 precursor RNA, GAM680 precursor RNA and GAM681 precursor RNA, herein schematically represented by GAM1 PRECURSOR, GAM2 PRECURSOR and GAM3 PRECURSOR respectively, each of which GAM precursor RNAs being a

hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37939] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM679 RNA, GAM680 RNA and GAM681 RNA respectively, herein schematically represented by GAM1 RNA, GAM2 RNA and GAM3 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37940] GAM679 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM679 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM679 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM679 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37941] GAM680 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM680 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM680 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM680 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37942] GAM681 RNA, herein schematically represented by GAM3 binds complementarily to a target binding site located in an untranslated region of GAM681 target RNA, herein schematically represented by GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM681 target RNA, herein schematically represented by GAM3 TARGET RNA into GAM681 target protein, herein schematically represented by GAM3 TARGET PROTEIN, both of Fig. 8.

[37943] It is appreciated that specific functions, and accordingly utilities, of GR2761 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2761 gene: GAM679 target protein, GAM680 target protein and GAM681 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM679, GAM680 and GAM681

[37944] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2762(GR2762) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37945] GR2762 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which

GR2762 gene was detected is described hereinabove with reference to Figs. 6-15.

[37946] GR2762 gene encodes GR2762 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37947] GR2762 precursor RNA folds spatially, forming GR2762 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2762 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2762 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37948] GR2762 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM689 precursor RNA and GAM690 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37949] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM689 RNA and GAM690 RNA respectively, herein schematically

represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37950] GAM689 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM689 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM689 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM689 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37951] GAM690 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM690 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM690 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM690 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37952] It is appreciated that specific functions, and accordingly utilities, of GR2762 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2762 gene: GAM689 target protein and GAM690 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The



function of these target genes is elaborated hereinabove with reference to GAM689 and GAM690

- [37953] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2763 (GR2763) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [37954] GR2763 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2763 gene was detected is described hereinabove with reference to Figs. 6-15.
- [37955] GR2763 gene encodes GR2763 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [37956] GR2763 precursor RNA folds spatially, forming GR2763 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2763 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2763 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

- [37957] GR2763 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM691 precursor RNA and GAM692 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [37958] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM691 RNA and GAM692 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.
- [37959] GAM691 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM691 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM691 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM691 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.
- [37960] GAM692 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM692 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM692 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM692 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37961] It is appreciated that specific functions, and accordingly utilities, of GR2763 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2763 gene: GAM691 target protein and GAM692 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM691 and GAM692

[37962] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2764 (GR2764) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37963] GR2764 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2764 gene was detected is described hereinabove with reference to Figs. 6-15.

[37964] GR2764 gene encodes GR2764 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides

long.

[37965] GR2764 precursor RNA folds spatially, forming GR2764 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2764 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2764 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37966] GR2764 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM694 precursor RNA, GAM695 precursor RNA, GAM696 precursor RNA and GAM697 precursor RNA, herein schematically represented by GAM1 PRECURSOR, GAM2 PRECURSOR, GAM3 PRECURSOR and GAM4 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37967] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM694 RNA, GAM695 RNA, GAM696 RNA and GAM697 RNA respectively, herein schematically represented by GAM1 RNA, GAM2 RNA, GAM3 RNA and GAM4 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37968] GAM694 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM694 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM694 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM694 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37969] GAM695 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM695 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM695 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM695 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37970] GAM696 RNA, herein schematically represented by GAM3 binds complementarily to a target binding site located in an untranslated region of GAM696 target RNA, herein schematically represented by GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM696 target RNA, herein schematically represented by GAM3 TARGET RNA into GAM696 target protein, herein schematically represented by GAM3 TARGET PROTEIN, both of Fig. 8.

[37971] GAM697 RNA, herein schematically represented by GAM4 binds complementarily to a target binding site located in an untranslated region of GAM697 target RNA, herein schematically represented by GAM4 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM697 target RNA, herein schematically represented by GAM4 TARGET RNA into GAM697 target protein, herein schematically represented by GAM4 TARGET PROTEIN, both of Fig. 8.

[37972] It is appreciated that specific functions, and accordingly utilities, of GR2764 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2764 gene: GAM694 target protein, GAM695 target protein, GAM696 target protein and GAM697 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM694, GAM695, GAM696 and GAM697

[37973] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2765(GR2765) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37974] GR2765 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR2765 gene was detected is described hereinabove with reference to Figs. 6-15.

[37975] GR2765 gene encodes GR2765 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37976] GR2765 precursor RNA folds spatially, forming GR2765 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2765 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2765 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37977] GR2765 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM702 precursor RNA and GAM703 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37978] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in

length, GAM702 RNA and GAM703 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37979] GAM702 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM702 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM702 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM702 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37980] GAM703 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM703 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM703 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM703 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37981] It is appreciated that specific functions, and accordingly utilities, of GR2765 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2765 gene: GAM702 target protein and GAM703 target protein, herein schematically represented by



GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM702 and GAM703

- [37982] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2766 (GR2766) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [37983] GR2766 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2766 gene was detected is described hereinabove with reference to Figs. 6-15.
- [37984] GR2766 gene encodes GR2766 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [37985] GR2766 precursor RNA folds spatially, forming GR2766 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2766 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2766 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

- [37986] GR2766 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM709 precursor RNA and GAM710 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [37987] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM709 RNA and GAM710 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.
- [37988] GAM709 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM709 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM709 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM709 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.
- [37989] GAM710 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM710 target RNA, herein schematically represented by GAM2 TARGET

RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM710 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM710 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37990] It is appreciated that specific functions, and accordingly utilities, of GR2766 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2766 gene: GAM709 target protein and GAM710 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM709 and GAM710

[37991] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2767 (GR2767) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[37992] GR2767 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2767 gene was detected is described hereinabove with reference to Figs. 6-15.

[37993] GR2767 gene encodes GR2767 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[37994] GR2767 precursor RNA folds spatially, forming GR2767 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2767 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2767 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[37995] GR2767 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM722 precursor RNA and GAM723 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[37996] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM722 RNA and GAM723 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[37997] GAM722 RNA, herein schematically represented by GAM1 binds

complimentarily to a target binding site located in an untranslated region of GAM722 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM722 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM722 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[37998] GAM723 RNA, herein schematically represented by GAM2 binds complimentarily to a target binding site located in an untranslated region of GAM723 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM723 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM723 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[37999] It is appreciated that specific functions, and accordingly utilities, of GR2767 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2767 gene: GAM722 target protein and GAM723 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM722 and GAM723

[38000] Fig. 16 further provides a conceptual description of novel bioinformatically

detected regulatory gene, referred to here as Genomic Record 2768(GR2768) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38001] GR2768 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2768 gene was detected is described hereinabove with reference to Figs. 6-15.

[38002] GR2768 gene encodes GR2768 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38003] GR2768 precursor RNA folds spatially, forming GR2768 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2768 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2768 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38004] GR2768 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM724 precursor RNA and

GAM725 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38005] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM724 RNA and GAM725 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38006] GAM724 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM724 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM724 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM724 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38007] GAM725 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM725 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM725 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM725 target protein, herein

schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38008] It is appreciated that specific functions, and accordingly utilities, of GR2768 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2768 gene: GAM724 target protein and GAM725 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM724 and GAM725

[38009] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2769 (GR2769) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38010] GR2769 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2769 gene was detected is described hereinabove with reference to Figs. 6-15.

[38011] GR2769 gene encodes GR2769 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38012] GR2769 precursor RNA folds spatially, forming GR2769 folded precursor



RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2769 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2769 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38013] GR2769 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM730 precursor RNA and GAM731 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38014] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM730 RNA and GAM731 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38015] GAM730 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM730 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM730 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM730 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38016] GAM731 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM731 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM731 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM731 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38017] It is appreciated that specific functions, and accordingly utilities, of GR2769 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2769 gene: GAM730 target protein and GAM731 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM730 and GAM731

[38018] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2770 (GR2770) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

[38019] GR2770 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2770 gene was detected is described hereinabove with reference to Figs. 6-15.

[38020] GR2770 gene encodes GR2770 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38021] GR2770 precursor RNA folds spatially, forming GR2770 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2770 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2770 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38022] GR2770 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM734 precursor RNA and GAM735 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to

GAM PRECURSOR RNA of Fig. 8.

[38023] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM734 RNA and GAM735 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38024] GAM734 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM734 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM734 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM734 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38025] GAM735 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM735 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM735 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM735 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38026] It is appreciated that specific functions, and accordingly utilities, of GR2770 gene, herein designated GR GENE, correlate with, and may be deduced

from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2770 gene: GAM734 target protein and GAM735 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM734 and GAM735

[38027] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2771 (GR2771) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38028] GR2771 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2771 gene was detected is described hereinabove with reference to Figs. 6-15.

[38029] GR2771 gene encodes GR2771 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38030] GR2771 precursor RNA folds spatially, forming GR2771 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2771 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the

nucleotide sequence of GR2771 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

- [38031] GR2771 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM739 precursor RNA and GAM740 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [38032] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM739 RNA and GAM740 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.
- [38033] GAM739 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM739 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM739 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM739 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38034] GAM740 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM740 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM740 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM740 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38035] It is appreciated that specific functions, and accordingly utilities, of GR2771 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2771 gene: GAM739 target protein and GAM740 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM739 and GAM740

[38036] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2772 (GR2772) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38037] GR2772 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which

GR2772 gene was detected is described hereinabove with reference to Figs. 6-15.

[38038] GR2772 gene encodes GR2772 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38039] GR2772 precursor RNA folds spatially, forming GR2772 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2772 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2772 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38040] GR2772 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM745 precursor RNA and GAM746 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38041] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM745 RNA and GAM746 RNA respectively, herein schematically



represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38042] GAM745 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM745 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM745 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM745 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38043] GAM746 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM746 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM746 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM746 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38044] It is appreciated that specific functions, and accordingly utilities, of GR2772 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2772 gene: GAM745 target protein and GAM746 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The

function of these target genes is elaborated hereinabove with reference to GAM745 and GAM746

- [38045] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2773(GR2773) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [38046] GR2773 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2773 gene was detected is described hereinabove with reference to Figs. 6-15.
- [38047] GR2773 gene encodes GR2773 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [38048] GR2773 precursor RNA folds spatially, forming GR2773 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2773 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2773 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38049] GR2773 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM750 precursor RNA and GAM751 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38050] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM750 RNA and GAM751 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38051] GAM750 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM750 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM750 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM750 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38052] GAM751 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM751 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM751 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM751 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38053] It is appreciated that specific functions, and accordingly utilities, of GR2773 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2773 gene: GAM750 target protein and GAM751 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM750 and GAM751

[38054] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2774 (GR2774) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38055] GR2774 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2774 gene was detected is described hereinabove with reference to Figs. 6-15.

[38056] GR2774 gene encodes GR2774 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides

long.

[38057] GR2774 precursor RNA folds spatially, forming GR2774 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2774 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2774 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38058] GR2774 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM755 precursor RNA, GAM756 precursor RNA and GAM757 precursor RNA, herein schematically represented by GAM1 PRECURSOR, GAM2 PRECURSOR and GAM3 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38059] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM755 RNA, GAM756 RNA and GAM757 RNA respectively, herein schematically represented by GAM1 RNA, GAM2 RNA and GAM3 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38060] GAM755 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM755 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM755 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM755 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38061] GAM756 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM756 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM756 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM756 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38062] GAM757 RNA, herein schematically represented by GAM3 binds complementarily to a target binding site located in an untranslated region of GAM757 target RNA, herein schematically represented by GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM757 target RNA, herein schematically represented by GAM3 TARGET RNA into GAM757 target protein, herein schematically represented by GAM3 TARGET PROTEIN, both of Fig. 8.

[38063] It is appreciated that specific functions, and accordingly utilities, of GR2774 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2774 gene: GAM755 target protein, GAM756 target protein and GAM757 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM755, GAM756 and GAM757

[38064] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2775(GR2775) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38065] GR2775 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2775 gene was detected is described hereinabove with reference to Figs. 6-15.

[38066] GR2775 gene encodes GR2775 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38067] GR2775 precursor RNA folds spatially, forming GR2775 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2775 folded precursor RNA, herein designated GR FOLDED

PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2775 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38068] GR2775 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM763 precursor RNA, GAM764 precursor RNA and GAM765 precursor RNA, herein schematically represented by GAM1 PRECURSOR, GAM2 PRECURSOR and GAM3 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38069] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM763 RNA, GAM764 RNA and GAM765 RNA respectively, herein schematically represented by GAM1 RNA, GAM2 RNA and GAM3 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38070] GAM763 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM763 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as



BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM763 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM763 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38071] GAM764 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM764 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM764 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM764 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38072] GAM765 RNA, herein schematically represented by GAM3 binds complementarily to a target binding site located in an untranslated region of GAM765 target RNA, herein schematically represented by GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM765 target RNA, herein schematically represented by GAM3 TARGET RNA into GAM765 target protein, herein schematically represented by GAM3 TARGET PROTEIN, both of Fig. 8.

[38073] It is appreciated that specific functions, and accordingly utilities, of GR2775 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2775 gene: GAM763 target

protein, GAM764 target protein and GAM765 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM763, GAM764 and GAM765

[38074] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2776(GR2776) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38075] GR2776 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2776 gene was detected is described hereinabove with reference to Figs. 6-15.

[38076] GR2776 gene encodes GR2776 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38077] GR2776 precursor RNA folds spatially, forming GR2776 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2776 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2776 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38078] GR2776 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM766 precursor RNA, GAM767 precursor RNA, GAM768 precursor RNA and GAM769 precursor RNA, herein schematically represented by GAM1 PRECURSOR, GAM2 PRECURSOR, GAM3 PRECURSOR and GAM4 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38079] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM766 RNA, GAM767 RNA, GAM768 RNA and GAM769 RNA respectively, herein schematically represented by GAM1 RNA, GAM2 RNA, GAM3 RNA and GAM4 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38080] GAM766 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM766 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM766 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM766 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38081] GAM767 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM767 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM767 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM767 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38082] GAM768 RNA, herein schematically represented by GAM3 binds complementarily to a target binding site located in an untranslated region of GAM768 target RNA, herein schematically represented by GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM768 target RNA, herein schematically represented by GAM3 TARGET RNA into GAM768 target protein, herein schematically represented by GAM3 TARGET PROTEIN, both of Fig. 8.

[38083] GAM769 RNA, herein schematically represented by GAM4 binds complementarily to a target binding site located in an untranslated region of GAM769 target RNA, herein schematically represented by GAM4 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM769 target RNA, herein schematically represented by GAM4 TARGET RNA into GAM769 target protein, herein schematically represented by GAM4 TARGET PROTEIN, both of Fig. 8.

[38084] It is appreciated that specific functions, and accordingly utilities, of GR2776 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2776 gene: GAM766 target protein, GAM767 target protein, GAM768 target protein and GAM769 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM766, GAM767, GAM768 and GAM769

[38085] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2777(GR2777) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38086] GR2777 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2777 gene was detected is described hereinabove with reference to Figs. 6-15.

[38087] GR2777 gene encodes GR2777 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38088] GR2777 precursor RNA folds spatially, forming GR2777 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated

that GR2777 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2777 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38089] GR2777 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM775 precursor RNA, GAM776 precursor RNA and GAM777 precursor RNA, herein schematically represented by GAM1 PRECURSOR, GAM2 PRECURSOR and GAM3 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38090] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM775 RNA, GAM776 RNA and GAM777 RNA respectively, herein schematically represented by GAM1 RNA, GAM2 RNA and GAM3 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38091] GAM775 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM775 target RNA, herein schematically represented by GAM1 TARGET

RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM775 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM775 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38092] GAM776 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM776 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM776 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM776 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38093] GAM777 RNA, herein schematically represented by GAM3 binds complementarily to a target binding site located in an untranslated region of GAM777 target RNA, herein schematically represented by GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM777 target RNA, herein schematically represented by GAM3 TARGET RNA into GAM777 target protein, herein schematically represented by GAM3 TARGET PROTEIN, both of Fig. 8.

[38094] It is appreciated that specific functions, and accordingly utilities, of GR2777 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs

comprised in the operon-like cluster of GR2777 gene: GAM775 target protein, GAM776 target protein and GAM777 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM775, GAM776 and GAM777

[38095] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2778(GR2778) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38096] GR2778 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2778 gene was detected is described hereinabove with reference to Figs. 6-15.

[38097] GR2778 gene encodes GR2778 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38098] GR2778 precursor RNA folds spatially, forming GR2778 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2778 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2778 precursor RNA comprises a plurality of



segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38099] GR2778 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM783 precursor RNA and GAM784 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38100] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM783 RNA and GAM784 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38101] GAM783 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM783 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM783 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM783 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38102] GAM784 RNA, herein schematically represented by GAM2 binds

complimentarily to a target binding site located in an untranslated region of GAM784 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM784 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM784 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38103] It is appreciated that specific functions, and accordingly utilities, of GR2778 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2778 gene: GAM783 target protein and GAM784 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM783 and GAM784

[38104] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2779 (GR2779) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38105] GR2779 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2779 gene was detected is described hereinabove with reference to Figs.

- [38106] GR2779 gene encodes GR2779 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [38107] GR2779 precursor RNA folds spatially, forming GR2779 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2779 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2779 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.
- [38108] GR2779 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM788 precursor RNA and GAM789 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [38109] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM788 RNA and GAM789 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which

GAM RNAs corresponding to GAM RNA of Fig. 8.

[38110] GAM788 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM788 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM788 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM788 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38111] GAM789 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM789 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM789 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM789 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38112] It is appreciated that specific functions, and accordingly utilities, of GR2779 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2779 gene: GAM788 target protein and GAM789 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to

- [38113] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2780 (GR2780) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [38114] GR2780 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2780 gene was detected is described hereinabove with reference to Figs. 6-15.
- [38115] GR2780 gene encodes GR2780 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [38116] GR2780 precursor RNA folds spatially, forming GR2780 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2780 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2780 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

- [38117] GR2780 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM798 precursor RNA and GAM799 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [38118] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM798 RNA and GAM799 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.
- [38119] GAM798 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM798 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM798 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM798 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.
- [38120] GAM799 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM799 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM799 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM799 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38121] It is appreciated that specific functions, and accordingly utilities, of GR2780 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2780 gene: GAM798 target protein and GAM799 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM798 and GAM799

[38122] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2781 (GR2781) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38123] GR2781 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2781 gene was detected is described hereinabove with reference to Figs. 6-15.

[38124] GR2781 gene encodes GR2781 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides

long.

[38125] GR2781 precursor RNA folds spatially, forming GR2781 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2781 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2781 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38126] GR2781 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM805 precursor RNA and GAM806 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38127] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM805 RNA and GAM806 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38128] GAM805 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of



GAM805 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM805 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM805 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38129] GAM806 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM806 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM806 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM806 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38130] It is appreciated that specific functions, and accordingly utilities, of GR2781 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2781 gene: GAM805 target protein and GAM806 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM805 and GAM806

[38131] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record

2782(GR2782) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38132] GR2782 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2782 gene was detected is described hereinabove with reference to Figs. 6-15.

[38133] GR2782 gene encodes GR2782 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38134] GR2782 precursor RNA folds spatially, forming GR2782 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2782 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2782 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38135] GR2782 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM816 precursor RNA, GAM817 precursor RNA, GAM818 precursor RNA and GAM819 precursor

RNA, herein schematically represented by GAM1 PRECURSOR, GAM2 PRECURSOR, GAM3 PRECURSOR and GAM4 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38136] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM816 RNA, GAM817 RNA, GAM818 RNA and GAM819 RNA respectively, herein schematically represented by GAM1 RNA, GAM2 RNA, GAM3 RNA and GAM4 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38137] GAM816 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM816 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM816 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM816 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38138] GAM817 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM817 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM817 target RNA, herein schematically

represented by GAM2 TARGET RNA into GAM817 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38139] GAM818 RNA, herein schematically represented by GAM3 binds complementarily to a target binding site located in an untranslated region of GAM818 target RNA, herein schematically represented by GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM818 target RNA, herein schematically represented by GAM3 TARGET RNA into GAM818 target protein, herein schematically represented by GAM3 TARGET PROTEIN, both of Fig. 8.

[38140] GAM819 RNA, herein schematically represented by GAM4 binds complementarily to a target binding site located in an untranslated region of GAM819 target RNA, herein schematically represented by GAM4 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM819 target RNA, herein schematically represented by GAM4 TARGET RNA into GAM819 target protein, herein schematically represented by GAM4 TARGET PROTEIN, both of Fig. 8.

[38141] It is appreciated that specific functions, and accordingly utilities, of GR2782 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2782 gene: GAM816 target protein, GAM817 target protein, GAM818 target protein and GAM819 target protein, herein schematically represented by GAM1 TARGET PROTEIN

through GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM816, GAM817, GAM818 and GAM819

- [38142] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2783(GR2783) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [38143] GR2783 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2783 gene was detected is described hereinabove with reference to Figs. 6-15.
- [38144] GR2783 gene encodes GR2783 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [38145] GR2783 precursor RNA folds spatially, forming GR2783 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2783 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2783 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

- [38146] GR2783 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM824 precursor RNA and GAM825 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [38147] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM824 RNA and GAM825 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.
- [38148] GAM824 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM824 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM824 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM824 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.
- [38149] GAM825 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM825 target RNA, herein schematically represented by GAM2 TARGET

RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM825 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM825 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38150] It is appreciated that specific functions, and accordingly utilities, of GR2783 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2783 gene: GAM824 target protein and GAM825 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM824 and GAM825

[38151] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2784 (GR2784) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38152] GR2784 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2784 gene was detected is described hereinabove with reference to Figs. 6-15.

[38153] GR2784 gene encodes GR2784 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38154] GR2784 precursor RNA folds spatially, forming GR2784 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2784 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2784 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38155] GR2784 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM831 precursor RNA and GAM832 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38156] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM831 RNA and GAM832 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38157] GAM831 RNA, herein schematically represented by GAM1 binds



complimentarily to a target binding site located in an untranslated region of GAM831 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM831 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM831 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38158] GAM832 RNA, herein schematically represented by GAM2 binds complimentarily to a target binding site located in an untranslated region of GAM832 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM832 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM832 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38159] It is appreciated that specific functions, and accordingly utilities, of GR2784 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2784 gene: GAM831 target protein and GAM832 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM831 and GAM832

[38160] Fig. 16 further provides a conceptual description of novel bioinformatically

detected regulatory gene, referred to here as Genomic Record 2785(GR2785) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38161] GR2785 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2785 gene was detected is described hereinabove with reference to Figs. 6-15.

[38162] GR2785 gene encodes GR2785 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38163] GR2785 precursor RNA folds spatially, forming GR2785 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2785 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2785 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38164] GR2785 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM835 precursor RNA and

GAM836 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38165] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM835 RNA and GAM836 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38166] GAM835 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM835 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM835 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM835 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38167] GAM836 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM836 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM836 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM836 target protein, herein

schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38168] It is appreciated that specific functions, and accordingly utilities, of GR2785 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2785 gene: GAM835 target protein and GAM836 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM835 and GAM836

[38169] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2786 (GR2786) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38170] GR2786 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2786 gene was detected is described hereinabove with reference to Figs. 6-15.

[38171] GR2786 gene encodes GR2786 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38172] GR2786 precursor RNA folds spatially, forming GR2786 folded precursor

RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2786 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2786 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38173] GR2786 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM841 precursor RNA, GAM842 precursor RNA and GAM843 precursor RNA, herein schematically represented by GAM1 PRECURSOR, GAM2 PRECURSOR and GAM3 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38174] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM841 RNA, GAM842 RNA and GAM843 RNA respectively, herein schematically represented by GAM1 RNA, GAM2 RNA and GAM3 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38175] GAM841 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of

GAM841 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM841 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM841 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38176] GAM842 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM842 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM842 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM842 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38177] GAM843 RNA, herein schematically represented by GAM3 binds complementarily to a target binding site located in an untranslated region of GAM843 target RNA, herein schematically represented by GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM843 target RNA, herein schematically represented by GAM3 TARGET RNA into GAM843 target protein, herein schematically represented by GAM3 TARGET PROTEIN, both of Fig. 8.

[38178] It is appreciated that specific functions, and accordingly utilities, of GR2786 gene, herein designated GR GENE, correlate with, and may be deduced

from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2786 gene: GAM841 target protein, GAM842 target protein and GAM843 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM841, GAM842 and GAM843

[38179] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2787(GR2787) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38180] GR2787 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2787 gene was detected is described hereinabove with reference to Figs. 6-15.

[38181] GR2787 gene encodes GR2787 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38182] GR2787 precursor RNA folds spatially, forming GR2787 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2787 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the

nucleotide sequence of GR2787 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

- [38183] GR2787 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM845 precursor RNA and GAM846 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [38184] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM845 RNA and GAM846 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.
- [38185] GAM845 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM845 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM845 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM845 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.



[38186] GAM846 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM846 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM846 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM846 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38187] It is appreciated that specific functions, and accordingly utilities, of GR2787 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2787 gene: GAM845 target protein and GAM846 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM845 and GAM846

[38188] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2788 (GR2788) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38189] GR2788 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which

GR2788 gene was detected is described hereinabove with reference to Figs. 6-15.

[38190] GR2788 gene encodes GR2788 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38191] GR2788 precursor RNA folds spatially, forming GR2788 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2788 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2788 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38192] GR2788 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM858 precursor RNA and GAM859 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38193] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM858 RNA and GAM859 RNA respectively, herein schematically

represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38194] GAM858 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM858 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM858 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM858 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38195] GAM859 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM859 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM859 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM859 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38196] It is appreciated that specific functions, and accordingly utilities, of GR2788 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2788 gene: GAM858 target protein and GAM859 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The

function of these target genes is elaborated hereinabove with reference to GAM858 and GAM859

- [38197] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2789 (GR2789) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [38198] GR2789 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2789 gene was detected is described hereinabove with reference to Figs. 6-15.
- [38199] GR2789 gene encodes GR2789 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [38200] GR2789 precursor RNA folds spatially, forming GR2789 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2789 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2789 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

- [38201] GR2789 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM860 precursor RNA, GAM861 precursor RNA and GAM862 precursor RNA, herein schematically represented by GAM1 PRECURSOR, GAM2 PRECURSOR and GAM3 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [38202] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM860 RNA, GAM861 RNA and GAM862 RNA respectively, herein schematically represented by GAM1 RNA, GAM2 RNA and GAM3 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.
- [38203] GAM860 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM860 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM860 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM860 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.
- [38204] GAM861 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of

GAM861 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM861 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM861 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38205] GAM862 RNA, herein schematically represented by GAM3 binds complementarily to a target binding site located in an untranslated region of GAM862 target RNA, herein schematically represented by GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM862 target RNA, herein schematically represented by GAM3 TARGET RNA into GAM862 target protein, herein schematically represented by GAM3 TARGET PROTEIN, both of Fig. 8.

[38206] It is appreciated that specific functions, and accordingly utilities, of GR2789 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2789 gene: GAM860 target protein, GAM861 target protein and GAM862 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM860, GAM861 and GAM862

[38207] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record

2790(GR2790) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38208] GR2790 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2790 gene was detected is described hereinabove with reference to Figs. 6-15.

[38209] GR2790 gene encodes GR2790 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38210] GR2790 precursor RNA folds spatially, forming GR2790 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2790 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2790 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38211] GR2790 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM864 precursor RNA and GAM865 precursor RNA, herein schematically represented by GAM1

PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38212] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM864 RNA and GAM865 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38213] GAM864 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM864 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM864 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM864 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38214] GAM865 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM865 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM865 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM865 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.



[38215] It is appreciated that specific functions, and accordingly utilities, of GR2790 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2790 gene: GAM864 target protein and GAM865 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM864 and GAM865

[38216] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2791 (GR2791) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38217] GR2791 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2791 gene was detected is described hereinabove with reference to Figs. 6-15.

[38218] GR2791 gene encodes GR2791 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38219] GR2791 precursor RNA folds spatially, forming GR2791 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2791 folded precursor RNA, herein designated GR FOLDED

PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2791 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38220] GR2791 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM872 precursor RNA and GAM873 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38221] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM872 RNA and GAM873 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38222] GAM872 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM872 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM872 target RNA, herein schematically

represented by GAM1 TARGET RNA into GAM872 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38223] GAM873 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM873 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM873 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM873 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38224] It is appreciated that specific functions, and accordingly utilities, of GR2791 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2791 gene: GAM872 target protein and GAM873 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM872 and GAM873

[38225] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2792 (GR2792) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38226] GR2792 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2792 gene was detected is described hereinabove with reference to Figs. 6-15.

[38227] GR2792 gene encodes GR2792 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38228] GR2792 precursor RNA folds spatially, forming GR2792 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2792 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2792 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38229] GR2792 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM876 precursor RNA, GAM877 precursor RNA and GAM878 precursor RNA, herein schematically represented by GAM1 PRECURSOR, GAM2 PRECURSOR and GAM3 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38230] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM876 RNA, GAM877 RNA and GAM878 RNA respectively, herein schematically represented by GAM1 RNA, GAM2 RNA and GAM3 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38231] GAM876 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM876 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM876 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM876 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38232] GAM877 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM877 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM877 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM877 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38233] GAM878 RNA, herein schematically represented by GAM3 binds complementarily to a target binding site located in an untranslated region of

GAM878 target RNA, herein schematically represented by GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM878 target RNA, herein schematically represented by GAM3 TARGET RNA into GAM878 target protein, herein schematically represented by GAM3 TARGET PROTEIN, both of Fig. 8.

[38234] It is appreciated that specific functions, and accordingly utilities, of GR2792 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2792 gene: GAM876 target protein, GAM877 target protein and GAM878 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM876, GAM877 and GAM878

[38235] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2793(GR2793) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38236] GR2793 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2793 gene was detected is described hereinabove with reference to Figs. 6-15.

[38237] GR2793 gene encodes GR2793 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38238] GR2793 precursor RNA folds spatially, forming GR2793 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2793 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2793 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38239] GR2793 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM882 precursor RNA and GAM883 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38240] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM882 RNA and GAM883 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38241] GAM882 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM882 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM882 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM882 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38242] GAM883 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM883 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM883 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM883 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38243] It is appreciated that specific functions, and accordingly utilities, of GR2793 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2793 gene: GAM882 target protein and GAM883 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM882 and GAM883



- [38244] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2794(GR2794) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [38245] GR2794 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2794 gene was detected is described hereinabove with reference to Figs. 6-15.
- [38246] GR2794 gene encodes GR2794 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [38247] GR2794 precursor RNA folds spatially, forming GR2794 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2794 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2794 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.
- [38248] GR2794 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into

at least 2 separate GAM precursor RNAs, GAM890 precursor RNA and GAM891 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38249] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM890 RNA and GAM891 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38250] GAM890 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM890 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM890 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM890 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38251] GAM891 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM891 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM891 target RNA, herein schematically

represented by GAM2 TARGET RNA into GAM891 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38252] It is appreciated that specific functions, and accordingly utilities, of GR2794 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2794 gene: GAM890 target protein and GAM891 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM890 and GAM891

[38253] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2795 (GR2795) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38254] GR2795 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2795 gene was detected is described hereinabove with reference to Figs. 6-15.

[38255] GR2795 gene encodes GR2795 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38256] GR2795 precursor RNA folds spatially, forming GR2795 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2795 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2795 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38257] GR2795 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM894 precursor RNA and GAM895 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38258] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM894 RNA and GAM895 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38259] GAM894 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM894 target RNA, herein schematically represented by GAM1 TARGET

RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM894 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM894 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38260] GAM895 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM895 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM895 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM895 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38261] It is appreciated that specific functions, and accordingly utilities, of GR2795 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2795 gene: GAM894 target protein and GAM895 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM894 and GAM895

[38262] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2796(GR2796) gene, which encodes an operon-like cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38263] GR2796 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2796 gene was detected is described hereinabove with reference to Figs. 6-15.

[38264] GR2796 gene encodes GR2796 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38265] GR2796 precursor RNA folds spatially, forming GR2796 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2796 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2796 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38266] GR2796 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM901 precursor RNA and GAM902 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM

precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38267] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM901 RNA and GAM902 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38268] GAM901 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM901 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM901 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM901 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38269] GAM902 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM902 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM902 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM902 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38270] It is appreciated that specific functions, and accordingly utilities, of GR2796

gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2796 gene: GAM901 target protein and GAM902 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM901 and GAM902

[38271] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2797 (GR2797) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38272] GR2797 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2797 gene was detected is described hereinabove with reference to Figs. 6-15.

[38273] GR2797 gene encodes GR2797 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38274] GR2797 precursor RNA folds spatially, forming GR2797 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2797 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as



hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2797 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38275] GR2797 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM909 precursor RNA and GAM910 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38276] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM909 RNA and GAM910 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38277] GAM909 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM909 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM909 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM909 target protein, herein

schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38278] GAM910 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM910 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM910 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM910 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38279] It is appreciated that specific functions, and accordingly utilities, of GR2797 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2797 gene: GAM909 target protein and GAM910 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM909 and GAM910

[38280] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2798 (GR2798) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38281] GR2798 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR2798 gene was detected is described hereinabove with reference to Figs. 6-15.

[38282] GR2798 gene encodes GR2798 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38283] GR2798 precursor RNA folds spatially, forming GR2798 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2798 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2798 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38284] GR2798 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM911 precursor RNA and GAM912 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38285] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in

length, GAM911 RNA and GAM912 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38286] GAM911 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM911 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM911 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM911 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38287] GAM912 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM912 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM912 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM912 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38288] It is appreciated that specific functions, and accordingly utilities, of GR2798 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2798 gene: GAM911 target protein and GAM912 target protein, herein schematically represented by

GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM911 and GAM912

- [38289] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2799 (GR2799) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [38290] GR2799 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2799 gene was detected is described hereinabove with reference to Figs. 6-15.
- [38291] GR2799 gene encodes GR2799 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [38292] GR2799 precursor RNA folds spatially, forming GR2799 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2799 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2799 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

- [38293] GR2799 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM917 precursor RNA and GAM918 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [38294] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM917 RNA and GAM918 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.
- [38295] GAM917 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM917 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM917 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM917 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.
- [38296] GAM918 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM918 target RNA, herein schematically represented by GAM2 TARGET

RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM918 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM918 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38297] It is appreciated that specific functions, and accordingly utilities, of GR2799 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2799 gene: GAM917 target protein and GAM918 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM917 and GAM918

[38298] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2800 (GR2800) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38299] GR2800 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2800 gene was detected is described hereinabove with reference to Figs. 6-15.

[38300] GR2800 gene encodes GR2800 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38301] GR2800 precursor RNA folds spatially, forming GR2800 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2800 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2800 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38302] GR2800 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM932 precursor RNA and GAM933 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38303] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM932 RNA and GAM933 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38304] GAM932 RNA, herein schematically represented by GAM1 binds



complimentarily to a target binding site located in an untranslated region of GAM932 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM932 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM932 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38305] GAM933 RNA, herein schematically represented by GAM2 binds complimentarily to a target binding site located in an untranslated region of GAM933 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM933 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM933 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38306] It is appreciated that specific functions, and accordingly utilities, of GR2800 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2800 gene: GAM932 target protein and GAM933 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM932 and GAM933

[38307] Fig. 16 further provides a conceptual description of novel bioinformatically

detected regulatory gene, referred to here as Genomic Record

2801(GR2801) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38308] GR2801 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2801 gene was detected is described hereinabove with reference to Figs. 6-15.

[38309] GR2801 gene encodes GR2801 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38310] GR2801 precursor RNA folds spatially, forming GR2801 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2801 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2801 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38311] GR2801 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM934 precursor RNA and

GAM935 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38312] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM934 RNA and GAM935 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38313] GAM934 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM934 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM934 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM934 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38314] GAM935 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM935 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM935 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM935 target protein, herein

schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38315] It is appreciated that specific functions, and accordingly utilities, of GR2801 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2801 gene: GAM934 target protein and GAM935 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM934 and GAM935

[38316] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2802 (GR2802) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38317] GR2802 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2802 gene was detected is described hereinabove with reference to Figs. 6-15.

[38318] GR2802 gene encodes GR2802 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38319] GR2802 precursor RNA folds spatially, forming GR2802 folded precursor

RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2802 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2802 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38320] GR2802 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM942 precursor RNA and GAM943 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38321] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM942 RNA and GAM943 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38322] GAM942 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM942 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM942 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM942 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38323] GAM943 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM943 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM943 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM943 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38324] It is appreciated that specific functions, and accordingly utilities, of GR2802 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2802 gene: GAM942 target protein and GAM943 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM942 and GAM943

[38325] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2803 (GR2803) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

[38326] GR2803 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2803 gene was detected is described hereinabove with reference to Figs. 6-15.

[38327] GR2803 gene encodes GR2803 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38328] GR2803 precursor RNA folds spatially, forming GR2803 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2803 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2803 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38329] GR2803 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM950 precursor RNA and GAM951 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to

GAM PRECURSOR RNA of Fig. 8.

[38330] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM950 RNA and GAM951 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38331] GAM950 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM950 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM950 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM950 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38332] GAM951 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM951 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM951 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM951 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38333] It is appreciated that specific functions, and accordingly utilities, of GR2803 gene, herein designated GR GENE, correlate with, and may be deduced



from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2803 gene: GAM950 target protein and GAM951 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM950 and GAM951

[38334] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2804 (GR2804) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38335] GR2804 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2804 gene was detected is described hereinabove with reference to Figs. 6-15.

[38336] GR2804 gene encodes GR2804 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38337] GR2804 precursor RNA folds spatially, forming GR2804 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2804 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the

nucleotide sequence of GR2804 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38338] GR2804 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM953 precursor RNA and GAM954 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38339] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM953 RNA and GAM954 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38340] GAM953 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM953 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM953 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM953 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38341] GAM954 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM954 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM954 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM954 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38342] It is appreciated that specific functions, and accordingly utilities, of GR2804 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2804 gene: GAM953 target protein and GAM954 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM953 and GAM954

[38343] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2805 (GR2805) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38344] GR2805 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which

GR2805 gene was detected is described hereinabove with reference to Figs. 6-15.

[38345] GR2805 gene encodes GR2805 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38346] GR2805 precursor RNA folds spatially, forming GR2805 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2805 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2805 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38347] GR2805 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM957 precursor RNA and GAM958 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38348] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM957 RNA and GAM958 RNA respectively, herein schematically

represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38349] GAM957 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM957 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM957 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM957 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38350] GAM958 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM958 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM958 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM958 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38351] It is appreciated that specific functions, and accordingly utilities, of GR2805 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2805 gene: GAM957 target protein and GAM958 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The

function of these target genes is elaborated hereinabove with reference to GAM957 and GAM958

- [38352] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2806 (GR2806) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [38353] GR2806 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2806 gene was detected is described hereinabove with reference to Figs. 6-15.
- [38354] GR2806 gene encodes GR2806 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [38355] GR2806 precursor RNA folds spatially, forming GR2806 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2806 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2806 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

- [38356] GR2806 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM965 precursor RNA and GAM966 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [38357] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM965 RNA and GAM966 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.
- [38358] GAM965 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM965 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM965 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM965 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.
- [38359] GAM966 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM966 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM966 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM966 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38360] It is appreciated that specific functions, and accordingly utilities, of GR2806 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2806 gene: GAM965 target protein and GAM966 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM965 and GAM966

[38361] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2807 (GR2807) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38362] GR2807 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2807 gene was detected is described hereinabove with reference to Figs. 6-15.

[38363] GR2807 gene encodes GR2807 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides



long.

[38364] GR2807 precursor RNA folds spatially, forming GR2807 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2807 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2807 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38365] GR2807 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM969 precursor RNA and GAM970 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38366] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM969 RNA and GAM970 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38367] GAM969 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of

GAM969 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM969 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM969 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38368] GAM970 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM970 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM970 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM970 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38369] It is appreciated that specific functions, and accordingly utilities, of GR2807 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2807 gene: GAM969 target protein and GAM970 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM969 and GAM970

[38370] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record

2808(GR2808) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38371] GR2808 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2808 gene was detected is described hereinabove with reference to Figs. 6-15.

[38372] GR2808 gene encodes GR2808 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38373] GR2808 precursor RNA folds spatially, forming GR2808 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2808 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2808 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38374] GR2808 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM972 precursor RNA and GAM973 precursor RNA, herein schematically represented by GAM1

PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38375] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM972 RNA and GAM973 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38376] GAM972 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM972 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM972 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM972 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38377] GAM973 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM973 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM973 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM973 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38378] It is appreciated that specific functions, and accordingly utilities, of GR2808 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2808 gene: GAM972 target protein and GAM973 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM972 and GAM973

[38379] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2809 (GR2809) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38380] GR2809 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2809 gene was detected is described hereinabove with reference to Figs. 6-15.

[38381] GR2809 gene encodes GR2809 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38382] GR2809 precursor RNA folds spatially, forming GR2809 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2809 folded precursor RNA, herein designated GR FOLDED

PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2809 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38383] GR2809 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM974 precursor RNA, GAM975 precursor RNA and GAM976 precursor RNA, herein schematically represented by GAM1 PRECURSOR, GAM2 PRECURSOR and GAM3 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38384] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM974 RNA, GAM975 RNA and GAM976 RNA respectively, herein schematically represented by GAM1 RNA, GAM2 RNA and GAM3 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38385] GAM974 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM974 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM974 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM974 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38386] GAM975 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM975 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM975 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM975 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38387] GAM976 RNA, herein schematically represented by GAM3 binds complementarily to a target binding site located in an untranslated region of GAM976 target RNA, herein schematically represented by GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM976 target RNA, herein schematically represented by GAM3 TARGET RNA into GAM976 target protein, herein schematically represented by GAM3 TARGET PROTEIN, both of Fig. 8.

[38388] It is appreciated that specific functions, and accordingly utilities, of GR2809 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2809 gene: GAM974 target

protein, GAM975 target protein and GAM976 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM974, GAM975 and GAM976

[38389] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2810(GR2810) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38390] GR2810 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2810 gene was detected is described hereinabove with reference to Figs. 6-15.

[38391] GR2810 gene encodes GR2810 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38392] GR2810 precursor RNA folds spatially, forming GR2810 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2810 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2810 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence



which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38393] GR2810 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM980 precursor RNA and GAM981 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38394] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM980 RNA and GAM981 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38395] GAM980 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM980 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM980 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM980 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38396] GAM981 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of

GAM981 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM981 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM981 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38397] It is appreciated that specific functions, and accordingly utilities, of GR2810 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2810 gene: GAM980 target protein and GAM981 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM980 and GAM981

[38398] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2811 (GR2811) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38399] GR2811 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2811 gene was detected is described hereinabove with reference to Figs. 6-15.

[38400] GR2811 gene encodes GR2811 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38401] GR2811 precursor RNA folds spatially, forming GR2811 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2811 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2811 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38402] GR2811 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM985 precursor RNA and GAM986 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38403] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM985 RNA and GAM986 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38404] GAM985 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM985 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM985 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM985 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38405] GAM986 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM986 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM986 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM986 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38406] It is appreciated that specific functions, and accordingly utilities, of GR2811 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2811 gene: GAM985 target protein and GAM986 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM985 and GAM986

- [38407] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2812(GR2812) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [38408] GR2812 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2812 gene was detected is described hereinabove with reference to Figs. 6-15.
- [38409] GR2812 gene encodes GR2812 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [38410] GR2812 precursor RNA folds spatially, forming GR2812 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2812 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2812 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.
- [38411] GR2812 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into

at least 3 separate GAM precursor RNAs, GAM989 precursor RNA, GAM990 precursor RNA and GAM991 precursor RNA, herein schematically represented by GAM1 PRECURSOR, GAM2 PRECURSOR and GAM3 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38412] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM989 RNA, GAM990 RNA and GAM991 RNA respectively, herein schematically represented by GAM1 RNA, GAM2 RNA and GAM3 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38413] GAM989 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM989 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM989 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM989 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38414] GAM990 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM990 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM990 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM990 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38415] GAM991 RNA, herein schematically represented by GAM3 binds complementarily to a target binding site located in an untranslated region of GAM991 target RNA, herein schematically represented by GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM991 target RNA, herein schematically represented by GAM3 TARGET RNA into GAM991 target protein, herein schematically represented by GAM3 TARGET PROTEIN, both of Fig. 8.

[38416] It is appreciated that specific functions, and accordingly utilities, of GR2812 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2812 gene: GAM989 target protein, GAM990 target protein and GAM991 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM989, GAM990 and GAM991

[38417] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2813(GR2813) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

[38418] GR2813 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2813 gene was detected is described hereinabove with reference to Figs. 6-15.

[38419] GR2813 gene encodes GR2813 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38420] GR2813 precursor RNA folds spatially, forming GR2813 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2813 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2813 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38421] GR2813 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM993 precursor RNA and GAM994 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to



GAM PRECURSOR RNA of Fig. 8.

[38422] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM993 RNA and GAM994 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38423] GAM993 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM993 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM993 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM993 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38424] GAM994 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM994 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM994 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM994 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38425] It is appreciated that specific functions, and accordingly utilities, of GR2813 gene, herein designated GR GENE, correlate with, and may be deduced

from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2813 gene: GAM993 target protein and GAM994 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM993 and GAM994

[38426] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2814 (GR2814) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38427] GR2814 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2814 gene was detected is described hereinabove with reference to Figs. 6-15.

[38428] GR2814 gene encodes GR2814 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38429] GR2814 precursor RNA folds spatially, forming GR2814 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2814 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the

nucleotide sequence of GR2814 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38430] GR2814 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1002 precursor RNA and GAM1003 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38431] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1002 RNA and GAM1003 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38432] GAM1002 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1002 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1002 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1002 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38433] GAM1003 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1003 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1003 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1003 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38434] It is appreciated that specific functions, and accordingly utilities, of GR2814 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2814 gene: GAM1002 target protein and GAM1003 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1002 and GAM1003

[38435] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2815 (GR2815) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38436] GR2815 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which

GR2815 gene was detected is described hereinabove with reference to Figs. 6-15.

[38437] GR2815 gene encodes GR2815 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38438] GR2815 precursor RNA folds spatially, forming GR2815 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2815 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2815 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38439] GR2815 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1013 precursor RNA and GAM1014 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38440] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1013 RNA and GAM1014 RNA respectively, herein

schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38441] GAM1013 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1013 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1013 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1013 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38442] GAM1014 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1014 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1014 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1014 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38443] It is appreciated that specific functions, and accordingly utilities, of GR2815 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2815 gene: GAM1013 target protein and GAM1014 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The

function of these target genes is elaborated hereinabove with reference to GAM1013 and GAM1014

- [38444] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2816 (GR2816) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [38445] GR2816 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2816 gene was detected is described hereinabove with reference to Figs. 6-15.
- [38446] GR2816 gene encodes GR2816 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [38447] GR2816 precursor RNA folds spatially, forming GR2816 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2816 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2816 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38448] GR2816 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1018 precursor RNA and GAM1019 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38449] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1018 RNA and GAM1019 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38450] GAM1018 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1018 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1018 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1018 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38451] GAM1019 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1019 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as



BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1019 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1019 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38452] It is appreciated that specific functions, and accordingly utilities, of GR2816 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2816 gene: GAM1018 target protein and GAM1019 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1018 and GAM1019

[38453] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2817 (GR2817) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38454] GR2817 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2817 gene was detected is described hereinabove with reference to Figs. 6-15.

[38455] GR2817 gene encodes GR2817 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides

long.

[38456] GR2817 precursor RNA folds spatially, forming GR2817 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2817 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2817 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38457] GR2817 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1020 precursor RNA and GAM1021 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38458] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1020 RNA and GAM1021 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38459] GAM1020 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of

GAM1020 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1020 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1020 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38460] GAM1021 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1021 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1021 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1021 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38461] It is appreciated that specific functions, and accordingly utilities, of GR2817 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2817 gene: GAM1020 target protein and GAM1021 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1020 and GAM1021

[38462] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record

2818(GR2818) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38463] GR2818 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2818 gene was detected is described hereinabove with reference to Figs. 6-15.

[38464] GR2818 gene encodes GR2818 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38465] GR2818 precursor RNA folds spatially, forming GR2818 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2818 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2818 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38466] GR2818 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1027 precursor RNA, GAM1028 precursor RNA and GAM1029 precursor RNA, herein

schematically represented by GAM1 PRECURSOR, GAM2 PRECURSOR and GAM3 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38467] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1027 RNA, GAM1028 RNA and GAM1029 RNA respectively, herein schematically represented by GAM1 RNA, GAM2 RNA and GAM3 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38468] GAM1027 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1027 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1027 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1027 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38469] GAM1028 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1028 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1028 target RNA, herein schematically

represented by GAM2 TARGET RNA into GAM1028 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38470] GAM1029 RNA, herein schematically represented by GAM3 binds complementarily to a target binding site located in an untranslated region of GAM1029 target RNA, herein schematically represented by GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1029 target RNA, herein schematically represented by GAM3 TARGET RNA into GAM1029 target protein, herein schematically represented by GAM3 TARGET PROTEIN, both of Fig. 8.

[38471] It is appreciated that specific functions, and accordingly utilities, of GR2818 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2818 gene: GAM1027 target protein, GAM1028 target protein and GAM1029 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1027, GAM1028 and GAM1029

[38472] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2819(GR2819) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

[38473] GR2819 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2819 gene was detected is described hereinabove with reference to Figs. 6-15.

[38474] GR2819 gene encodes GR2819 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38475] GR2819 precursor RNA folds spatially, forming GR2819 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2819 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2819 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38476] GR2819 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1032 precursor RNA and GAM1033 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38477] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1032 RNA and GAM1033 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38478] GAM1032 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1032 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1032 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1032 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38479] GAM1033 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1033 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1033 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1033 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38480] It is appreciated that specific functions, and accordingly utilities, of GR2819 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs



comprised in the operon-like cluster of GR2819 gene: GAM1032 target protein and GAM1033 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1032 and GAM1033

[38481] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2820 (GR2820) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38482] GR2820 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2820 gene was detected is described hereinabove with reference to Figs. 6-15.

[38483] GR2820 gene encodes GR2820 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38484] GR2820 precursor RNA folds spatially, forming GR2820 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2820 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2820 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38485] GR2820 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1036 precursor RNA and GAM1037 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38486] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1036 RNA and GAM1037 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38487] GAM1036 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1036 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1036 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1036 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38488] GAM1037 RNA, herein schematically represented by GAM2 binds

complimentarily to a target binding site located in an untranslated region of GAM1037 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1037 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1037 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38489] It is appreciated that specific functions, and accordingly utilities, of GR2820 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2820 gene: GAM1036 target protein and GAM1037 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1036 and GAM1037

[38490] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2821 (GR2821) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38491] GR2821 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2821 gene was detected is described hereinabove with reference to Figs.

- [38492] GR2821 gene encodes GR2821 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [38493] GR2821 precursor RNA folds spatially, forming GR2821 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2821 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2821 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.
- [38494] GR2821 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1041 precursor RNA and GAM1042 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [38495] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1041 RNA and GAM1042 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively,

each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38496] GAM1041 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1041 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1041 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1041 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38497] GAM1042 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1042 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1042 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1042 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38498] It is appreciated that specific functions, and accordingly utilities, of GR2821 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2821 gene: GAM1041 target protein and GAM1042 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to

- [38499] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2822(GR2822) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [38500] GR2822 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2822 gene was detected is described hereinabove with reference to Figs. 6-15.
- [38501] GR2822 gene encodes GR2822 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [38502] GR2822 precursor RNA folds spatially, forming GR2822 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2822 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2822 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

- [38503] GR2822 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1051 precursor RNA, GAM1052 precursor RNA and GAM1053 precursor RNA, herein schematically represented by GAM1 PRECURSOR, GAM2 PRECURSOR and GAM3 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [38504] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1051 RNA, GAM1052 RNA and GAM1053 RNA respectively, herein schematically represented by GAM1 RNA, GAM2 RNA and GAM3 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.
- [38505] GAM1051 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1051 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1051 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1051 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.
- [38506] GAM1052 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of

GAM1052 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1052 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1052 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38507] GAM1053 RNA, herein schematically represented by GAM3 binds complementarily to a target binding site located in an untranslated region of GAM1053 target RNA, herein schematically represented by GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1053 target RNA, herein schematically represented by GAM3 TARGET RNA into GAM1053 target protein, herein schematically represented by GAM3 TARGET PROTEIN, both of Fig. 8.

[38508] It is appreciated that specific functions, and accordingly utilities, of GR2822 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2822 gene: GAM1051 target protein, GAM1052 target protein and GAM1053 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1051, GAM1052 and GAM1053

[38509] Fig. 16 further provides a conceptual description of novel bioinformatically



detected regulatory gene, referred to here as Genomic Record

2823(GR2823) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38510] GR2823 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2823 gene was detected is described hereinabove with reference to Figs. 6-15.

[38511] GR2823 gene encodes GR2823 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38512] GR2823 precursor RNA folds spatially, forming GR2823 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2823 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2823 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38513] GR2823 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1054 precursor RNA,

GAM1055 precursor RNA and GAM1056 precursor RNA, herein schematically represented by GAM1 PRECURSOR, GAM2 PRECURSOR and GAM3 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38514] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1054 RNA, GAM1055 RNA and GAM1056 RNA respectively, herein schematically represented by GAM1 RNA, GAM2 RNA and GAM3 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38515] GAM1054 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1054 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1054 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1054 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38516] GAM1055 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1055 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby

inhibiting translation of GAM1055 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1055 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38517] GAM1056 RNA, herein schematically represented by GAM3 binds complementarily to a target binding site located in an untranslated region of GAM1056 target RNA, herein schematically represented by GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1056 target RNA, herein schematically represented by GAM3 TARGET RNA into GAM1056 target protein, herein schematically represented by GAM3 TARGET PROTEIN, both of Fig. 8.

[38518] It is appreciated that specific functions, and accordingly utilities, of GR2823 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2823 gene: GAM1054 target protein, GAM1055 target protein and GAM1056 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1054, GAM1055 and GAM1056

[38519] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2824(GR2824) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

[38520] GR2824 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2824 gene was detected is described hereinabove with reference to Figs. 6-15.

[38521] GR2824 gene encodes GR2824 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38522] GR2824 precursor RNA folds spatially, forming GR2824 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2824 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2824 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38523] GR2824 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1060 precursor RNA and GAM1061 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to

## GAM PRECURSOR RNA of Fig. 8.

[38524] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1060 RNA and GAM1061 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38525] GAM1060 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1060 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1060 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1060 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38526] GAM1061 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1061 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1061 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1061 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38527] It is appreciated that specific functions, and accordingly utilities, of GR2824 gene, herein designated GR GENE, correlate with, and may be deduced

from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2824 gene: GAM1060 target protein and GAM1061 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1060 and GAM1061

[38528] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2825 (GR2825) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38529] GR2825 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2825 gene was detected is described hereinabove with reference to Figs. 6-15.

[38530] GR2825 gene encodes GR2825 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38531] GR2825 precursor RNA folds spatially, forming GR2825 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2825 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the

nucleotide sequence of GR2825 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38532] GR2825 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1070 precursor RNA and GAM1071 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38533] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1070 RNA and GAM1071 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38534] GAM1070 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1070 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1070 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1070 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38535] GAM1071 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1071 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1071 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1071 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38536] It is appreciated that specific functions, and accordingly utilities, of GR2825 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2825 gene: GAM1070 target protein and GAM1071 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1070 and GAM1071

[38537] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2826 (GR2826) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38538] GR2826 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which



GR2826 gene was detected is described hereinabove with reference to Figs. 6-15.

[38539] GR2826 gene encodes GR2826 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38540] GR2826 precursor RNA folds spatially, forming GR2826 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2826 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2826 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38541] GR2826 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1080 precursor RNA and GAM1081 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38542] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1080 RNA and GAM1081 RNA respectively, herein

schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38543] GAM1080 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1080 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1080 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1080 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38544] GAM1081 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1081 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1081 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1081 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38545] It is appreciated that specific functions, and accordingly utilities, of GR2826 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2826 gene: GAM1080 target protein and GAM1081 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The

function of these target genes is elaborated hereinabove with reference to GAM1080 and GAM1081

- [38546] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2827 (GR2827) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [38547] GR2827 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2827 gene was detected is described hereinabove with reference to Figs. 6-15.
- [38548] GR2827 gene encodes GR2827 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [38549] GR2827 precursor RNA folds spatially, forming GR2827 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2827 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2827 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

- [38550] GR2827 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1093 precursor RNA and GAM1094 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [38551] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1093 RNA and GAM1094 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.
- [38552] GAM1093 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1093 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1093 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1093 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.
- [38553] GAM1094 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1094 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1094 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1094 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38554] It is appreciated that specific functions, and accordingly utilities, of GR2827 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2827 gene: GAM1093 target protein and GAM1094 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1093 and GAM1094

[38555] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2828 (GR2828) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38556] GR2828 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2828 gene was detected is described hereinabove with reference to Figs. 6-15.

[38557] GR2828 gene encodes GR2828 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides

long.

[38558] GR2828 precursor RNA folds spatially, forming GR2828 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2828 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2828 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38559] GR2828 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1095 precursor RNA and GAM1096 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38560] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1095 RNA and GAM1096 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38561] GAM1095 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of

GAM1095 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1095 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1095 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38562] GAM1096 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1096 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1096 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1096 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38563] It is appreciated that specific functions, and accordingly utilities, of GR2828 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2828 gene: GAM1095 target protein and GAM1096 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1095 and GAM1096

[38564] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record

2829(GR2829) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38565] GR2829 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2829 gene was detected is described hereinabove with reference to Figs. 6-15.

[38566] GR2829 gene encodes GR2829 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38567] GR2829 precursor RNA folds spatially, forming GR2829 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2829 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2829 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38568] GR2829 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1097 precursor RNA and GAM1098 precursor RNA, herein schematically represented by GAM1



PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38569] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1097 RNA and GAM1098 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38570] GAM1097 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1097 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1097 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1097 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38571] GAM1098 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1098 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1098 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1098 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38572] It is appreciated that specific functions, and accordingly utilities, of GR2829 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2829 gene: GAM1097 target protein and GAM1098 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1097 and GAM1098

[38573] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2830 (GR2830) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38574] GR2830 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2830 gene was detected is described hereinabove with reference to Figs. 6-15.

[38575] GR2830 gene encodes GR2830 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38576] GR2830 precursor RNA folds spatially, forming GR2830 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2830 folded precursor RNA, herein designated GR FOLDED

PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2830 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38577] GR2830 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1099 precursor RNA and GAM1100 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38578] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1099 RNA and GAM1100 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38579] GAM1099 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1099 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1099 target RNA, herein schematically

represented by GAM1 TARGET RNA into GAM1099 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38580] GAM1100 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1100 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1100 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1100 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38581] It is appreciated that specific functions, and accordingly utilities, of GR2830 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2830 gene: GAM1099 target protein and GAM1100 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1099 and GAM1100

[38582] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2831 (GR2831) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38583] GR2831 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2831 gene was detected is described hereinabove with reference to Figs. 6-15.

[38584] GR2831 gene encodes GR2831 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38585] GR2831 precursor RNA folds spatially, forming GR2831 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2831 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2831 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38586] GR2831 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1107 precursor RNA and GAM1108 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38587] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX

of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1107 RNA and GAM1108 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38588] GAM1107 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1107 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1107 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1107 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38589] GAM1108 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1108 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1108 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1108 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38590] It is appreciated that specific functions, and accordingly utilities, of GR2831 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2831 gene: GAM1107 target

protein and GAM1108 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1107 and GAM1108

[38591] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2832 (GR2832) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38592] GR2832 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2832 gene was detected is described hereinabove with reference to Figs. 6-15.

[38593] GR2832 gene encodes GR2832 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38594] GR2832 precursor RNA folds spatially, forming GR2832 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2832 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2832 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38595] GR2832 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1114 precursor RNA and GAM1115 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38596] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1114 RNA and GAM1115 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38597] GAM1114 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1114 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1114 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1114 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38598] GAM1115 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of



GAM1115 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1115 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1115 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38599] It is appreciated that specific functions, and accordingly utilities, of GR2832 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2832 gene: GAM1114 target protein and GAM1115 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1114 and GAM1115

[38600] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2833 (GR2833) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38601] GR2833 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2833 gene was detected is described hereinabove with reference to Figs. 6-15.

[38602] GR2833 gene encodes GR2833 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38603] GR2833 precursor RNA folds spatially, forming GR2833 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2833 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2833 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38604] GR2833 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1129 precursor RNA and GAM1130 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38605] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1129 RNA and GAM1130 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38606] GAM1129 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1129 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1129 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1129 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38607] GAM1130 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1130 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1130 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1130 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38608] It is appreciated that specific functions, and accordingly utilities, of GR2833 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2833 gene: GAM1129 target protein and GAM1130 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1129 and GAM1130

- [38609] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2834(GR2834) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [38610] GR2834 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2834 gene was detected is described hereinabove with reference to Figs. 6-15.
- [38611] GR2834 gene encodes GR2834 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [38612] GR2834 precursor RNA folds spatially, forming GR2834 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2834 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2834 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.
- [38613] GR2834 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into

at least 2 separate GAM precursor RNAs, GAM1145 precursor RNA and GAM1146 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38614] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1145 RNA and GAM1146 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38615] GAM1145 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1145 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1145 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1145 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38616] GAM1146 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1146 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1146 target RNA, herein schematically

represented by GAM2 TARGET RNA into GAM1146 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38617] It is appreciated that specific functions, and accordingly utilities, of GR2834 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2834 gene: GAM1145 target protein and GAM1146 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1145 and GAM1146

[38618] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2835 (GR2835) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38619] GR2835 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2835 gene was detected is described hereinabove with reference to Figs. 6-15.

[38620] GR2835 gene encodes GR2835 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38621] GR2835 precursor RNA folds spatially, forming GR2835 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2835 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2835 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38622] GR2835 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1151 precursor RNA and GAM1152 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38623] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1151 RNA and GAM1152 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38624] GAM1151 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1151 target RNA, herein schematically represented by GAM1 TARGET

RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1151 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1151 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38625] GAM1152 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1152 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1152 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1152 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38626] It is appreciated that specific functions, and accordingly utilities, of GR2835 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2835 gene: GAM1151 target protein and GAM1152 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1151 and GAM1152

[38627] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2836(GR2836) gene, which encodes an operon-like cluster of novel micro



RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38628] GR2836 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2836 gene was detected is described hereinabove with reference to Figs. 6-15.

[38629] GR2836 gene encodes GR2836 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38630] GR2836 precursor RNA folds spatially, forming GR2836 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2836 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2836 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38631] GR2836 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1153 precursor RNA and GAM1154 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM

precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38632] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1153 RNA and GAM1154 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38633] GAM1153 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1153 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1153 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1153 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38634] GAM1154 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1154 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1154 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1154 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38635] It is appreciated that specific functions, and accordingly utilities, of GR2836

gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2836 gene: GAM1153 target protein and GAM1154 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1153 and GAM1154

[38636] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2837 (GR2837) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38637] GR2837 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2837 gene was detected is described hereinabove with reference to Figs. 6-15.

[38638] GR2837 gene encodes GR2837 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38639] GR2837 precursor RNA folds spatially, forming GR2837 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2837 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as

hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2837 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38640] GR2837 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1156 precursor RNA and GAM1157 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38641] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1156 RNA and GAM1157 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38642] GAM1156 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1156 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1156 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1156 target protein, herein

schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38643] GAM1157 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1157 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1157 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1157 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38644] It is appreciated that specific functions, and accordingly utilities, of GR2837 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2837 gene: GAM1156 target protein and GAM1157 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1156 and GAM1157

[38645] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2838 (GR2838) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38646] GR2838 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR2838 gene was detected is described hereinabove with reference to Figs. 6-15.

[38647] GR2838 gene encodes GR2838 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38648] GR2838 precursor RNA folds spatially, forming GR2838 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2838 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2838 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38649] GR2838 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1162 precursor RNA and GAM1163 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38650] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in

length, GAM1162 RNA and GAM1163 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38651] GAM1162 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1162 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1162 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1162 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38652] GAM1163 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1163 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1163 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1163 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38653] It is appreciated that specific functions, and accordingly utilities, of GR2838 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2838 gene: GAM1162 target protein and GAM1163 target protein, herein schematically represented by

GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1162 and GAM1163

[38654] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2839 (GR2839) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38655] GR2839 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2839 gene was detected is described hereinabove with reference to Figs. 6-15.

[38656] GR2839 gene encodes GR2839 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38657] GR2839 precursor RNA folds spatially, forming GR2839 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2839 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2839 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half



thereof, as is well known in the art.

[38658] GR2839 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM1168 precursor RNA, GAM1169 precursor RNA, GAM1170 precursor RNA and GAM1171 precursor RNA, herein schematically represented by GAM1 PRECURSOR, GAM2 PRECURSOR, GAM3 PRECURSOR and GAM4 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38659] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1168 RNA, GAM1169 RNA, GAM1170 RNA and GAM1171 RNA respectively, herein schematically represented by GAM1 RNA, GAM2 RNA, GAM3 RNA and GAM4 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38660] GAM1168 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1168 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1168 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1168 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38661] GAM1169 RNA, herein schematically represented by GAM2 binds

complimentarily to a target binding site located in an untranslated region of GAM1169 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1169 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1169 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38662] GAM1170 RNA, herein schematically represented by GAM3 binds complimentarily to a target binding site located in an untranslated region of GAM1170 target RNA, herein schematically represented by GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1170 target RNA, herein schematically represented by GAM3 TARGET RNA into GAM1170 target protein, herein schematically represented by GAM3 TARGET PROTEIN, both of Fig. 8.

[38663] GAM1171 RNA, herein schematically represented by GAM4 binds complimentarily to a target binding site located in an untranslated region of GAM1171 target RNA, herein schematically represented by GAM4 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1171 target RNA, herein schematically represented by GAM4 TARGET RNA into GAM1171 target protein, herein schematically represented by GAM4 TARGET PROTEIN, both of Fig. 8.

[38664] It is appreciated that specific functions, and accordingly utilities, of GR2839

gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2839 gene: GAM1168 target protein, GAM1169 target protein, GAM1170 target protein and GAM1171 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1168, GAM1169, GAM1170 and GAM1171

[38665] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2840(GR2840) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38666] GR2840 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2840 gene was detected is described hereinabove with reference to Figs. 6-15.

[38667] GR2840 gene encodes GR2840 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38668] GR2840 precursor RNA folds spatially, forming GR2840 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2840 folded precursor RNA, herein designated GR FOLDED

PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2840 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38669] GR2840 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1183 precursor RNA and GAM1184 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38670] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1183 RNA and GAM1184 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38671] GAM1183 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1183 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1183 target RNA, herein schematically

represented by GAM1 TARGET RNA into GAM1183 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38672] GAM1184 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1184 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1184 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1184 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38673] It is appreciated that specific functions, and accordingly utilities, of GR2840 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2840 gene: GAM1183 target protein and GAM1184 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1183 and GAM1184

[38674] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2841 (GR2841) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38675] GR2841 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2841 gene was detected is described hereinabove with reference to Figs. 6-15.

[38676] GR2841 gene encodes GR2841 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38677] GR2841 precursor RNA folds spatially, forming GR2841 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2841 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2841 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38678] GR2841 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1188 precursor RNA and GAM1189 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38679] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX

of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1188 RNA and GAM1189 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38680] GAM1188 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1188 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1188 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1188 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38681] GAM1189 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1189 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1189 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1189 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38682] It is appreciated that specific functions, and accordingly utilities, of GR2841 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2841 gene: GAM1188 target

protein and GAM1189 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1188 and GAM1189

[38683] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2842 (GR2842) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38684] GR2842 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2842 gene was detected is described hereinabove with reference to Figs. 6-15.

[38685] GR2842 gene encodes GR2842 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38686] GR2842 precursor RNA folds spatially, forming GR2842 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2842 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2842 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence



which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38687] GR2842 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1193 precursor RNA and GAM1194 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38688] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1193 RNA and GAM1194 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38689] GAM1193 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1193 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1193 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1193 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38690] GAM1194 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of

GAM1194 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1194 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1194 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38691] It is appreciated that specific functions, and accordingly utilities, of GR2842 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2842 gene: GAM1193 target protein and GAM1194 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1193 and GAM1194

[38692] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2843 (GR2843) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38693] GR2843 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2843 gene was detected is described hereinabove with reference to Figs. 6-15.

[38694] GR2843 gene encodes GR2843 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38695] GR2843 precursor RNA folds spatially, forming GR2843 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2843 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2843 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38696] GR2843 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1200 precursor RNA and GAM1201 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38697] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1200 RNA and GAM1201 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38698] GAM1200 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1200 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1200 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1200 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38699] GAM1201 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1201 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1201 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1201 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38700] It is appreciated that specific functions, and accordingly utilities, of GR2843 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2843 gene: GAM1200 target protein and GAM1201 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1200 and GAM1201

- [38701] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2844(GR2844) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [38702] GR2844 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2844 gene was detected is described hereinabove with reference to Figs. 6-15.
- [38703] GR2844 gene encodes GR2844 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [38704] GR2844 precursor RNA folds spatially, forming GR2844 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2844 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2844 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.
- [38705] GR2844 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into

at least 2 separate GAM precursor RNAs, GAM1203 precursor RNA and GAM1204 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38706] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1203 RNA and GAM1204 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38707] GAM1203 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1203 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1203 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1203 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38708] GAM1204 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1204 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1204 target RNA, herein schematically

represented by GAM2 TARGET RNA into GAM1204 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38709] It is appreciated that specific functions, and accordingly utilities, of GR2844 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2844 gene: GAM1203 target protein and GAM1204 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1203 and GAM1204

[38710] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2845 (GR2845) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38711] GR2845 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2845 gene was detected is described hereinabove with reference to Figs. 6-15.

[38712] GR2845 gene encodes GR2845 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38713] GR2845 precursor RNA folds spatially, forming GR2845 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2845 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2845 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38714] GR2845 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1211 precursor RNA and GAM1212 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38715] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1211 RNA and GAM1212 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38716] GAM1211 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1211 target RNA, herein schematically represented by GAM1 TARGET



RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1211 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1211 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38717] GAM1212 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1212 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1212 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1212 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38718] It is appreciated that specific functions, and accordingly utilities, of GR2845 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2845 gene: GAM1211 target protein and GAM1212 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1211 and GAM1212

[38719] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2846(GR2846) gene, which encodes an operon-like cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38720] GR2846 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2846 gene was detected is described hereinabove with reference to Figs. 6-15.

[38721] GR2846 gene encodes GR2846 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38722] GR2846 precursor RNA folds spatially, forming GR2846 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2846 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2846 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38723] GR2846 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1220 precursor RNA, GAM1221 precursor RNA and GAM1222 precursor RNA, herein schematically represented by GAM1 PRECURSOR, GAM2 PRECURSOR

and GAM3 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38724] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1220 RNA, GAM1221 RNA and GAM1222 RNA respectively, herein schematically represented by GAM1 RNA, GAM2 RNA and GAM3 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38725] GAM1220 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1220 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1220 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1220 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38726] GAM1221 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1221 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1221 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1221 target protein, herein

schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38727] GAM1222 RNA, herein schematically represented by GAM3 binds complementarily to a target binding site located in an untranslated region of GAM1222 target RNA, herein schematically represented by GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1222 target RNA, herein schematically represented by GAM3 TARGET RNA into GAM1222 target protein, herein schematically represented by GAM3 TARGET PROTEIN, both of Fig. 8.

[38728] It is appreciated that specific functions, and accordingly utilities, of GR2846 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2846 gene: GAM1220 target protein, GAM1221 target protein and GAM1222 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1220, GAM1221 and GAM1222

[38729] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2847(GR2847) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

- [38730] GR2847 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2847 gene was detected is described hereinabove with reference to Figs. 6-15.
- [38731] GR2847 gene encodes GR2847 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [38732] GR2847 precursor RNA folds spatially, forming GR2847 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2847 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2847 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.
- [38733] GR2847 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1223 precursor RNA and GAM1224 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [38734] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX

of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1223 RNA and GAM1224 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38735] GAM1223 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1223 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1223 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1223 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38736] GAM1224 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1224 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1224 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1224 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38737] It is appreciated that specific functions, and accordingly utilities, of GR2847 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2847 gene: GAM1223 target

protein and GAM1224 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1223 and GAM1224

[38738] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2848 (GR2848) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38739] GR2848 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2848 gene was detected is described hereinabove with reference to Figs. 6-15.

[38740] GR2848 gene encodes GR2848 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38741] GR2848 precursor RNA folds spatially, forming GR2848 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2848 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2848 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38742] GR2848 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1227 precursor RNA and GAM1228 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38743] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1227 RNA and GAM1228 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38744] GAM1227 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1227 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1227 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1227 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38745] GAM1228 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of



GAM1228 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1228 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1228 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38746] It is appreciated that specific functions, and accordingly utilities, of GR2848 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2848 gene: GAM1227 target protein and GAM1228 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1227 and GAM1228

[38747] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2849 (GR2849) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

- [38748] GR2849 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2849 gene was detected is described hereinabove with reference to Figs. 6-15.
- [38749] GR2849 gene encodes GR2849 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [38750] GR2849 precursor RNA folds spatially, forming GR2849 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2849 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2849 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.
- [38751] GR2849 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1233 precursor RNA, GAM1234 precursor RNA and GAM1235 precursor RNA, herein schematically represented by GAM1 PRECURSOR, GAM2 PRECURSOR and GAM3 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38752] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1233 RNA, GAM1234 RNA and GAM1235 RNA respectively, herein schematically represented by GAM1 RNA, GAM2 RNA and GAM3 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38753] GAM1233 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1233 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1233 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1233 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38754] GAM1234 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1234 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1234 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1234 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38755] GAM1235 RNA, herein schematically represented by GAM3 binds complementarily to a target binding site located in an untranslated region of

GAM1235 target RNA, herein schematically represented by GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1235 target RNA, herein schematically represented by GAM3 TARGET RNA into GAM1235 target protein, herein schematically represented by GAM3 TARGET PROTEIN, both of Fig. 8.

[38756] It is appreciated that specific functions, and accordingly utilities, of GR2849 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2849 gene: GAM1233 target protein, GAM1234 target protein and GAM1235 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1233, GAM1234 and GAM1235

[38757] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2850 (GR2850) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38758] GR2850 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2850 gene was detected is described hereinabove with reference to Figs.

- [38759] GR2850 gene encodes GR2850 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [38760] GR2850 precursor RNA folds spatially, forming GR2850 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2850 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2850 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.
- [38761] GR2850 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1249 precursor RNA and GAM1250 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [38762] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1249 RNA and GAM1250 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively,

each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38763] GAM1249 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1249 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1249 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1249 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38764] GAM1250 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1250 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1250 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1250 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38765] It is appreciated that specific functions, and accordingly utilities, of GR2850 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2850 gene: GAM1249 target protein and GAM1250 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to

- [38766] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2851 (GR2851) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [38767] GR2851 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2851 gene was detected is described hereinabove with reference to Figs. 6-15.
- [38768] GR2851 gene encodes GR2851 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [38769] GR2851 precursor RNA folds spatially, forming GR2851 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2851 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2851 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

- [38770] GR2851 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1254 precursor RNA and GAM1255 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [38771] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1254 RNA and GAM1255 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.
- [38772] GAM1254 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1254 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1254 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1254 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.
- [38773] GAM1255 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1255 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as



BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1255 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1255 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38774] It is appreciated that specific functions, and accordingly utilities, of GR2851 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2851 gene: GAM1254 target protein and GAM1255 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1254 and GAM1255

[38775] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2852 (GR2852) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38776] GR2852 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2852 gene was detected is described hereinabove with reference to Figs. 6-15.

[38777] GR2852 gene encodes GR2852 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides

long.

[38778] GR2852 precursor RNA folds spatially, forming GR2852 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2852 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2852 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38779] GR2852 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1256 precursor RNA and GAM1257 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38780] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1256 RNA and GAM1257 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38781] GAM1256 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of

GAM1256 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1256 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1256 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38782] GAM1257 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1257 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1257 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1257 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38783] It is appreciated that specific functions, and accordingly utilities, of GR2852 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2852 gene: GAM1256 target protein and GAM1257 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1256 and GAM1257

[38784] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record

2853(GR2853) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38785] GR2853 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2853 gene was detected is described hereinabove with reference to Figs. 6-15.

[38786] GR2853 gene encodes GR2853 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38787] GR2853 precursor RNA folds spatially, forming GR2853 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2853 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2853 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38788] GR2853 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1260 precursor RNA, GAM1261 precursor RNA and GAM1262 precursor RNA, herein

schematically represented by GAM1 PRECURSOR, GAM2 PRECURSOR and GAM3 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38789] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1260 RNA, GAM1261 RNA and GAM1262 RNA respectively, herein schematically represented by GAM1 RNA, GAM2 RNA and GAM3 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38790] GAM1260 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1260 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1260 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1260 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38791] GAM1261 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1261 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1261 target RNA, herein schematically

represented by GAM2 TARGET RNA into GAM1261 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38792] GAM1262 RNA, herein schematically represented by GAM3 binds complementarily to a target binding site located in an untranslated region of GAM1262 target RNA, herein schematically represented by GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1262 target RNA, herein schematically represented by GAM3 TARGET RNA into GAM1262 target protein, herein schematically represented by GAM3 TARGET PROTEIN, both of Fig. 8.

[38793] It is appreciated that specific functions, and accordingly utilities, of GR2853 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2853 gene: GAM1260 target protein, GAM1261 target protein and GAM1262 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1260, GAM1261 and GAM1262

[38794] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2854(GR2854) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

[38795] GR2854 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2854 gene was detected is described hereinabove with reference to Figs. 6-15.

[38796] GR2854 gene encodes GR2854 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38797] GR2854 precursor RNA folds spatially, forming GR2854 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2854 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2854 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38798] GR2854 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1263 precursor RNA and GAM1264 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38799] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1263 RNA and GAM1264 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38800] GAM1263 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1263 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1263 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1263 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38801] GAM1264 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1264 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1264 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1264 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38802] It is appreciated that specific functions, and accordingly utilities, of GR2854 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs



comprised in the operon-like cluster of GR2854 gene: GAM1263 target protein and GAM1264 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1263 and GAM1264

[38803] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2855 (GR2855) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38804] GR2855 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2855 gene was detected is described hereinabove with reference to Figs. 6-15.

[38805] GR2855 gene encodes GR2855 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38806] GR2855 precursor RNA folds spatially, forming GR2855 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2855 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2855 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38807] GR2855 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1270 precursor RNA and GAM1271 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38808] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1270 RNA and GAM1271 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38809] GAM1270 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1270 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1270 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1270 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38810] GAM1271 RNA, herein schematically represented by GAM2 binds

complimentarily to a target binding site located in an untranslated region of GAM1271 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1271 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1271 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38811] It is appreciated that specific functions, and accordingly utilities, of GR2855 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2855 gene: GAM1270 target protein and GAM1271 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1270 and GAM1271

[38812] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2856 (GR2856) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38813] GR2856 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2856 gene was detected is described hereinabove with reference to Figs.

- [38814] GR2856 gene encodes GR2856 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [38815] GR2856 precursor RNA folds spatially, forming GR2856 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2856 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2856 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.
- [38816] GR2856 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1281 precursor RNA and GAM1282 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [38817] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1281 RNA and GAM1282 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively,

each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38818] GAM1281 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1281 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1281 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1281 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38819] GAM1282 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1282 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1282 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1282 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38820] It is appreciated that specific functions, and accordingly utilities, of GR2856 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2856 gene: GAM1281 target protein and GAM1282 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to

- [38821] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2857 (GR2857) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [38822] GR2857 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2857 gene was detected is described hereinabove with reference to Figs. 6-15.
- [38823] GR2857 gene encodes GR2857 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [38824] GR2857 precursor RNA folds spatially, forming GR2857 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2857 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2857 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38825] GR2857 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1287 precursor RNA and GAM1288 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38826] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1287 RNA and GAM1288 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38827] GAM1287 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1287 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1287 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1287 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38828] GAM1288 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1288 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1288 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1288 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38829] It is appreciated that specific functions, and accordingly utilities, of GR2857 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2857 gene: GAM1287 target protein and GAM1288 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1287 and GAM1288

[38830] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2858 (GR2858) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38831] GR2858 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2858 gene was detected is described hereinabove with reference to Figs. 6-15.

[38832] GR2858 gene encodes GR2858 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides



long.

[38833] GR2858 precursor RNA folds spatially, forming GR2858 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2858 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2858 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38834] GR2858 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1289 precursor RNA and GAM1290 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38835] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1289 RNA and GAM1290 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38836] GAM1289 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of

GAM1289 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1289 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1289 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38837] GAM1290 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1290 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1290 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1290 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38838] It is appreciated that specific functions, and accordingly utilities, of GR2858 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2858 gene: GAM1289 target protein and GAM1290 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1289 and GAM1290

[38839] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record

2859(GR2859) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38840] GR2859 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2859 gene was detected is described hereinabove with reference to Figs. 6-15.

[38841] GR2859 gene encodes GR2859 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38842] GR2859 precursor RNA folds spatially, forming GR2859 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2859 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2859 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38843] GR2859 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1308 precursor RNA, GAM1309 precursor RNA and GAM1310 precursor RNA, herein

schematically represented by GAM1 PRECURSOR, GAM2 PRECURSOR and GAM3 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38844] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1308 RNA, GAM1309 RNA and GAM1310 RNA respectively, herein schematically represented by GAM1 RNA, GAM2 RNA and GAM3 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38845] GAM1308 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1308 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1308 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1308 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38846] GAM1309 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1309 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1309 target RNA, herein schematically

represented by GAM2 TARGET RNA into GAM1309 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38847] GAM1310 RNA, herein schematically represented by GAM3 binds complementarily to a target binding site located in an untranslated region of GAM1310 target RNA, herein schematically represented by GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1310 target RNA, herein schematically represented by GAM3 TARGET RNA into GAM1310 target protein, herein schematically represented by GAM3 TARGET PROTEIN, both of Fig. 8.

[38848] It is appreciated that specific functions, and accordingly utilities, of GR2859 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2859 gene: GAM1308 target protein, GAM1309 target protein and GAM1310 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1308, GAM1309 and GAM1310

[38849] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2860 (GR2860) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

[38850] GR2860 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2860 gene was detected is described hereinabove with reference to Figs. 6-15.

[38851] GR2860 gene encodes GR2860 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38852] GR2860 precursor RNA folds spatially, forming GR2860 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2860 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2860 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38853] GR2860 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1315 precursor RNA and GAM1316 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38854] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1315 RNA and GAM1316 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38855] GAM1315 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1315 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1315 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1315 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38856] GAM1316 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1316 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1316 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1316 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38857] It is appreciated that specific functions, and accordingly utilities, of GR2860 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs

comprised in the operon-like cluster of GR2860 gene: GAM1315 target protein and GAM1316 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1315 and GAM1316

[38858] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2861 (GR2861) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38859] GR2861 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2861 gene was detected is described hereinabove with reference to Figs. 6-15.

[38860] GR2861 gene encodes GR2861 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38861] GR2861 precursor RNA folds spatially, forming GR2861 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2861 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2861 precursor RNA comprises a plurality of



segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38862] GR2861 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1317 precursor RNA and GAM1318 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38863] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1317 RNA and GAM1318 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38864] GAM1317 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1317 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1317 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1317 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38865] GAM1318 RNA, herein schematically represented by GAM2 binds

complimentarily to a target binding site located in an untranslated region of GAM1318 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1318 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1318 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38866] It is appreciated that specific functions, and accordingly utilities, of GR2861 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2861 gene: GAM1317 target protein and GAM1318 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1317 and GAM1318

[38867] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2862 (GR2862) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38868] GR2862 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2862 gene was detected is described hereinabove with reference to Figs.

- [38869] GR2862 gene encodes GR2862 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [38870] GR2862 precursor RNA folds spatially, forming GR2862 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2862 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2862 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.
- [38871] GR2862 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1321 precursor RNA and GAM1322 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [38872] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1321 RNA and GAM1322 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively,

each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38873] GAM1321 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1321 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1321 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1321 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38874] GAM1322 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1322 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1322 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1322 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38875] It is appreciated that specific functions, and accordingly utilities, of GR2862 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2862 gene: GAM1321 target protein and GAM1322 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to

- [38876] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2863(GR2863) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [38877] GR2863 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2863 gene was detected is described hereinabove with reference to Figs. 6-15.
- [38878] GR2863 gene encodes GR2863 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [38879] GR2863 precursor RNA folds spatially, forming GR2863 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2863 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2863 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38880] GR2863 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1326 precursor RNA, GAM1327 precursor RNA and GAM1328 precursor RNA, herein schematically represented by GAM1 PRECURSOR, GAM2 PRECURSOR and GAM3 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38881] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1326 RNA, GAM1327 RNA and GAM1328 RNA respectively, herein schematically represented by GAM1 RNA, GAM2 RNA and GAM3 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38882] GAM1326 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1326 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1326 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1326 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38883] GAM1327 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of

GAM1327 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1327 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1327 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38884] GAM1328 RNA, herein schematically represented by GAM3 binds complementarily to a target binding site located in an untranslated region of GAM1328 target RNA, herein schematically represented by GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1328 target RNA, herein schematically represented by GAM3 TARGET RNA into GAM1328 target protein, herein schematically represented by GAM3 TARGET PROTEIN, both of Fig. 8.

[38885] It is appreciated that specific functions, and accordingly utilities, of GR2863 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2863 gene: GAM1326 target protein, GAM1327 target protein and GAM1328 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1326, GAM1327 and GAM1328

[38886] Fig. 16 further provides a conceptual description of novel bioinformatically

detected regulatory gene, referred to here as Genomic Record

2864(GR2864) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38887] GR2864 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2864 gene was detected is described hereinabove with reference to Figs. 6-15.

[38888] GR2864 gene encodes GR2864 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38889] GR2864 precursor RNA folds spatially, forming GR2864 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2864 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2864 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38890] GR2864 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1344 precursor RNA and



GAM1345 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38891] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1344 RNA and GAM1345 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38892] GAM1344 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1344 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1344 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1344 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38893] GAM1345 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1345 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1345 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1345 target protein, herein

schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38894] It is appreciated that specific functions, and accordingly utilities, of GR2864 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2864 gene: GAM1344 target protein and GAM1345 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1344 and GAM1345

[38895] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2865 (GR2865) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38896] GR2865 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2865 gene was detected is described hereinabove with reference to Figs. 6-15.

[38897] GR2865 gene encodes GR2865 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38898] GR2865 precursor RNA folds spatially, forming GR2865 folded precursor

RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2865 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2865 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38899] GR2865 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1353 precursor RNA and GAM1354 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38900] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1353 RNA and GAM1354 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38901] GAM1353 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1353 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1353 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1353 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38902] GAM1354 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1354 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1354 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1354 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38903] It is appreciated that specific functions, and accordingly utilities, of GR2865 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2865 gene: GAM1353 target protein and GAM1354 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1353 and GAM1354

[38904] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2866 (GR2866) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

[38905] GR2866 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2866 gene was detected is described hereinabove with reference to Figs. 6-15.

[38906] GR2866 gene encodes GR2866 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38907] GR2866 precursor RNA folds spatially, forming GR2866 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2866 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2866 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38908] GR2866 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1355 precursor RNA and GAM1356 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to

## GAM PRECURSOR RNA of Fig. 8.

[38909] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1355 RNA and GAM1356 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38910] GAM1355 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1355 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1355 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1355 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38911] GAM1356 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1356 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1356 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1356 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38912] It is appreciated that specific functions, and accordingly utilities, of GR2866 gene, herein designated GR GENE, correlate with, and may be deduced

from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2866 gene: GAM1355 target protein and GAM1356 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1355 and GAM1356

[38913] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2867 (GR2867) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38914] GR2867 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2867 gene was detected is described hereinabove with reference to Figs. 6-15.

[38915] GR2867 gene encodes GR2867 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38916] GR2867 precursor RNA folds spatially, forming GR2867 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2867 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the

nucleotide sequence of GR2867 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

- [38917] GR2867 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1357 precursor RNA and GAM1358 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [38918] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1357 RNA and GAM1358 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.
- [38919] GAM1357 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1357 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1357 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1357 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.



[38920] GAM1358 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1358 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1358 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1358 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38921] It is appreciated that specific functions, and accordingly utilities, of GR2867 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2867 gene: GAM1357 target protein and GAM1358 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1357 and GAM1358

[38922] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2868 (GR2868) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38923] GR2868 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which

GR2868 gene was detected is described hereinabove with reference to Figs. 6-15.

[38924] GR2868 gene encodes GR2868 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38925] GR2868 precursor RNA folds spatially, forming GR2868 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2868 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2868 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38926] GR2868 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1361 precursor RNA and GAM1362 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38927] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1361 RNA and GAM1362 RNA respectively, herein

schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38928] GAM1361 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1361 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1361 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1361 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38929] GAM1362 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1362 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1362 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1362 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38930] It is appreciated that specific functions, and accordingly utilities, of GR2868 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2868 gene: GAM1361 target protein and GAM1362 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The

function of these target genes is elaborated hereinabove with reference to GAM1361 and GAM1362

- [38931] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2869 (GR2869) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [38932] GR2869 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2869 gene was detected is described hereinabove with reference to Figs. 6-15.
- [38933] GR2869 gene encodes GR2869 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [38934] GR2869 precursor RNA folds spatially, forming GR2869 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2869 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2869 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

- [38935] GR2869 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1364 precursor RNA and GAM1365 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [38936] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1364 RNA and GAM1365 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.
- [38937] GAM1364 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1364 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1364 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1364 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.
- [38938] GAM1365 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1365 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1365 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1365 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38939] It is appreciated that specific functions, and accordingly utilities, of GR2869 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2869 gene: GAM1364 target protein and GAM1365 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1364 and GAM1365

[38940] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2870 (GR2870) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38941] GR2870 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2870 gene was detected is described hereinabove with reference to Figs. 6-15.

[38942] GR2870 gene encodes GR2870 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides

long.

[38943] GR2870 precursor RNA folds spatially, forming GR2870 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2870 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2870 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38944] GR2870 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1368 precursor RNA and GAM1369 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38945] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1368 RNA and GAM1369 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38946] GAM1368 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of

GAM1368 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1368 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1368 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38947] GAM1369 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1369 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1369 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1369 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38948] It is appreciated that specific functions, and accordingly utilities, of GR2870 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2870 gene: GAM1368 target protein and GAM1369 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1368 and GAM1369

[38949] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record



2871(GR2871) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38950] GR2871 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2871 gene was detected is described hereinabove with reference to Figs. 6-15.

[38951] GR2871 gene encodes GR2871 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38952] GR2871 precursor RNA folds spatially, forming GR2871 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2871 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2871 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38953] GR2871 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1389 precursor RNA and GAM1390 precursor RNA, herein schematically represented by GAM1

PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38954] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1389 RNA and GAM1390 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38955] GAM1389 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1389 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1389 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1389 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38956] GAM1390 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1390 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1390 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1390 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38957] It is appreciated that specific functions, and accordingly utilities, of GR2871 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2871 gene: GAM1389 target protein and GAM1390 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1389 and GAM1390

[38958] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2872 (GR2872) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38959] GR2872 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2872 gene was detected is described hereinabove with reference to Figs. 6-15.

[38960] GR2872 gene encodes GR2872 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38961] GR2872 precursor RNA folds spatially, forming GR2872 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2872 folded precursor RNA, herein designated GR FOLDED

PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2872 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38962] GR2872 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1396 precursor RNA and GAM1397 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38963] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1396 RNA and GAM1397 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38964] GAM1396 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1396 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1396 target RNA, herein schematically

represented by GAM1 TARGET RNA into GAM1396 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38965] GAM1397 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1397 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1397 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1397 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38966] It is appreciated that specific functions, and accordingly utilities, of GR2872 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2872 gene: GAM1396 target protein and GAM1397 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1396 and GAM1397

[38967] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2873 (GR2873) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

- [38968] GR2873 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2873 gene was detected is described hereinabove with reference to Figs. 6-15.
- [38969] GR2873 gene encodes GR2873 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [38970] GR2873 precursor RNA folds spatially, forming GR2873 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2873 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2873 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.
- [38971] GR2873 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1421 precursor RNA and GAM1422 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [38972] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX

of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1421 RNA and GAM1422 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38973] GAM1421 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1421 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1421 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1421 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38974] GAM1422 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1422 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1422 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1422 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38975] It is appreciated that specific functions, and accordingly utilities, of GR2873 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2873 gene: GAM1421 target

protein and GAM1422 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1421 and GAM1422

[38976] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2874 (GR2874) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38977] GR2874 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2874 gene was detected is described hereinabove with reference to Figs. 6-15.

[38978] GR2874 gene encodes GR2874 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38979] GR2874 precursor RNA folds spatially, forming GR2874 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2874 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2874 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence



which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38980] GR2874 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1427 precursor RNA, GAM1428 precursor RNA and GAM1429 precursor RNA, herein schematically represented by GAM1 PRECURSOR, GAM2 PRECURSOR and GAM3 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38981] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1427 RNA, GAM1428 RNA and GAM1429 RNA respectively, herein schematically represented by GAM1 RNA, GAM2 RNA and GAM3 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38982] GAM1427 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1427 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1427 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1427 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

- [38983] GAM1428 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1428 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1428 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1428 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.
- [38984] GAM1429 RNA, herein schematically represented by GAM3 binds complementarily to a target binding site located in an untranslated region of GAM1429 target RNA, herein schematically represented by GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1429 target RNA, herein schematically represented by GAM3 TARGET RNA into GAM1429 target protein, herein schematically represented by GAM3 TARGET PROTEIN, both of Fig. 8.
- [38985] It is appreciated that specific functions, and accordingly utilities, of GR2874 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2874 gene: GAM1427 target protein, GAM1428 target protein and GAM1429 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1427, GAM1428 and GAM1429

- [38986] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2875(GR2875) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [38987] GR2875 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2875 gene was detected is described hereinabove with reference to Figs. 6-15.
- [38988] GR2875 gene encodes GR2875 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [38989] GR2875 precursor RNA folds spatially, forming GR2875 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2875 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2875 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.
- [38990] GR2875 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into

at least 2 separate GAM precursor RNAs, GAM1433 precursor RNA and GAM1434 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[38991] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1433 RNA and GAM1434 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[38992] GAM1433 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1433 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1433 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1433 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[38993] GAM1434 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1434 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1434 target RNA, herein schematically

represented by GAM2 TARGET RNA into GAM1434 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[38994] It is appreciated that specific functions, and accordingly utilities, of GR2875 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2875 gene: GAM1433 target protein and GAM1434 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1433 and GAM1434

[38995] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2876 (GR2876) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[38996] GR2876 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2876 gene was detected is described hereinabove with reference to Figs. 6-15.

[38997] GR2876 gene encodes GR2876 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[38998] GR2876 precursor RNA folds spatially, forming GR2876 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2876 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2876 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[38999] GR2876 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1435 precursor RNA and GAM1436 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39000] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1435 RNA and GAM1436 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39001] GAM1435 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1435 target RNA, herein schematically represented by GAM1 TARGET

RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1435 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1435 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39002] GAM1436 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1436 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1436 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1436 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39003] It is appreciated that specific functions, and accordingly utilities, of GR2876 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2876 gene: GAM1435 target protein and GAM1436 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1435 and GAM1436

[39004] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2877(GR2877) gene, which encodes an operon-like cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39005] GR2877 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2877 gene was detected is described hereinabove with reference to Figs. 6-15.

[39006] GR2877 gene encodes GR2877 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39007] GR2877 precursor RNA folds spatially, forming GR2877 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2877 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2877 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39008] GR2877 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1440 precursor RNA and GAM1441 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM



precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39009] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1440 RNA and GAM1441 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39010] GAM1440 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1440 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1440 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1440 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39011] GAM1441 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1441 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1441 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1441 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39012] It is appreciated that specific functions, and accordingly utilities, of GR2877

gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2877 gene: GAM1440 target protein and GAM1441 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1440 and GAM1441

[39013] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2878 (GR2878) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39014] GR2878 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2878 gene was detected is described hereinabove with reference to Figs. 6-15.

[39015] GR2878 gene encodes GR2878 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39016] GR2878 precursor RNA folds spatially, forming GR2878 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2878 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as

hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2878 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39017] GR2878 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1445 precursor RNA, GAM1446 precursor RNA and GAM1447 precursor RNA, herein schematically represented by GAM1 PRECURSOR, GAM2 PRECURSOR and GAM3 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39018] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1445 RNA, GAM1446 RNA and GAM1447 RNA respectively, herein schematically represented by GAM1 RNA, GAM2 RNA and GAM3 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39019] GAM1445 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1445 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby

inhibiting translation of GAM1445 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1445 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39020] GAM1446 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1446 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1446 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1446 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39021] GAM1447 RNA, herein schematically represented by GAM3 binds complementarily to a target binding site located in an untranslated region of GAM1447 target RNA, herein schematically represented by GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1447 target RNA, herein schematically represented by GAM3 TARGET RNA into GAM1447 target protein, herein schematically represented by GAM3 TARGET PROTEIN, both of Fig. 8.

[39022] It is appreciated that specific functions, and accordingly utilities, of GR2878 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2878 gene: GAM1445 target protein, GAM1446 target protein and GAM1447 target protein, herein

schematically represented by GAM1 TARGET PROTEIN through GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1445, GAM1446 and GAM1447

- [39023] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2879(GR2879) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [39024] GR2879 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2879 gene was detected is described hereinabove with reference to Figs. 6-15.
- [39025] GR2879 gene encodes GR2879 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [39026] GR2879 precursor RNA folds spatially, forming GR2879 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2879 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2879 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

- [39027] GR2879 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1457 precursor RNA and GAM1458 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [39028] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1457 RNA and GAM1458 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.
- [39029] GAM1457 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1457 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1457 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1457 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.
- [39030] GAM1458 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of

GAM1458 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1458 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1458 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39031] It is appreciated that specific functions, and accordingly utilities, of GR2879 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2879 gene: GAM1457 target protein and GAM1458 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1457 and GAM1458

[39032] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2880 (GR2880) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39033] GR2880 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2880 gene was detected is described hereinabove with reference to Figs. 6-15.

[39034] GR2880 gene encodes GR2880 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39035] GR2880 precursor RNA folds spatially, forming GR2880 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2880 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2880 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39036] GR2880 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1472 precursor RNA and GAM1473 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39037] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1472 RNA and GAM1473 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.



[39038] GAM1472 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1472 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1472 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1472 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39039] GAM1473 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1473 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1473 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1473 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39040] It is appreciated that specific functions, and accordingly utilities, of GR2880 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2880 gene: GAM1472 target protein and GAM1473 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1472 and GAM1473

- [39041] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2881 (GR2881) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [39042] GR2881 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2881 gene was detected is described hereinabove with reference to Figs. 6-15.
- [39043] GR2881 gene encodes GR2881 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [39044] GR2881 precursor RNA folds spatially, forming GR2881 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2881 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2881 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.
- [39045] GR2881 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into

at least 2 separate GAM precursor RNAs, GAM1483 precursor RNA and GAM1484 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39046] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1483 RNA and GAM1484 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39047] GAM1483 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1483 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1483 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1483 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39048] GAM1484 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1484 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1484 target RNA, herein schematically

represented by GAM2 TARGET RNA into GAM1484 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39049] It is appreciated that specific functions, and accordingly utilities, of GR2881 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2881 gene: GAM1483 target protein and GAM1484 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1483 and GAM1484

[39050] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2882 (GR2882) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39051] GR2882 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2882 gene was detected is described hereinabove with reference to Figs. 6-15.

[39052] GR2882 gene encodes GR2882 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39053] GR2882 precursor RNA folds spatially, forming GR2882 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2882 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2882 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39054] GR2882 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1488 precursor RNA and GAM1489 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39055] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1488 RNA and GAM1489 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39056] GAM1488 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1488 target RNA, herein schematically represented by GAM1 TARGET

RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1488 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1488 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39057] GAM1489 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1489 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1489 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1489 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39058] It is appreciated that specific functions, and accordingly utilities, of GR2882 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2882 gene: GAM1488 target protein and GAM1489 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1488 and GAM1489

[39059] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2883(GR2883) gene, which encodes an operon-like cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39060] GR2883 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2883 gene was detected is described hereinabove with reference to Figs. 6-15.

[39061] GR2883 gene encodes GR2883 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39062] GR2883 precursor RNA folds spatially, forming GR2883 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2883 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2883 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39063] GR2883 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1490 precursor RNA and GAM1491 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM

precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39064] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1490 RNA and GAM1491 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39065] GAM1490 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1490 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1490 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1490 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39066] GAM1491 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1491 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1491 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1491 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39067] It is appreciated that specific functions, and accordingly utilities, of GR2883



gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2883 gene: GAM1490 target protein and GAM1491 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1490 and GAM1491

[39068] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2884 (GR2884) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39069] GR2884 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2884 gene was detected is described hereinabove with reference to Figs. 6-15.

[39070] GR2884 gene encodes GR2884 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39071] GR2884 precursor RNA folds spatially, forming GR2884 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2884 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as

hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2884 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39072] GR2884 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1492 precursor RNA and GAM1493 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39073] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1492 RNA and GAM1493 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39074] GAM1492 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1492 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1492 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1492 target protein, herein

schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39075] GAM1493 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1493 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1493 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1493 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39076] It is appreciated that specific functions, and accordingly utilities, of GR2884 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2884 gene: GAM1492 target protein and GAM1493 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1492 and GAM1493

[39077] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2885 (GR2885) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39078] GR2885 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR2885 gene was detected is described hereinabove with reference to Figs. 6-15.

[39079] GR2885 gene encodes GR2885 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39080] GR2885 precursor RNA folds spatially, forming GR2885 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2885 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2885 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39081] GR2885 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1495 precursor RNA and GAM1496 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39082] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in

length, GAM1495 RNA and GAM1496 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39083] GAM1495 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1495 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1495 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1495 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39084] GAM1496 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1496 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1496 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1496 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39085] It is appreciated that specific functions, and accordingly utilities, of GR2885 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2885 gene: GAM1495 target protein and GAM1496 target protein, herein schematically represented by

GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1495 and GAM1496

- [39086] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2886 (GR2886) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [39087] GR2886 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2886 gene was detected is described hereinabove with reference to Figs. 6-15.
- [39088] GR2886 gene encodes GR2886 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [39089] GR2886 precursor RNA folds spatially, forming GR2886 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2886 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2886 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

- [39090] GR2886 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1497 precursor RNA and GAM1498 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [39091] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1497 RNA and GAM1498 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.
- [39092] GAM1497 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1497 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1497 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1497 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.
- [39093] GAM1498 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1498 target RNA, herein schematically represented by GAM2 TARGET

RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1498 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1498 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39094] It is appreciated that specific functions, and accordingly utilities, of GR2886 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2886 gene: GAM1497 target protein and GAM1498 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1497 and GAM1498

[39095] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2887 (GR2887) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39096] GR2887 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2887 gene was detected is described hereinabove with reference to Figs. 6-15.

[39097] GR2887 gene encodes GR2887 precursor RNA, herein designated GR



PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39098] GR2887 precursor RNA folds spatially, forming GR2887 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2887 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2887 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39099] GR2887 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1519 precursor RNA and GAM1520 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39100] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1519 RNA and GAM1520 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39101] GAM1519 RNA, herein schematically represented by GAM1 binds

complimentarily to a target binding site located in an untranslated region of GAM1519 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1519 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1519 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39102] GAM1520 RNA, herein schematically represented by GAM2 binds complimentarily to a target binding site located in an untranslated region of GAM1520 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1520 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1520 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39103] It is appreciated that specific functions, and accordingly utilities, of GR2887 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2887 gene: GAM1519 target protein and GAM1520 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1519 and GAM1520

[39104] Fig. 16 further provides a conceptual description of novel bioinformatically

detected regulatory gene, referred to here as Genomic Record 2888(GR2888) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39105] GR2888 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2888 gene was detected is described hereinabove with reference to Figs. 6-15.

[39106] GR2888 gene encodes GR2888 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39107] GR2888 precursor RNA folds spatially, forming GR2888 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2888 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2888 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39108] GR2888 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1523 precursor RNA and

GAM1524 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39109] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1523 RNA and GAM1524 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39110] GAM1523 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1523 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1523 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1523 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39111] GAM1524 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1524 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1524 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1524 target protein, herein

schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39112] It is appreciated that specific functions, and accordingly utilities, of GR2888 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2888 gene: GAM1523 target protein and GAM1524 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1523 and GAM1524

[39113] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2889 (GR2889) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39114] GR2889 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2889 gene was detected is described hereinabove with reference to Figs. 6-15.

[39115] GR2889 gene encodes GR2889 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39116] GR2889 precursor RNA folds spatially, forming GR2889 folded precursor

RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2889 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2889 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39117] GR2889 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1526 precursor RNA and GAM1527 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39118] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1526 RNA and GAM1527 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39119] GAM1526 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1526 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1526 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1526 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39120] GAM1527 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1527 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1527 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1527 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39121] It is appreciated that specific functions, and accordingly utilities, of GR2889 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2889 gene: GAM1526 target protein and GAM1527 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1526 and GAM1527

[39122] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2890 (GR2890) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

[39123] GR2890 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2890 gene was detected is described hereinabove with reference to Figs. 6-15.

[39124] GR2890 gene encodes GR2890 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39125] GR2890 precursor RNA folds spatially, forming GR2890 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2890 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2890 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39126] GR2890 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1531 precursor RNA and GAM1532 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to



## GAM PRECURSOR RNA of Fig. 8.

[39127] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1531 RNA and GAM1532 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39128] GAM1531 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1531 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1531 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1531 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39129] GAM1532 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1532 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1532 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1532 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39130] It is appreciated that specific functions, and accordingly utilities, of GR2890 gene, herein designated GR GENE, correlate with, and may be deduced

from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2890 gene: GAM1531 target protein and GAM1532 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1531 and GAM1532

[39131] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2891 (GR2891) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39132] GR2891 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2891 gene was detected is described hereinabove with reference to Figs. 6-15.

[39133] GR2891 gene encodes GR2891 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39134] GR2891 precursor RNA folds spatially, forming GR2891 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2891 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the

nucleotide sequence of GR2891 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

- [39135] GR2891 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1534 precursor RNA and GAM1535 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [39136] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1534 RNA and GAM1535 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.
- [39137] GAM1534 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1534 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1534 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1534 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39138] GAM1535 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1535 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1535 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1535 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39139] It is appreciated that specific functions, and accordingly utilities, of GR2891 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2891 gene: GAM1534 target protein and GAM1535 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1534 and GAM1535

[39140] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2892 (GR2892) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39141] GR2892 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which

GR2892 gene was detected is described hereinabove with reference to Figs. 6-15.

[39142] GR2892 gene encodes GR2892 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39143] GR2892 precursor RNA folds spatially, forming GR2892 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2892 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2892 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39144] GR2892 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1537 precursor RNA and GAM1538 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39145] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1537 RNA and GAM1538 RNA respectively, herein

schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39146] GAM1537 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1537 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1537 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1537 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39147] GAM1538 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1538 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1538 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1538 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39148] It is appreciated that specific functions, and accordingly utilities, of GR2892 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2892 gene: GAM1537 target protein and GAM1538 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The

function of these target genes is elaborated hereinabove with reference to GAM1537 and GAM1538

- [39149] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2893 (GR2893) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [39150] GR2893 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2893 gene was detected is described hereinabove with reference to Figs. 6-15.
- [39151] GR2893 gene encodes GR2893 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [39152] GR2893 precursor RNA folds spatially, forming GR2893 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2893 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2893 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

- [39153] GR2893 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1552 precursor RNA and GAM1553 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [39154] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1552 RNA and GAM1553 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.
- [39155] GAM1552 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1552 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1552 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1552 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.
- [39156] GAM1553 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1553 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as



BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1553 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1553 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39157] It is appreciated that specific functions, and accordingly utilities, of GR2893 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2893 gene: GAM1552 target protein and GAM1553 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1552 and GAM1553

[39158] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2894 (GR2894) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39159] GR2894 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2894 gene was detected is described hereinabove with reference to Figs. 6-15.

[39160] GR2894 gene encodes GR2894 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides

long.

[39161] GR2894 precursor RNA folds spatially, forming GR2894 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2894 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2894 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39162] GR2894 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1558 precursor RNA and GAM1559 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39163] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1558 RNA and GAM1559 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39164] GAM1558 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of

GAM1558 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1558 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1558 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39165] GAM1559 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1559 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1559 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1559 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39166] It is appreciated that specific functions, and accordingly utilities, of GR2894 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2894 gene: GAM1558 target protein and GAM1559 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1558 and GAM1559

[39167] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record

2895(GR2895) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39168] GR2895 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2895 gene was detected is described hereinabove with reference to Figs. 6-15.

[39169] GR2895 gene encodes GR2895 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39170] GR2895 precursor RNA folds spatially, forming GR2895 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2895 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2895 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39171] GR2895 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1564 precursor RNA and GAM1565 precursor RNA, herein schematically represented by GAM1

PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39172] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1564 RNA and GAM1565 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39173] GAM1564 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1564 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1564 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1564 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39174] GAM1565 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1565 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1565 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1565 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39175] It is appreciated that specific functions, and accordingly utilities, of GR2895 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2895 gene: GAM1564 target protein and GAM1565 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1564 and GAM1565

[39176] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2896 (GR2896) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39177] GR2896 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2896 gene was detected is described hereinabove with reference to Figs. 6-15.

[39178] GR2896 gene encodes GR2896 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39179] GR2896 precursor RNA folds spatially, forming GR2896 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2896 folded precursor RNA, herein designated GR FOLDED

PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2896 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39180] GR2896 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1567 precursor RNA and GAM1568 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39181] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1567 RNA and GAM1568 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39182] GAM1567 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1567 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1567 target RNA, herein schematically

represented by GAM1 TARGET RNA into GAM1567 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39183] GAM1568 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1568 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1568 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1568 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39184] It is appreciated that specific functions, and accordingly utilities, of GR2896 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2896 gene: GAM1567 target protein and GAM1568 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1567 and GAM1568

[39185] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2897 (GR2897) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.



[39186] GR2897 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2897 gene was detected is described hereinabove with reference to Figs. 6-15.

[39187] GR2897 gene encodes GR2897 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39188] GR2897 precursor RNA folds spatially, forming GR2897 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2897 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2897 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39189] GR2897 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1569 precursor RNA and GAM1570 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39190] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX

of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1569 RNA and GAM1570 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39191] GAM1569 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1569 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1569 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1569 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39192] GAM1570 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1570 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1570 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1570 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39193] It is appreciated that specific functions, and accordingly utilities, of GR2897 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2897 gene: GAM1569 target

protein and GAM1570 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1569 and GAM1570

[39194] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2898 (GR2898) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39195] GR2898 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2898 gene was detected is described hereinabove with reference to Figs. 6-15.

[39196] GR2898 gene encodes GR2898 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39197] GR2898 precursor RNA folds spatially, forming GR2898 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2898 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2898 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39198] GR2898 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1573 precursor RNA and GAM1574 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39199] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1573 RNA and GAM1574 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39200] GAM1573 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1573 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1573 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1573 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39201] GAM1574 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of

GAM1574 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1574 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1574 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39202] It is appreciated that specific functions, and accordingly utilities, of GR2898 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2898 gene: GAM1573 target protein and GAM1574 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1573 and GAM1574

[39203] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2899 (GR2899) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39204] GR2899 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2899 gene was detected is described hereinabove with reference to Figs. 6-15.

- [39205] GR2899 gene encodes GR2899 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [39206] GR2899 precursor RNA folds spatially, forming GR2899 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2899 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2899 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.
- [39207] GR2899 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1576 precursor RNA and GAM1577 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [39208] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1576 RNA and GAM1577 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39209] GAM1576 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1576 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1576 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1576 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39210] GAM1577 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1577 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1577 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1577 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39211] It is appreciated that specific functions, and accordingly utilities, of GR2899 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2899 gene: GAM1576 target protein and GAM1577 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1576 and GAM1577

- [39212] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2900 (GR2900) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [39213] GR2900 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2900 gene was detected is described hereinabove with reference to Figs. 6-15.
- [39214] GR2900 gene encodes GR2900 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [39215] GR2900 precursor RNA folds spatially, forming GR2900 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2900 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2900 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.
- [39216] GR2900 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into



at least 2 separate GAM precursor RNAs, GAM1583 precursor RNA and GAM1584 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39217] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1583 RNA and GAM1584 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39218] GAM1583 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1583 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1583 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1583 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39219] GAM1584 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1584 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1584 target RNA, herein schematically

represented by GAM2 TARGET RNA into GAM1584 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39220] It is appreciated that specific functions, and accordingly utilities, of GR2900 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2900 gene: GAM1583 target protein and GAM1584 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1583 and GAM1584

[39221] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2901 (GR2901) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39222] GR2901 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2901 gene was detected is described hereinabove with reference to Figs. 6-15.

[39223] GR2901 gene encodes GR2901 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39224] GR2901 precursor RNA folds spatially, forming GR2901 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2901 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2901 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39225] GR2901 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1586 precursor RNA, GAM1587 precursor RNA and GAM1588 precursor RNA, herein schematically represented by GAM1 PRECURSOR, GAM2 PRECURSOR and GAM3 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39226] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1586 RNA, GAM1587 RNA and GAM1588 RNA respectively, herein schematically represented by GAM1 RNA, GAM2 RNA and GAM3 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39227] GAM1586 RNA, herein schematically represented by GAM1 binds

complimentarily to a target binding site located in an untranslated region of GAM1586 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1586 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1586 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39228] GAM1587 RNA, herein schematically represented by GAM2 binds complimentarily to a target binding site located in an untranslated region of GAM1587 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1587 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1587 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39229] GAM1588 RNA, herein schematically represented by GAM3 binds complimentarily to a target binding site located in an untranslated region of GAM1588 target RNA, herein schematically represented by GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1588 target RNA, herein schematically represented by GAM3 TARGET RNA into GAM1588 target protein, herein schematically represented by GAM3 TARGET PROTEIN, both of Fig. 8.

[39230] It is appreciated that specific functions, and accordingly utilities, of GR2901

gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2901 gene: GAM1586 target protein, GAM1587 target protein and GAM1588 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1586, GAM1587 and GAM1588

[39231] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2902(GR2902) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39232] GR2902 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2902 gene was detected is described hereinabove with reference to Figs. 6-15.

[39233] GR2902 gene encodes GR2902 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39234] GR2902 precursor RNA folds spatially, forming GR2902 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2902 folded precursor RNA, herein designated GR FOLDED

PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2902 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39235] GR2902 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1594 precursor RNA and GAM1595 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39236] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1594 RNA and GAM1595 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39237] GAM1594 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1594 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1594 target RNA, herein schematically

represented by GAM1 TARGET RNA into GAM1594 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39238] GAM1595 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1595 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1595 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1595 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39239] It is appreciated that specific functions, and accordingly utilities, of GR2902 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2902 gene: GAM1594 target protein and GAM1595 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1594 and GAM1595

[39240] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2903 (GR2903) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

- [39241] GR2903 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2903 gene was detected is described hereinabove with reference to Figs. 6-15.
- [39242] GR2903 gene encodes GR2903 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [39243] GR2903 precursor RNA folds spatially, forming GR2903 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2903 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2903 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.
- [39244] GR2903 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM1596 precursor RNA, GAM1597 precursor RNA, GAM1598 precursor RNA and GAM1599 precursor RNA, herein schematically represented by GAM1 PRECURSOR, GAM2 PRECURSOR, GAM3 PRECURSOR and GAM4 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.



[39245] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1596 RNA, GAM1597 RNA, GAM1598 RNA and GAM1599 RNA respectively, herein schematically represented by GAM1 RNA, GAM2 RNA, GAM3 RNA and GAM4 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39246] GAM1596 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1596 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1596 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1596 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39247] GAM1597 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1597 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1597 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1597 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39248] GAM1598 RNA, herein schematically represented by GAM3 binds complementarily to a target binding site located in an untranslated region of

GAM1598 target RNA, herein schematically represented by GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1598 target RNA, herein schematically represented by GAM3 TARGET RNA into GAM1598 target protein, herein schematically represented by GAM3 TARGET PROTEIN, both of Fig. 8.

[39249] GAM1599 RNA, herein schematically represented by GAM4 binds complementarily to a target binding site located in an untranslated region of GAM1599 target RNA, herein schematically represented by GAM4 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1599 target RNA, herein schematically represented by GAM4 TARGET RNA into GAM1599 target protein, herein schematically represented by GAM4 TARGET PROTEIN, both of Fig. 8.

[39250] It is appreciated that specific functions, and accordingly utilities, of GR2903 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2903 gene: GAM1596 target protein, GAM1597 target protein, GAM1598 target protein and GAM1599 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1596, GAM1597, GAM1598 and GAM1599

[39251] Fig. 16 further provides a conceptual description of novel bioinformatically

detected regulatory gene, referred to here as Genomic Record 2904 (GR2904) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39252] GR2904 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2904 gene was detected is described hereinabove with reference to Figs. 6-15.

[39253] GR2904 gene encodes GR2904 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39254] GR2904 precursor RNA folds spatially, forming GR2904 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2904 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2904 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39255] GR2904 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1607 precursor RNA and

GAM1608 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39256] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1607 RNA and GAM1608 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39257] GAM1607 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1607 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1607 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1607 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39258] GAM1608 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1608 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1608 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1608 target protein, herein

schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39259] It is appreciated that specific functions, and accordingly utilities, of GR2904 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2904 gene: GAM1607 target protein and GAM1608 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1607 and GAM1608

[39260] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2905 (GR2905) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39261] GR2905 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2905 gene was detected is described hereinabove with reference to Figs. 6-15.

[39262] GR2905 gene encodes GR2905 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39263] GR2905 precursor RNA folds spatially, forming GR2905 folded precursor

RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2905 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2905 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39264] GR2905 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1612 precursor RNA and GAM1613 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39265] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1612 RNA and GAM1613 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39266] GAM1612 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1612 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1612 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1612 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39267] GAM1613 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1613 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1613 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1613 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39268] It is appreciated that specific functions, and accordingly utilities, of GR2905 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2905 gene: GAM1612 target protein and GAM1613 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1612 and GAM1613

[39269] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2906 (GR2906) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

[39270] GR2906 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2906 gene was detected is described hereinabove with reference to Figs. 6-15.

[39271] GR2906 gene encodes GR2906 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39272] GR2906 precursor RNA folds spatially, forming GR2906 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2906 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2906 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39273] GR2906 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1616 precursor RNA and GAM1617 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to



GAM PRECURSOR RNA of Fig. 8.

[39274] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1616 RNA and GAM1617 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39275] GAM1616 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1616 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1616 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1616 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39276] GAM1617 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1617 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1617 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1617 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39277] It is appreciated that specific functions, and accordingly utilities, of GR2906 gene, herein designated GR GENE, correlate with, and may be deduced

from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2906 gene: GAM1616 target protein and GAM1617 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1616 and GAM1617

[39278] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2907 (GR2907) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39279] GR2907 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2907 gene was detected is described hereinabove with reference to Figs. 6-15.

[39280] GR2907 gene encodes GR2907 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39281] GR2907 precursor RNA folds spatially, forming GR2907 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2907 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the

nucleotide sequence of GR2907 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39282] GR2907 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1618 precursor RNA and GAM1619 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39283] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1618 RNA and GAM1619 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39284] GAM1618 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1618 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1618 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1618 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39285] GAM1619 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1619 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1619 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1619 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39286] It is appreciated that specific functions, and accordingly utilities, of GR2907 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2907 gene: GAM1618 target protein and GAM1619 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1618 and GAM1619

[39287] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2908 (GR2908) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39288] GR2908 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which

GR2908 gene was detected is described hereinabove with reference to Figs. 6-15.

[39289] GR2908 gene encodes GR2908 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39290] GR2908 precursor RNA folds spatially, forming GR2908 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2908 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2908 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39291] GR2908 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1620 precursor RNA and GAM1621 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39292] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1620 RNA and GAM1621 RNA respectively, herein

schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39293] GAM1620 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1620 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1620 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1620 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39294] GAM1621 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1621 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1621 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1621 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39295] It is appreciated that specific functions, and accordingly utilities, of GR2908 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2908 gene: GAM1620 target protein and GAM1621 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The

function of these target genes is elaborated hereinabove with reference to GAM1620 and GAM1621

- [39296] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2909 (GR2909) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [39297] GR2909 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2909 gene was detected is described hereinabove with reference to Figs. 6-15.
- [39298] GR2909 gene encodes GR2909 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [39299] GR2909 precursor RNA folds spatially, forming GR2909 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2909 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2909 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

- [39300] GR2909 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1626 precursor RNA and GAM1627 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [39301] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1626 RNA and GAM1627 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.
- [39302] GAM1626 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1626 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1626 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1626 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.
- [39303] GAM1627 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1627 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as



BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1627 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1627 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39304] It is appreciated that specific functions, and accordingly utilities, of GR2909 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2909 gene: GAM1626 target protein and GAM1627 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1626 and GAM1627

[39305] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2910 (GR2910) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39306] GR2910 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2910 gene was detected is described hereinabove with reference to Figs. 6-15.

[39307] GR2910 gene encodes GR2910 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides

long.

[39308] GR2910 precursor RNA folds spatially, forming GR2910 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2910 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2910 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39309] GR2910 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1630 precursor RNA and GAM1631 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39310] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1630 RNA and GAM1631 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39311] GAM1630 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of

GAM1630 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1630 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1630 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39312] GAM1631 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1631 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1631 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1631 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39313] It is appreciated that specific functions, and accordingly utilities, of GR2910 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2910 gene: GAM1630 target protein and GAM1631 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1630 and GAM1631

[39314] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record

2911(GR2911) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39315] GR2911 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2911 gene was detected is described hereinabove with reference to Figs. 6-15.

[39316] GR2911 gene encodes GR2911 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39317] GR2911 precursor RNA folds spatially, forming GR2911 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2911 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2911 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39318] GR2911 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1636 precursor RNA and GAM1637 precursor RNA, herein schematically represented by GAM1

PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39319] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1636 RNA and GAM1637 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39320] GAM1636 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1636 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1636 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1636 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39321] GAM1637 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1637 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1637 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1637 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39322] It is appreciated that specific functions, and accordingly utilities, of GR2911 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2911 gene: GAM1636 target protein and GAM1637 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1636 and GAM1637

[39323] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2912 (GR2912) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39324] GR2912 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2912 gene was detected is described hereinabove with reference to Figs. 6-15.

[39325] GR2912 gene encodes GR2912 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39326] GR2912 precursor RNA folds spatially, forming GR2912 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2912 folded precursor RNA, herein designated GR FOLDED

PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2912 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39327] GR2912 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1643 precursor RNA and GAM1644 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39328] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1643 RNA and GAM1644 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39329] GAM1643 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1643 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1643 target RNA, herein schematically

represented by GAM1 TARGET RNA into GAM1643 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39330] GAM1644 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1644 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1644 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1644 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39331] It is appreciated that specific functions, and accordingly utilities, of GR2912 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2912 gene: GAM1643 target protein and GAM1644 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1643 and GAM1644

[39332] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2913 (GR2913) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.



[39333] GR2913 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2913 gene was detected is described hereinabove with reference to Figs. 6-15.

[39334] GR2913 gene encodes GR2913 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39335] GR2913 precursor RNA folds spatially, forming GR2913 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2913 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2913 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39336] GR2913 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1650 precursor RNA, GAM1651 precursor RNA and GAM1652 precursor RNA, herein schematically represented by GAM1 PRECURSOR, GAM2 PRECURSOR and GAM3 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39337] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1650 RNA, GAM1651 RNA and GAM1652 RNA respectively, herein schematically represented by GAM1 RNA, GAM2 RNA and GAM3 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39338] GAM1650 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1650 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1650 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1650 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39339] GAM1651 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1651 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1651 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1651 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39340] GAM1652 RNA, herein schematically represented by GAM3 binds complementarily to a target binding site located in an untranslated region of

GAM1652 target RNA, herein schematically represented by GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1652 target RNA, herein schematically represented by GAM3 TARGET RNA into GAM1652 target protein, herein schematically represented by GAM3 TARGET PROTEIN, both of Fig. 8.

[39341] It is appreciated that specific functions, and accordingly utilities, of GR2913 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2913 gene: GAM1650 target protein, GAM1651 target protein and GAM1652 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1650, GAM1651 and GAM1652

[39342] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2914(GR2914) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39343] GR2914 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2914 gene was detected is described hereinabove with reference to Figs.

- [39344] GR2914 gene encodes GR2914 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [39345] GR2914 precursor RNA folds spatially, forming GR2914 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2914 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2914 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.
- [39346] GR2914 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1662 precursor RNA and GAM1663 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [39347] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1662 RNA and GAM1663 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively,

each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39348] GAM1662 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1662 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1662 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1662 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39349] GAM1663 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1663 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1663 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1663 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39350] It is appreciated that specific functions, and accordingly utilities, of GR2914 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2914 gene: GAM1662 target protein and GAM1663 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to

- [39351] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2915(GR2915) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [39352] GR2915 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2915 gene was detected is described hereinabove with reference to Figs. 6-15.
- [39353] GR2915 gene encodes GR2915 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [39354] GR2915 precursor RNA folds spatially, forming GR2915 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2915 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2915 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

- [39355] GR2915 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1670 precursor RNA and GAM1671 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [39356] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1670 RNA and GAM1671 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.
- [39357] GAM1670 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1670 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1670 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1670 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.
- [39358] GAM1671 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1671 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1671 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1671 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39359] It is appreciated that specific functions, and accordingly utilities, of GR2915 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2915 gene: GAM1670 target protein and GAM1671 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1670 and GAM1671

[39360] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2916 (GR2916) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39361] GR2916 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2916 gene was detected is described hereinabove with reference to Figs. 6-15.

[39362] GR2916 gene encodes GR2916 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides



long.

[39363] GR2916 precursor RNA folds spatially, forming GR2916 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2916 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2916 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39364] GR2916 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1674 precursor RNA and GAM1675 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39365] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1674 RNA and GAM1675 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39366] GAM1674 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of

GAM1674 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1674 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1674 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39367] GAM1675 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1675 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1675 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1675 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39368] It is appreciated that specific functions, and accordingly utilities, of GR2916 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2916 gene: GAM1674 target protein and GAM1675 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1674 and GAM1675

[39369] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record

2917(GR2917) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39370] GR2917 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2917 gene was detected is described hereinabove with reference to Figs. 6-15.

[39371] GR2917 gene encodes GR2917 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39372] GR2917 precursor RNA folds spatially, forming GR2917 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2917 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2917 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39373] GR2917 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1678 precursor RNA and GAM1679 precursor RNA, herein schematically represented by GAM1

PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39374] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1678 RNA and GAM1679 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39375] GAM1678 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1678 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1678 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1678 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39376] GAM1679 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1679 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1679 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1679 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39377] It is appreciated that specific functions, and accordingly utilities, of GR2917 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2917 gene: GAM1678 target protein and GAM1679 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1678 and GAM1679

[39378] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2918 (GR2918) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39379] GR2918 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2918 gene was detected is described hereinabove with reference to Figs. 6-15.

[39380] GR2918 gene encodes GR2918 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39381] GR2918 precursor RNA folds spatially, forming GR2918 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2918 folded precursor RNA, herein designated GR FOLDED

PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2918 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39382] GR2918 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1681 precursor RNA and GAM1682 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39383] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1681 RNA and GAM1682 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39384] GAM1681 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1681 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1681 target RNA, herein schematically

represented by GAM1 TARGET RNA into GAM1681 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39385] GAM1682 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1682 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1682 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1682 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39386] It is appreciated that specific functions, and accordingly utilities, of GR2918 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2918 gene: GAM1681 target protein and GAM1682 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1681 and GAM1682

[39387] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2919 (GR2919) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39388] GR2919 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2919 gene was detected is described hereinabove with reference to Figs. 6-15.

[39389] GR2919 gene encodes GR2919 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39390] GR2919 precursor RNA folds spatially, forming GR2919 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2919 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2919 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39391] GR2919 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1686 precursor RNA and GAM1687 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39392] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX



of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1686 RNA and GAM1687 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39393] GAM1686 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1686 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1686 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1686 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39394] GAM1687 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1687 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1687 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1687 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39395] It is appreciated that specific functions, and accordingly utilities, of GR2919 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2919 gene: GAM1686 target

protein and GAM1687 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1686 and GAM1687

[39396] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2920 (GR2920) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39397] GR2920 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2920 gene was detected is described hereinabove with reference to Figs. 6-15.

[39398] GR2920 gene encodes GR2920 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39399] GR2920 precursor RNA folds spatially, forming GR2920 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2920 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2920 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39400] GR2920 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1695 precursor RNA, GAM1696 precursor RNA and GAM1697 precursor RNA, herein schematically represented by GAM1 PRECURSOR, GAM2 PRECURSOR and GAM3 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39401] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1695 RNA, GAM1696 RNA and GAM1697 RNA respectively, herein schematically represented by GAM1 RNA, GAM2 RNA and GAM3 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39402] GAM1695 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1695 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1695 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1695 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

- [39403] GAM1696 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1696 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1696 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1696 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.
- [39404] GAM1697 RNA, herein schematically represented by GAM3 binds complementarily to a target binding site located in an untranslated region of GAM1697 target RNA, herein schematically represented by GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1697 target RNA, herein schematically represented by GAM3 TARGET RNA into GAM1697 target protein, herein schematically represented by GAM3 TARGET PROTEIN, both of Fig. 8.
- [39405] It is appreciated that specific functions, and accordingly utilities, of GR2920 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2920 gene: GAM1695 target protein, GAM1696 target protein and GAM1697 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1695, GAM1696 and GAM1697

- [39406] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2921 (GR2921) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [39407] GR2921 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2921 gene was detected is described hereinabove with reference to Figs. 6-15.
- [39408] GR2921 gene encodes GR2921 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [39409] GR2921 precursor RNA folds spatially, forming GR2921 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2921 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2921 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.
- [39410] GR2921 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into

at least 2 separate GAM precursor RNAs, GAM1699 precursor RNA and GAM1700 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39411] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1699 RNA and GAM1700 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39412] GAM1699 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1699 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1699 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1699 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39413] GAM1700 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1700 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1700 target RNA, herein schematically

represented by GAM2 TARGET RNA into GAM1700 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39414] It is appreciated that specific functions, and accordingly utilities, of GR2921 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2921 gene: GAM1699 target protein and GAM1700 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1699 and GAM1700

[39415] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2922 (GR2922) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39416] GR2922 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2922 gene was detected is described hereinabove with reference to Figs. 6-15.

[39417] GR2922 gene encodes GR2922 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39418] GR2922 precursor RNA folds spatially, forming GR2922 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2922 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2922 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39419] GR2922 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1704 precursor RNA and GAM1705 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39420] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1704 RNA and GAM1705 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39421] GAM1704 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1704 target RNA, herein schematically represented by GAM1 TARGET



RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1704 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1704 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39422] GAM1705 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1705 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1705 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1705 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39423] It is appreciated that specific functions, and accordingly utilities, of GR2922 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2922 gene: GAM1704 target protein and GAM1705 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1704 and GAM1705

[39424] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2923(GR2923) gene, which encodes an operon-like cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39425] GR2923 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2923 gene was detected is described hereinabove with reference to Figs. 6-15.

[39426] GR2923 gene encodes GR2923 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39427] GR2923 precursor RNA folds spatially, forming GR2923 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2923 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2923 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39428] GR2923 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1708 precursor RNA and GAM1709 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM

precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39429] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1708 RNA and GAM1709 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39430] GAM1708 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1708 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1708 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1708 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39431] GAM1709 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1709 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1709 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1709 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39432] It is appreciated that specific functions, and accordingly utilities, of GR2923

gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2923 gene: GAM1708 target protein and GAM1709 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1708 and GAM1709

[39433] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2924 (GR2924) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39434] GR2924 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2924 gene was detected is described hereinabove with reference to Figs. 6-15.

[39435] GR2924 gene encodes GR2924 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39436] GR2924 precursor RNA folds spatially, forming GR2924 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2924 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as

hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2924 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39437] GR2924 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1712 precursor RNA, GAM1713 precursor RNA and GAM1714 precursor RNA, herein schematically represented by GAM1 PRECURSOR, GAM2 PRECURSOR and GAM3 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39438] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1712 RNA, GAM1713 RNA and GAM1714 RNA respectively, herein schematically represented by GAM1 RNA, GAM2 RNA and GAM3 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39439] GAM1712 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1712 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby

inhibiting translation of GAM1712 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1712 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39440] GAM1713 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1713 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1713 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1713 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39441] GAM1714 RNA, herein schematically represented by GAM3 binds complementarily to a target binding site located in an untranslated region of GAM1714 target RNA, herein schematically represented by GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1714 target RNA, herein schematically represented by GAM3 TARGET RNA into GAM1714 target protein, herein schematically represented by GAM3 TARGET PROTEIN, both of Fig. 8.

[39442] It is appreciated that specific functions, and accordingly utilities, of GR2924 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2924 gene: GAM1712 target protein, GAM1713 target protein and GAM1714 target protein, herein

schematically represented by GAM1 TARGET PROTEIN through GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1712, GAM1713 and GAM1714

- [39443] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2925(GR2925) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [39444] GR2925 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2925 gene was detected is described hereinabove with reference to Figs. 6-15.
- [39445] GR2925 gene encodes GR2925 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [39446] GR2925 precursor RNA folds spatially, forming GR2925 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2925 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2925 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39447] GR2925 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1715 precursor RNA, GAM1716 precursor RNA and GAM1717 precursor RNA, herein schematically represented by GAM1 PRECURSOR, GAM2 PRECURSOR and GAM3 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39448] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1715 RNA, GAM1716 RNA and GAM1717 RNA respectively, herein schematically represented by GAM1 RNA, GAM2 RNA and GAM3 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39449] GAM1715 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1715 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1715 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1715 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.



[39450] GAM1716 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1716 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1716 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1716 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39451] GAM1717 RNA, herein schematically represented by GAM3 binds complementarily to a target binding site located in an untranslated region of GAM1717 target RNA, herein schematically represented by GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1717 target RNA, herein schematically represented by GAM3 TARGET RNA into GAM1717 target protein, herein schematically represented by GAM3 TARGET PROTEIN, both of Fig. 8.

[39452] It is appreciated that specific functions, and accordingly utilities, of GR2925 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2925 gene: GAM1715 target protein, GAM1716 target protein and GAM1717 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1715, GAM1716 and GAM1717

- [39453] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2926(GR2926) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [39454] GR2926 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2926 gene was detected is described hereinabove with reference to Figs. 6-15.
- [39455] GR2926 gene encodes GR2926 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [39456] GR2926 precursor RNA folds spatially, forming GR2926 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2926 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2926 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.
- [39457] GR2926 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into

at least 2 separate GAM precursor RNAs, GAM1718 precursor RNA and GAM1719 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39458] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1718 RNA and GAM1719 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39459] GAM1718 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1718 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1718 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1718 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39460] GAM1719 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1719 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1719 target RNA, herein schematically

represented by GAM2 TARGET RNA into GAM1719 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39461] It is appreciated that specific functions, and accordingly utilities, of GR2926 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2926 gene: GAM1718 target protein and GAM1719 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1718 and GAM1719

[39462] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2927 (GR2927) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39463] GR2927 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2927 gene was detected is described hereinabove with reference to Figs. 6-15.

[39464] GR2927 gene encodes GR2927 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39465] GR2927 precursor RNA folds spatially, forming GR2927 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2927 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2927 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39466] GR2927 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1723 precursor RNA and GAM1724 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39467] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1723 RNA and GAM1724 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39468] GAM1723 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1723 target RNA, herein schematically represented by GAM1 TARGET

RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1723 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1723 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39469] GAM1724 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1724 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1724 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1724 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39470] It is appreciated that specific functions, and accordingly utilities, of GR2927 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2927 gene: GAM1723 target protein and GAM1724 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1723 and GAM1724

[39471] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2928(GR2928) gene, which encodes an operon-like cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39472] GR2928 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2928 gene was detected is described hereinabove with reference to Figs. 6-15.

[39473] GR2928 gene encodes GR2928 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39474] GR2928 precursor RNA folds spatially, forming GR2928 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2928 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2928 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39475] GR2928 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM1735 precursor RNA, GAM1736 precursor RNA, GAM1737 precursor RNA and GAM1738 precursor RNA, herein schematically represented by GAM1 PRECURSOR,

GAM2 PRECURSOR, GAM3 PRECURSOR and GAM4 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39476] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1735 RNA, GAM1736 RNA, GAM1737 RNA and GAM1738 RNA respectively, herein schematically represented by GAM1 RNA, GAM2 RNA, GAM3 RNA and GAM4 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39477] GAM1735 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1735 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1735 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1735 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39478] GAM1736 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1736 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1736 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1736 target protein, herein



schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39479] GAM1737 RNA, herein schematically represented by GAM3 binds complementarily to a target binding site located in an untranslated region of GAM1737 target RNA, herein schematically represented by GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1737 target RNA, herein schematically represented by GAM3 TARGET RNA into GAM1737 target protein, herein schematically represented by GAM3 TARGET PROTEIN, both of Fig. 8.

[39480] GAM1738 RNA, herein schematically represented by GAM4 binds complementarily to a target binding site located in an untranslated region of GAM1738 target RNA, herein schematically represented by GAM4 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1738 target RNA, herein schematically represented by GAM4 TARGET RNA into GAM1738 target protein, herein schematically represented by GAM4 TARGET PROTEIN, both of Fig. 8.

[39481] It is appreciated that specific functions, and accordingly utilities, of GR2928 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2928 gene: GAM1735 target protein, GAM1736 target protein, GAM1737 target protein and GAM1738 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM TARGET PROTEIN respectively. The function of

these target genes is elaborated hereinabove with reference to GAM1735, GAM1736, GAM1737 and GAM1738

- [39482] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2929(GR2929) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [39483] GR2929 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2929 gene was detected is described hereinabove with reference to Figs. 6-15.
- [39484] GR2929 gene encodes GR2929 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [39485] GR2929 precursor RNA folds spatially, forming GR2929 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2929 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2929 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

- [39486] GR2929 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1744 precursor RNA and GAM1745 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [39487] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1744 RNA and GAM1745 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.
- [39488] GAM1744 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1744 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1744 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1744 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.
- [39489] GAM1745 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1745 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1745 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1745 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39490] It is appreciated that specific functions, and accordingly utilities, of GR2929 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2929 gene: GAM1744 target protein and GAM1745 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1744 and GAM1745

[39491] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2930 (GR2930) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39492] GR2930 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2930 gene was detected is described hereinabove with reference to Figs. 6-15.

[39493] GR2930 gene encodes GR2930 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides

long.

[39494] GR2930 precursor RNA folds spatially, forming GR2930 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2930 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2930 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39495] GR2930 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1749 precursor RNA and GAM1750 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39496] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1749 RNA and GAM1750 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39497] GAM1749 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of

GAM1749 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1749 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1749 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39498] GAM1750 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1750 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1750 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1750 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39499] It is appreciated that specific functions, and accordingly utilities, of GR2930 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2930 gene: GAM1749 target protein and GAM1750 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1749 and GAM1750

[39500] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record

2931(GR2931) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39501] GR2931 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2931 gene was detected is described hereinabove with reference to Figs. 6-15.

[39502] GR2931 gene encodes GR2931 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39503] GR2931 precursor RNA folds spatially, forming GR2931 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2931 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2931 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39504] GR2931 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1751 precursor RNA and GAM1752 precursor RNA, herein schematically represented by GAM1

PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39505] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1751 RNA and GAM1752 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39506] GAM1751 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1751 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1751 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1751 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39507] GAM1752 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1752 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1752 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1752 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.



[39508] It is appreciated that specific functions, and accordingly utilities, of GR2931 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2931 gene: GAM1751 target protein and GAM1752 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1751 and GAM1752

[39509] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2932 (GR2932) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39510] GR2932 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2932 gene was detected is described hereinabove with reference to Figs. 6-15.

[39511] GR2932 gene encodes GR2932 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39512] GR2932 precursor RNA folds spatially, forming GR2932 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2932 folded precursor RNA, herein designated GR FOLDED

PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2932 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39513] GR2932 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1755 precursor RNA and GAM1756 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39514] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1755 RNA and GAM1756 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39515] GAM1755 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1755 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1755 target RNA, herein schematically

represented by GAM1 TARGET RNA into GAM1755 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39516] GAM1756 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1756 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1756 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1756 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39517] It is appreciated that specific functions, and accordingly utilities, of GR2932 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2932 gene: GAM1755 target protein and GAM1756 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1755 and GAM1756

[39518] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2933 (GR2933) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39519] GR2933 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2933 gene was detected is described hereinabove with reference to Figs. 6-15.

[39520] GR2933 gene encodes GR2933 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39521] GR2933 precursor RNA folds spatially, forming GR2933 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2933 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2933 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39522] GR2933 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1761 precursor RNA and GAM1762 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39523] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX

of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1761 RNA and GAM1762 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39524] GAM1761 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1761 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1761 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1761 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39525] GAM1762 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1762 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1762 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1762 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39526] It is appreciated that specific functions, and accordingly utilities, of GR2933 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2933 gene: GAM1761 target

protein and GAM1762 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1761 and GAM1762

[39527] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2934 (GR2934) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39528] GR2934 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2934 gene was detected is described hereinabove with reference to Figs. 6-15.

[39529] GR2934 gene encodes GR2934 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39530] GR2934 precursor RNA folds spatially, forming GR2934 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2934 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2934 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39531] GR2934 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1764 precursor RNA and GAM1765 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39532] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1764 RNA and GAM1765 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39533] GAM1764 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1764 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1764 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1764 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39534] GAM1765 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of

GAM1765 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1765 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1765 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39535] It is appreciated that specific functions, and accordingly utilities, of GR2934 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2934 gene: GAM1764 target protein and GAM1765 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1764 and GAM1765

[39536] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2935 (GR2935) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39537] GR2935 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2935 gene was detected is described hereinabove with reference to Figs. 6-15.



[39538] GR2935 gene encodes GR2935 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39539] GR2935 precursor RNA folds spatially, forming GR2935 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2935 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2935 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39540] GR2935 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1768 precursor RNA and GAM1769 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39541] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1768 RNA and GAM1769 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39542] GAM1768 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1768 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1768 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1768 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39543] GAM1769 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1769 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1769 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1769 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39544] It is appreciated that specific functions, and accordingly utilities, of GR2935 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2935 gene: GAM1768 target protein and GAM1769 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1768 and GAM1769

- [39545] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2936 (GR2936) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [39546] GR2936 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2936 gene was detected is described hereinabove with reference to Figs. 6-15.
- [39547] GR2936 gene encodes GR2936 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [39548] GR2936 precursor RNA folds spatially, forming GR2936 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2936 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2936 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.
- [39549] GR2936 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into

at least 2 separate GAM precursor RNAs, GAM1775 precursor RNA and GAM1776 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39550] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1775 RNA and GAM1776 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39551] GAM1775 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1775 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1775 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1775 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39552] GAM1776 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1776 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1776 target RNA, herein schematically

represented by GAM2 TARGET RNA into GAM1776 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39553] It is appreciated that specific functions, and accordingly utilities, of GR2936 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2936 gene: GAM1775 target protein and GAM1776 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1775 and GAM1776

[39554] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2937 (GR2937) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39555] GR2937 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2937 gene was detected is described hereinabove with reference to Figs. 6-15.

[39556] GR2937 gene encodes GR2937 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39557] GR2937 precursor RNA folds spatially, forming GR2937 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2937 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2937 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39558] GR2937 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1777 precursor RNA and GAM1778 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39559] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1777 RNA and GAM1778 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39560] GAM1777 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1777 target RNA, herein schematically represented by GAM1 TARGET

RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1777 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1777 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39561] GAM1778 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1778 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1778 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1778 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39562] It is appreciated that specific functions, and accordingly utilities, of GR2937 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2937 gene: GAM1777 target protein and GAM1778 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1777 and GAM1778

[39563] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2938(GR2938) gene, which encodes an operon-like cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39564] GR2938 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2938 gene was detected is described hereinabove with reference to Figs. 6-15.

[39565] GR2938 gene encodes GR2938 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39566] GR2938 precursor RNA folds spatially, forming GR2938 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2938 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2938 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39567] GR2938 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1782 precursor RNA and GAM1783 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM



precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39568] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1782 RNA and GAM1783 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39569] GAM1782 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1782 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1782 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1782 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39570] GAM1783 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1783 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1783 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1783 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39571] It is appreciated that specific functions, and accordingly utilities, of GR2938

gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2938 gene: GAM1782 target protein and GAM1783 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1782 and GAM1783

[39572] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2939 (GR2939) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39573] GR2939 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2939 gene was detected is described hereinabove with reference to Figs. 6-15.

[39574] GR2939 gene encodes GR2939 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39575] GR2939 precursor RNA folds spatially, forming GR2939 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2939 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as

hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2939 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39576] GR2939 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1784 precursor RNA and GAM1785 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39577] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1784 RNA and GAM1785 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39578] GAM1784 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1784 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1784 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1784 target protein, herein

schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39579] GAM1785 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1785 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1785 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1785 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39580] It is appreciated that specific functions, and accordingly utilities, of GR2939 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2939 gene: GAM1784 target protein and GAM1785 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1784 and GAM1785

[39581] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2940 (GR2940) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39582] GR2940 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR2940 gene was detected is described hereinabove with reference to Figs. 6-15.

[39583] GR2940 gene encodes GR2940 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39584] GR2940 precursor RNA folds spatially, forming GR2940 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2940 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2940 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39585] GR2940 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1789 precursor RNA and GAM1790 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39586] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in

length, GAM1789 RNA and GAM1790 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39587] GAM1789 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1789 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1789 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1789 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39588] GAM1790 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1790 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1790 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1790 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39589] It is appreciated that specific functions, and accordingly utilities, of GR2940 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2940 gene: GAM1789 target protein and GAM1790 target protein, herein schematically represented by

GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1789 and GAM1790

[39590] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2941 (GR2941) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39591] GR2941 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2941 gene was detected is described hereinabove with reference to Figs. 6-15.

[39592] GR2941 gene encodes GR2941 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39593] GR2941 precursor RNA folds spatially, forming GR2941 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2941 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2941 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

- [39594] GR2941 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1796 precursor RNA and GAM1797 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [39595] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1796 RNA and GAM1797 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.
- [39596] GAM1796 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1796 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1796 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1796 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.
- [39597] GAM1797 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1797 target RNA, herein schematically represented by GAM2 TARGET



RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1797 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1797 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39598] It is appreciated that specific functions, and accordingly utilities, of GR2941 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2941 gene: GAM1796 target protein and GAM1797 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1796 and GAM1797

[39599] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2942 (GR2942) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39600] GR2942 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2942 gene was detected is described hereinabove with reference to Figs. 6-15.

[39601] GR2942 gene encodes GR2942 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39602] GR2942 precursor RNA folds spatially, forming GR2942 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2942 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2942 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39603] GR2942 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1800 precursor RNA and GAM1801 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39604] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1800 RNA and GAM1801 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39605] GAM1800 RNA, herein schematically represented by GAM1 binds

complimentarily to a target binding site located in an untranslated region of GAM1800 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1800 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1800 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39606] GAM1801 RNA, herein schematically represented by GAM2 binds complimentarily to a target binding site located in an untranslated region of GAM1801 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1801 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1801 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39607] It is appreciated that specific functions, and accordingly utilities, of GR2942 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2942 gene: GAM1800 target protein and GAM1801 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1800 and GAM1801

[39608] Fig. 16 further provides a conceptual description of novel bioinformatically

detected regulatory gene, referred to here as Genomic Record 2943(GR2943) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39609] GR2943 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2943 gene was detected is described hereinabove with reference to Figs. 6-15.

[39610] GR2943 gene encodes GR2943 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39611] GR2943 precursor RNA folds spatially, forming GR2943 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2943 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2943 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39612] GR2943 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1806 precursor RNA and

GAM1807 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39613] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1806 RNA and GAM1807 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39614] GAM1806 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1806 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1806 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1806 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39615] GAM1807 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1807 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1807 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1807 target protein, herein

schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39616] It is appreciated that specific functions, and accordingly utilities, of GR2943 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2943 gene: GAM1806 target protein and GAM1807 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1806 and GAM1807

[39617] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2944 (GR2944) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39618] GR2944 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2944 gene was detected is described hereinabove with reference to Figs. 6-15.

[39619] GR2944 gene encodes GR2944 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39620] GR2944 precursor RNA folds spatially, forming GR2944 folded precursor

RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2944 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2944 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39621] GR2944 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1812 precursor RNA and GAM1813 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39622] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1812 RNA and GAM1813 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39623] GAM1812 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1812 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1812 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1812 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39624] GAM1813 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1813 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1813 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1813 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39625] It is appreciated that specific functions, and accordingly utilities, of GR2944 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2944 gene: GAM1812 target protein and GAM1813 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1812 and GAM1813

[39626] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2945 (GR2945) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one



target gene, the function and utility of which at least one target gene is known in the art.

[39627] GR2945 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2945 gene was detected is described hereinabove with reference to Figs. 6-15.

[39628] GR2945 gene encodes GR2945 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39629] GR2945 precursor RNA folds spatially, forming GR2945 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2945 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2945 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39630] GR2945 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1830 precursor RNA and GAM1831 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to

## GAM PRECURSOR RNA of Fig. 8.

[39631] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1830 RNA and GAM1831 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39632] GAM1830 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1830 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1830 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1830 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39633] GAM1831 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1831 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1831 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1831 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39634] It is appreciated that specific functions, and accordingly utilities, of GR2945 gene, herein designated GR GENE, correlate with, and may be deduced

from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2945 gene: GAM1830 target protein and GAM1831 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1830 and GAM1831

[39635] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2946 (GR2946) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39636] GR2946 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2946 gene was detected is described hereinabove with reference to Figs. 6-15.

[39637] GR2946 gene encodes GR2946 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39638] GR2946 precursor RNA folds spatially, forming GR2946 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2946 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the

nucleotide sequence of GR2946 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

- [39639] GR2946 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1833 precursor RNA and GAM1834 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [39640] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1833 RNA and GAM1834 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.
- [39641] GAM1833 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1833 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1833 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1833 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39642] GAM1834 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1834 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1834 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1834 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39643] It is appreciated that specific functions, and accordingly utilities, of GR2946 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2946 gene: GAM1833 target protein and GAM1834 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1833 and GAM1834

[39644] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2947 (GR2947) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39645] GR2947 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which

GR2947 gene was detected is described hereinabove with reference to Figs. 6-15.

[39646] GR2947 gene encodes GR2947 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39647] GR2947 precursor RNA folds spatially, forming GR2947 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2947 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2947 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39648] GR2947 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1842 precursor RNA and GAM1843 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39649] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1842 RNA and GAM1843 RNA respectively, herein

schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39650] GAM1842 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1842 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1842 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1842 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39651] GAM1843 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1843 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1843 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1843 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39652] It is appreciated that specific functions, and accordingly utilities, of GR2947 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2947 gene: GAM1842 target protein and GAM1843 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The

function of these target genes is elaborated hereinabove with reference to GAM1842 and GAM1843

- [39653] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2948 (GR2948) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [39654] GR2948 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2948 gene was detected is described hereinabove with reference to Figs. 6-15.
- [39655] GR2948 gene encodes GR2948 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [39656] GR2948 precursor RNA folds spatially, forming GR2948 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2948 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2948 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.



- [39657] GR2948 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1850 precursor RNA and GAM1851 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [39658] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1850 RNA and GAM1851 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.
- [39659] GAM1850 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1850 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1850 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1850 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.
- [39660] GAM1851 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1851 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1851 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1851 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39661] It is appreciated that specific functions, and accordingly utilities, of GR2948 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2948 gene: GAM1850 target protein and GAM1851 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1850 and GAM1851

[39662] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2949 (GR2949) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39663] GR2949 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2949 gene was detected is described hereinabove with reference to Figs. 6-15.

[39664] GR2949 gene encodes GR2949 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides

long.

[39665] GR2949 precursor RNA folds spatially, forming GR2949 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2949 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2949 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39666] GR2949 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1857 precursor RNA and GAM1858 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39667] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1857 RNA and GAM1858 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39668] GAM1857 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of

GAM1857 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1857 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1857 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39669] GAM1858 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1858 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1858 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1858 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39670] It is appreciated that specific functions, and accordingly utilities, of GR2949 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2949 gene: GAM1857 target protein and GAM1858 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1857 and GAM1858

[39671] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record

2950(GR2950) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39672] GR2950 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2950 gene was detected is described hereinabove with reference to Figs. 6-15.

[39673] GR2950 gene encodes GR2950 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39674] GR2950 precursor RNA folds spatially, forming GR2950 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2950 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2950 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39675] GR2950 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1860 precursor RNA and GAM1861 precursor RNA, herein schematically represented by GAM1

PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39676] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1860 RNA and GAM1861 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39677] GAM1860 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1860 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1860 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1860 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39678] GAM1861 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1861 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1861 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1861 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39679] It is appreciated that specific functions, and accordingly utilities, of GR2950 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2950 gene: GAM1860 target protein and GAM1861 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1860 and GAM1861

[39680] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2951 (GR2951) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39681] GR2951 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2951 gene was detected is described hereinabove with reference to Figs. 6-15.

[39682] GR2951 gene encodes GR2951 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39683] GR2951 precursor RNA folds spatially, forming GR2951 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2951 folded precursor RNA, herein designated GR FOLDED

PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2951 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39684] GR2951 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1866 precursor RNA and GAM1867 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39685] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1866 RNA and GAM1867 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39686] GAM1866 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1866 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1866 target RNA, herein schematically



represented by GAM1 TARGET RNA into GAM1866 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39687] GAM1867 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1867 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1867 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1867 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39688] It is appreciated that specific functions, and accordingly utilities, of GR2951 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2951 gene: GAM1866 target protein and GAM1867 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1866 and GAM1867

[39689] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2952 (GR2952) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

- [39690] GR2952 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2952 gene was detected is described hereinabove with reference to Figs. 6-15.
- [39691] GR2952 gene encodes GR2952 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [39692] GR2952 precursor RNA folds spatially, forming GR2952 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2952 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2952 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.
- [39693] GR2952 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1875 precursor RNA and GAM1876 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [39694] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX

of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1875 RNA and GAM1876 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39695] GAM1875 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1875 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1875 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1875 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39696] GAM1876 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1876 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1876 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1876 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39697] It is appreciated that specific functions, and accordingly utilities, of GR2952 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2952 gene: GAM1875 target

protein and GAM1876 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1875 and GAM1876

[39698] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2953 (GR2953) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39699] GR2953 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2953 gene was detected is described hereinabove with reference to Figs. 6-15.

[39700] GR2953 gene encodes GR2953 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39701] GR2953 precursor RNA folds spatially, forming GR2953 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2953 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2953 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39702] GR2953 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1880 precursor RNA and GAM1881 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39703] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1880 RNA and GAM1881 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39704] GAM1880 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1880 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1880 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1880 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39705] GAM1881 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of

GAM1881 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1881 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1881 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39706] It is appreciated that specific functions, and accordingly utilities, of GR2953 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2953 gene: GAM1880 target protein and GAM1881 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1880 and GAM1881

[39707] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2954 (GR2954) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39708] GR2954 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2954 gene was detected is described hereinabove with reference to Figs. 6-15.

[39709] GR2954 gene encodes GR2954 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39710] GR2954 precursor RNA folds spatially, forming GR2954 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2954 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2954 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39711] GR2954 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1887 precursor RNA, GAM1888 precursor RNA and GAM1889 precursor RNA, herein schematically represented by GAM1 PRECURSOR, GAM2 PRECURSOR and GAM3 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39712] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1887 RNA, GAM1888 RNA and GAM1889 RNA respectively, herein schematically represented by GAM1 RNA, GAM2 RNA and GAM3

RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39713] GAM1887 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1887 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1887 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1887 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39714] GAM1888 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1888 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1888 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1888 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39715] GAM1889 RNA, herein schematically represented by GAM3 binds complementarily to a target binding site located in an untranslated region of GAM1889 target RNA, herein schematically represented by GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1889 target RNA, herein schematically



represented by GAM3 TARGET RNA into GAM1889 target protein, herein schematically represented by GAM3 TARGET PROTEIN, both of Fig. 8.

[39716] It is appreciated that specific functions, and accordingly utilities, of GR2954 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2954 gene: GAM1887 target protein, GAM1888 target protein and GAM1889 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1887, GAM1888 and GAM1889

[39717] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2955(GR2955) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39718] GR2955 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2955 gene was detected is described hereinabove with reference to Figs. 6-15.

[39719] GR2955 gene encodes GR2955 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39720] GR2955 precursor RNA folds spatially, forming GR2955 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2955 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2955 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39721] GR2955 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1896 precursor RNA and GAM1897 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39722] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1896 RNA and GAM1897 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39723] GAM1896 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1896 target RNA, herein schematically represented by GAM1 TARGET

RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1896 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1896 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39724] GAM1897 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1897 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1897 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1897 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39725] It is appreciated that specific functions, and accordingly utilities, of GR2955 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2955 gene: GAM1896 target protein and GAM1897 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1896 and GAM1897

[39726] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2956(GR2956) gene, which encodes an operon-like cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39727] GR2956 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2956 gene was detected is described hereinabove with reference to Figs. 6-15.

[39728] GR2956 gene encodes GR2956 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39729] GR2956 precursor RNA folds spatially, forming GR2956 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2956 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2956 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39730] GR2956 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1909 precursor RNA and GAM1910 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM

precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39731] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1909 RNA and GAM1910 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39732] GAM1909 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1909 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1909 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1909 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39733] GAM1910 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1910 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1910 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1910 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39734] It is appreciated that specific functions, and accordingly utilities, of GR2956

gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2956 gene: GAM1909 target protein and GAM1910 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1909 and GAM1910

[39735] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2957 (GR2957) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39736] GR2957 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2957 gene was detected is described hereinabove with reference to Figs. 6-15.

[39737] GR2957 gene encodes GR2957 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39738] GR2957 precursor RNA folds spatially, forming GR2957 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2957 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as

hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2957 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39739] GR2957 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1912 precursor RNA, GAM1913 precursor RNA and GAM1914 precursor RNA, herein schematically represented by GAM1 PRECURSOR, GAM2 PRECURSOR and GAM3 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39740] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1912 RNA, GAM1913 RNA and GAM1914 RNA respectively, herein schematically represented by GAM1 RNA, GAM2 RNA and GAM3 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39741] GAM1912 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1912 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby

inhibiting translation of GAM1912 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1912 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39742] GAM1913 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1913 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1913 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1913 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39743] GAM1914 RNA, herein schematically represented by GAM3 binds complementarily to a target binding site located in an untranslated region of GAM1914 target RNA, herein schematically represented by GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1914 target RNA, herein schematically represented by GAM3 TARGET RNA into GAM1914 target protein, herein schematically represented by GAM3 TARGET PROTEIN, both of Fig. 8.

[39744] It is appreciated that specific functions, and accordingly utilities, of GR2957 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2957 gene: GAM1912 target protein, GAM1913 target protein and GAM1914 target protein, herein



schematically represented by GAM1 TARGET PROTEIN through GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1912, GAM1913 and GAM1914

- [39745] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2958(GR2958) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [39746] GR2958 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2958 gene was detected is described hereinabove with reference to Figs. 6-15.
- [39747] GR2958 gene encodes GR2958 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [39748] GR2958 precursor RNA folds spatially, forming GR2958 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2958 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2958 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39749] GR2958 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1915 precursor RNA and GAM1916 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39750] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1915 RNA and GAM1916 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39751] GAM1915 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1915 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1915 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1915 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39752] GAM1916 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of

GAM1916 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1916 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1916 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39753] It is appreciated that specific functions, and accordingly utilities, of GR2958 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2958 gene: GAM1915 target protein and GAM1916 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1915 and GAM1916

[39754] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2959 (GR2959) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39755] GR2959 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2959 gene was detected is described hereinabove with reference to Figs. 6-15.

[39756] GR2959 gene encodes GR2959 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39757] GR2959 precursor RNA folds spatially, forming GR2959 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2959 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2959 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39758] GR2959 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1922 precursor RNA and GAM1923 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39759] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1922 RNA and GAM1923 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39760] GAM1922 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1922 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1922 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1922 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39761] GAM1923 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1923 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1923 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1923 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39762] It is appreciated that specific functions, and accordingly utilities, of GR2959 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2959 gene: GAM1922 target protein and GAM1923 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1922 and GAM1923

- [39763] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2960 (GR2960) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [39764] GR2960 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2960 gene was detected is described hereinabove with reference to Figs. 6-15.
- [39765] GR2960 gene encodes GR2960 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [39766] GR2960 precursor RNA folds spatially, forming GR2960 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2960 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2960 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

- [39767] GR2960 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1940 precursor RNA and GAM1941 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [39768] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1940 RNA and GAM1941 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.
- [39769] GAM1940 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1940 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1940 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1940 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.
- [39770] GAM1941 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1941 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1941 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1941 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39771] It is appreciated that specific functions, and accordingly utilities, of GR2960 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2960 gene: GAM1940 target protein and GAM1941 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1940 and GAM1941

[39772] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2961 (GR2961) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39773] GR2961 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2961 gene was detected is described hereinabove with reference to Figs. 6-15.

[39774] GR2961 gene encodes GR2961 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides



long.

[39775] GR2961 precursor RNA folds spatially, forming GR2961 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2961 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2961 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39776] GR2961 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1946 precursor RNA and GAM1947 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39777] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1946 RNA and GAM1947 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39778] GAM1946 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of

GAM1946 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1946 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1946 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39779] GAM1947 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1947 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1947 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1947 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39780] It is appreciated that specific functions, and accordingly utilities, of GR2961 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2961 gene: GAM1946 target protein and GAM1947 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1946 and GAM1947

[39781] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record

2962(GR2962) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39782] GR2962 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2962 gene was detected is described hereinabove with reference to Figs. 6-15.

[39783] GR2962 gene encodes GR2962 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39784] GR2962 precursor RNA folds spatially, forming GR2962 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2962 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2962 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39785] GR2962 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1949 precursor RNA and GAM1950 precursor RNA, herein schematically represented by GAM1

PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39786] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1949 RNA and GAM1950 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39787] GAM1949 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1949 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1949 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1949 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39788] GAM1950 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1950 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1950 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1950 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39789] It is appreciated that specific functions, and accordingly utilities, of GR2962 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2962 gene: GAM1949 target protein and GAM1950 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1949 and GAM1950

[39790] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2963 (GR2963) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39791] GR2963 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2963 gene was detected is described hereinabove with reference to Figs. 6-15.

[39792] GR2963 gene encodes GR2963 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39793] GR2963 precursor RNA folds spatially, forming GR2963 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2963 folded precursor RNA, herein designated GR FOLDED

PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2963 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39794] GR2963 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1952 precursor RNA and GAM1953 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39795] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1952 RNA and GAM1953 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39796] GAM1952 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1952 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1952 target RNA, herein schematically

represented by GAM1 TARGET RNA into GAM1952 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39797] GAM1953 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1953 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1953 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1953 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39798] It is appreciated that specific functions, and accordingly utilities, of GR2963 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2963 gene: GAM1952 target protein and GAM1953 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1952 and GAM1953

[39799] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2964 (GR2964) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39800] GR2964 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2964 gene was detected is described hereinabove with reference to Figs. 6-15.

[39801] GR2964 gene encodes GR2964 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39802] GR2964 precursor RNA folds spatially, forming GR2964 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2964 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2964 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39803] GR2964 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1954 precursor RNA and GAM1955 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39804] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX



of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1954 RNA and GAM1955 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39805] GAM1954 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1954 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1954 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1954 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39806] GAM1955 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1955 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1955 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1955 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39807] It is appreciated that specific functions, and accordingly utilities, of GR2964 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2964 gene: GAM1954 target

protein and GAM1955 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1954 and GAM1955

[39808] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2965 (GR2965) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39809] GR2965 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2965 gene was detected is described hereinabove with reference to Figs. 6-15.

[39810] GR2965 gene encodes GR2965 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39811] GR2965 precursor RNA folds spatially, forming GR2965 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2965 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2965 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

- [39812] GR2965 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1956 precursor RNA and GAM1957 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [39813] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1956 RNA and GAM1957 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.
- [39814] GAM1956 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1956 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1956 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1956 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.
- [39815] GAM1957 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of

GAM1957 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1957 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1957 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39816] It is appreciated that specific functions, and accordingly utilities, of GR2965 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2965 gene: GAM1956 target protein and GAM1957 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1956 and GAM1957

[39817] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2966 (GR2966) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39818] GR2966 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2966 gene was detected is described hereinabove with reference to Figs. 6-15.

[39819] GR2966 gene encodes GR2966 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39820] GR2966 precursor RNA folds spatially, forming GR2966 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2966 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2966 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39821] GR2966 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1960 precursor RNA and GAM1961 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39822] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1960 RNA and GAM1961 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39823] GAM1960 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1960 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1960 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1960 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39824] GAM1961 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1961 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1961 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1961 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39825] It is appreciated that specific functions, and accordingly utilities, of GR2966 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2966 gene: GAM1960 target protein and GAM1961 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1960 and GAM1961

- [39826] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2967 (GR2967) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [39827] GR2967 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2967 gene was detected is described hereinabove with reference to Figs. 6-15.
- [39828] GR2967 gene encodes GR2967 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [39829] GR2967 precursor RNA folds spatially, forming GR2967 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2967 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2967 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.
- [39830] GR2967 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into

at least 3 separate GAM precursor RNAs, GAM1963 precursor RNA, GAM1964 precursor RNA and GAM1965 precursor RNA, herein schematically represented by GAM1 PRECURSOR, GAM2 PRECURSOR and GAM3 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39831] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1963 RNA, GAM1964 RNA and GAM1965 RNA respectively, herein schematically represented by GAM1 RNA, GAM2 RNA and GAM3 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39832] GAM1963 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1963 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1963 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1963 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39833] GAM1964 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1964 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as



BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1964 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1964 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39834] GAM1965 RNA, herein schematically represented by GAM3 binds complementarily to a target binding site located in an untranslated region of GAM1965 target RNA, herein schematically represented by GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1965 target RNA, herein schematically represented by GAM3 TARGET RNA into GAM1965 target protein, herein schematically represented by GAM3 TARGET PROTEIN, both of Fig. 8.

[39835] It is appreciated that specific functions, and accordingly utilities, of GR2967 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2967 gene: GAM1963 target protein, GAM1964 target protein and GAM1965 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1963, GAM1964 and GAM1965

[39836] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2968(GR2968) gene, which encodes an operon-like cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39837] GR2968 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2968 gene was detected is described hereinabove with reference to Figs. 6-15.

[39838] GR2968 gene encodes GR2968 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39839] GR2968 precursor RNA folds spatially, forming GR2968 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2968 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2968 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39840] GR2968 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1969 precursor RNA and GAM1970 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM

precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39841] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1969 RNA and GAM1970 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39842] GAM1969 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1969 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1969 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1969 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39843] GAM1970 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1970 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1970 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1970 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39844] It is appreciated that specific functions, and accordingly utilities, of GR2968

gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2968 gene: GAM1969 target protein and GAM1970 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1969 and GAM1970

[39845] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2969 (GR2969) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39846] GR2969 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2969 gene was detected is described hereinabove with reference to Figs. 6-15.

[39847] GR2969 gene encodes GR2969 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39848] GR2969 precursor RNA folds spatially, forming GR2969 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2969 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as

hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2969 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39849] GR2969 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1981 precursor RNA and GAM1982 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39850] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1981 RNA and GAM1982 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39851] GAM1981 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1981 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1981 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1981 target protein, herein

schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39852] GAM1982 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1982 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1982 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1982 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39853] It is appreciated that specific functions, and accordingly utilities, of GR2969 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2969 gene: GAM1981 target protein and GAM1982 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1981 and GAM1982

[39854] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2970 (GR2970) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39855] GR2970 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR2970 gene was detected is described hereinabove with reference to Figs. 6-15.

[39856] GR2970 gene encodes GR2970 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39857] GR2970 precursor RNA folds spatially, forming GR2970 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2970 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2970 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39858] GR2970 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1983 precursor RNA and GAM1984 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39859] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in

length, GAM1983 RNA and GAM1984 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39860] GAM1983 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1983 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1983 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1983 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39861] GAM1984 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1984 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1984 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1984 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39862] It is appreciated that specific functions, and accordingly utilities, of GR2970 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2970 gene: GAM1983 target protein and GAM1984 target protein, herein schematically represented by



GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1983 and GAM1984

[39863] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2971 (GR2971) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39864] GR2971 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2971 gene was detected is described hereinabove with reference to Figs. 6-15.

[39865] GR2971 gene encodes GR2971 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39866] GR2971 precursor RNA folds spatially, forming GR2971 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2971 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2971 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

- [39867] GR2971 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1986 precursor RNA and GAM1987 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [39868] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1986 RNA and GAM1987 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.
- [39869] GAM1986 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM1986 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1986 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1986 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.
- [39870] GAM1987 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM1987 target RNA, herein schematically represented by GAM2 TARGET

RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1987 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1987 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39871] It is appreciated that specific functions, and accordingly utilities, of GR2971 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2971 gene: GAM1986 target protein and GAM1987 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1986 and GAM1987

[39872] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2972 (GR2972) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39873] GR2972 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2972 gene was detected is described hereinabove with reference to Figs. 6-15.

[39874] GR2972 gene encodes GR2972 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39875] GR2972 precursor RNA folds spatially, forming GR2972 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2972 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2972 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39876] GR2972 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1995 precursor RNA and GAM1996 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39877] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1995 RNA and GAM1996 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39878] GAM1995 RNA, herein schematically represented by GAM1 binds

complimentarily to a target binding site located in an untranslated region of GAM1995 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1995 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM1995 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39879] GAM1996 RNA, herein schematically represented by GAM2 binds complimentarily to a target binding site located in an untranslated region of GAM1996 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1996 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM1996 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39880] It is appreciated that specific functions, and accordingly utilities, of GR2972 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2972 gene: GAM1995 target protein and GAM1996 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM1995 and GAM1996

[39881] Fig. 16 further provides a conceptual description of novel bioinformatically

detected regulatory gene, referred to here as Genomic Record

2973(GR2973) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39882] GR2973 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2973 gene was detected is described hereinabove with reference to Figs. 6-15.

[39883] GR2973 gene encodes GR2973 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39884] GR2973 precursor RNA folds spatially, forming GR2973 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2973 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2973 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39885] GR2973 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2002 precursor RNA and

GAM2003 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39886] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2002 RNA and GAM2003 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39887] GAM2002 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2002 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2002 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2002 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39888] GAM2003 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2003 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2003 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2003 target protein, herein

schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39889] It is appreciated that specific functions, and accordingly utilities, of GR2973 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2973 gene: GAM2002 target protein and GAM2003 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2002 and GAM2003

[39890] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2974 (GR2974) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39891] GR2974 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2974 gene was detected is described hereinabove with reference to Figs. 6-15.

[39892] GR2974 gene encodes GR2974 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39893] GR2974 precursor RNA folds spatially, forming GR2974 folded precursor



RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2974 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2974 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39894] GR2974 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2010 precursor RNA and GAM2011 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39895] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2010 RNA and GAM2011 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39896] GAM2010 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2010 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2010 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2010 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39897] GAM2011 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2011 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2011 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2011 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39898] It is appreciated that specific functions, and accordingly utilities, of GR2974 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2974 gene: GAM2010 target protein and GAM2011 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2010 and GAM2011

[39899] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2975 (GR2975) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

[39900] GR2975 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2975 gene was detected is described hereinabove with reference to Figs. 6-15.

[39901] GR2975 gene encodes GR2975 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39902] GR2975 precursor RNA folds spatially, forming GR2975 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2975 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2975 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39903] GR2975 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2022 precursor RNA and GAM2023 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to

## GAM PRECURSOR RNA of Fig. 8.

[39904] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2022 RNA and GAM2023 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39905] GAM2022 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2022 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2022 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2022 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39906] GAM2023 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2023 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2023 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2023 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39907] It is appreciated that specific functions, and accordingly utilities, of GR2975 gene, herein designated GR GENE, correlate with, and may be deduced

from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2975 gene: GAM2022 target protein and GAM2023 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2022 and GAM2023

[39908] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2976 (GR2976) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39909] GR2976 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2976 gene was detected is described hereinabove with reference to Figs. 6-15.

[39910] GR2976 gene encodes GR2976 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39911] GR2976 precursor RNA folds spatially, forming GR2976 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2976 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the

nucleotide sequence of GR2976 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

- [39912] GR2976 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2026 precursor RNA and GAM2027 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [39913] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2026 RNA and GAM2027 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.
- [39914] GAM2026 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2026 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2026 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2026 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39915] GAM2027 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2027 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2027 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2027 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39916] It is appreciated that specific functions, and accordingly utilities, of GR2976 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2976 gene: GAM2026 target protein and GAM2027 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2026 and GAM2027

[39917] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2977 (GR2977) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39918] GR2977 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which

GR2977 gene was detected is described hereinabove with reference to Figs. 6-15.

[39919] GR2977 gene encodes GR2977 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39920] GR2977 precursor RNA folds spatially, forming GR2977 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2977 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2977 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39921] GR2977 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2032 precursor RNA and GAM2033 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39922] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2032 RNA and GAM2033 RNA respectively, herein



schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39923] GAM2032 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2032 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2032 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2032 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39924] GAM2033 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2033 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2033 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2033 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39925] It is appreciated that specific functions, and accordingly utilities, of GR2977 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2977 gene: GAM2032 target protein and GAM2033 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The

function of these target genes is elaborated hereinabove with reference to GAM2032 and GAM2033

- [39926] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2978 (GR2978) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [39927] GR2978 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2978 gene was detected is described hereinabove with reference to Figs. 6-15.
- [39928] GR2978 gene encodes GR2978 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [39929] GR2978 precursor RNA folds spatially, forming GR2978 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2978 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2978 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

- [39930] GR2978 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2039 precursor RNA and GAM2040 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [39931] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2039 RNA and GAM2040 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.
- [39932] GAM2039 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2039 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2039 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2039 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.
- [39933] GAM2040 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2040 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2040 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2040 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39934] It is appreciated that specific functions, and accordingly utilities, of GR2978 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2978 gene: GAM2039 target protein and GAM2040 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2039 and GAM2040

[39935] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2979 (GR2979) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39936] GR2979 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2979 gene was detected is described hereinabove with reference to Figs. 6-15.

[39937] GR2979 gene encodes GR2979 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides

long.

[39938] GR2979 precursor RNA folds spatially, forming GR2979 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2979 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2979 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39939] GR2979 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2042 precursor RNA and GAM2043 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39940] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2042 RNA and GAM2043 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39941] GAM2042 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of

GAM2042 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2042 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2042 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39942] GAM2043 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2043 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2043 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2043 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39943] It is appreciated that specific functions, and accordingly utilities, of GR2979 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2979 gene: GAM2042 target protein and GAM2043 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2042 and GAM2043

[39944] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record

2980(GR2980) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39945] GR2980 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2980 gene was detected is described hereinabove with reference to Figs. 6-15.

[39946] GR2980 gene encodes GR2980 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39947] GR2980 precursor RNA folds spatially, forming GR2980 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2980 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2980 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39948] GR2980 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2047 precursor RNA and GAM2048 precursor RNA, herein schematically represented by GAM1

PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39949] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2047 RNA and GAM2048 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39950] GAM2047 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2047 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2047 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2047 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39951] GAM2048 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2048 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2048 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2048 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.



[39952] It is appreciated that specific functions, and accordingly utilities, of GR2980 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2980 gene: GAM2047 target protein and GAM2048 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2047 and GAM2048

[39953] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2981 (GR2981) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39954] GR2981 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2981 gene was detected is described hereinabove with reference to Figs. 6-15.

[39955] GR2981 gene encodes GR2981 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[39956] GR2981 precursor RNA folds spatially, forming GR2981 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2981 folded precursor RNA, herein designated GR FOLDED

PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2981 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39957] GR2981 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2051 precursor RNA, GAM2052 precursor RNA and GAM2053 precursor RNA, herein schematically represented by GAM1 PRECURSOR, GAM2 PRECURSOR and GAM3 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39958] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2051 RNA, GAM2052 RNA and GAM2053 RNA respectively, herein schematically represented by GAM1 RNA, GAM2 RNA and GAM3 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39959] GAM2051 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2051 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2051 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2051 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39960] GAM2052 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2052 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2052 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2052 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39961] GAM2053 RNA, herein schematically represented by GAM3 binds complementarily to a target binding site located in an untranslated region of GAM2053 target RNA, herein schematically represented by GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2053 target RNA, herein schematically represented by GAM3 TARGET RNA into GAM2053 target protein, herein schematically represented by GAM3 TARGET PROTEIN, both of Fig. 8.

[39962] It is appreciated that specific functions, and accordingly utilities, of GR2981 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2981 gene: GAM2051 target

protein, GAM2052 target protein and GAM2053 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2051, GAM2052 and GAM2053

- [39963] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2982 (GR2982) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [39964] GR2982 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2982 gene was detected is described hereinabove with reference to Figs. 6-15.
- [39965] GR2982 gene encodes GR2982 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [39966] GR2982 precursor RNA folds spatially, forming GR2982 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2982 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2982 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39967] GR2982 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2054 precursor RNA and GAM2055 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39968] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2054 RNA and GAM2055 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39969] GAM2054 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2054 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2054 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2054 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39970] GAM2055 RNA, herein schematically represented by GAM2 binds

complimentarily to a target binding site located in an untranslated region of GAM2055 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2055 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2055 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39971] It is appreciated that specific functions, and accordingly utilities, of GR2982 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2982 gene: GAM2054 target protein and GAM2055 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2054 and GAM2055

[39972] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2983 (GR2983) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39973] GR2983 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2983 gene was detected is described hereinabove with reference to Figs.

- [39974] GR2983 gene encodes GR2983 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [39975] GR2983 precursor RNA folds spatially, forming GR2983 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2983 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2983 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.
- [39976] GR2983 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2088 precursor RNA and GAM2089 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [39977] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2088 RNA and GAM2089 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively,

each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[39978] GAM2088 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2088 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2088 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2088 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[39979] GAM2089 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2089 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2089 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2089 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39980] It is appreciated that specific functions, and accordingly utilities, of GR2983 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2983 gene: GAM2088 target protein and GAM2089 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to



- [39981] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2984 (GR2984) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [39982] GR2984 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2984 gene was detected is described hereinabove with reference to Figs. 6-15.
- [39983] GR2984 gene encodes GR2984 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [39984] GR2984 precursor RNA folds spatially, forming GR2984 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2984 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2984 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

- [39985] GR2984 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2093 precursor RNA and GAM2094 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [39986] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2093 RNA and GAM2094 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.
- [39987] GAM2093 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2093 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2093 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2093 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.
- [39988] GAM2094 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2094 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2094 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2094 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[39989] It is appreciated that specific functions, and accordingly utilities, of GR2984 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2984 gene: GAM2093 target protein and GAM2094 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2093 and GAM2094

[39990] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2985 (GR2985) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[39991] GR2985 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2985 gene was detected is described hereinabove with reference to Figs. 6-15.

[39992] GR2985 gene encodes GR2985 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides

long.

[39993] GR2985 precursor RNA folds spatially, forming GR2985 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2985 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2985 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[39994] GR2985 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2095 precursor RNA, GAM2096 precursor RNA and GAM2097 precursor RNA, herein schematically represented by GAM1 PRECURSOR, GAM2 PRECURSOR and GAM3 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[39995] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2095 RNA, GAM2096 RNA and GAM2097 RNA respectively, herein schematically represented by GAM1 RNA, GAM2 RNA and GAM3 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

- [39996] GAM2095 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2095 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2095 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2095 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.
- [39997] GAM2096 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2096 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2096 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2096 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.
- [39998] GAM2097 RNA, herein schematically represented by GAM3 binds complementarily to a target binding site located in an untranslated region of GAM2097 target RNA, herein schematically represented by GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2097 target RNA, herein schematically represented by GAM3 TARGET RNA into GAM2097 target protein, herein schematically represented by GAM3 TARGET PROTEIN, both of Fig. 8.

[39999] It is appreciated that specific functions, and accordingly utilities, of GR2985 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2985 gene: GAM2095 target protein, GAM2096 target protein and GAM2097 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2095, GAM2096 and GAM2097

[40000] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2986 (GR2986) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[40001] GR2986 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2986 gene was detected is described hereinabove with reference to Figs. 6-15.

[40002] GR2986 gene encodes GR2986 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40003] GR2986 precursor RNA folds spatially, forming GR2986 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated

that GR2986 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2986 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40004] GR2986 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2105 precursor RNA and GAM2106 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[40005] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2105 RNA and GAM2106 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40006] GAM2105 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2105 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby

inhibiting translation of GAM2105 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2105 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40007] GAM2106 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2106 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2106 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2106 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40008] It is appreciated that specific functions, and accordingly utilities, of GR2986 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2986 gene: GAM2105 target protein and GAM2106 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2105 and GAM2106

[40009] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2987 (GR2987) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is



known in the art.

[40010] GR2987 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2987 gene was detected is described hereinabove with reference to Figs. 6-15.

[40011] GR2987 gene encodes GR2987 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40012] GR2987 precursor RNA folds spatially, forming GR2987 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2987 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2987 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40013] GR2987 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2108 precursor RNA and GAM2109 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[40014] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2108 RNA and GAM2109 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40015] GAM2108 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2108 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2108 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2108 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40016] GAM2109 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2109 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2109 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2109 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40017] It is appreciated that specific functions, and accordingly utilities, of GR2987 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs

comprised in the operon-like cluster of GR2987 gene: GAM2108 target protein and GAM2109 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2108 and GAM2109

[40018] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2988 (GR2988) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[40019] GR2988 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2988 gene was detected is described hereinabove with reference to Figs. 6-15.

[40020] GR2988 gene encodes GR2988 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40021] GR2988 precursor RNA folds spatially, forming GR2988 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2988 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2988 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40022] GR2988 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2110 precursor RNA and GAM2111 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[40023] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2110 RNA and GAM2111 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40024] GAM2110 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2110 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2110 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2110 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40025] GAM2111 RNA, herein schematically represented by GAM2 binds

complimentarily to a target binding site located in an untranslated region of GAM2111 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2111 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2111 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40026] It is appreciated that specific functions, and accordingly utilities, of GR2988 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2988 gene: GAM2110 target protein and GAM2111 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2110 and GAM2111

[40027] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2989 (GR2989) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[40028] GR2989 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2989 gene was detected is described hereinabove with reference to Figs.

- [40029] GR2989 gene encodes GR2989 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [40030] GR2989 precursor RNA folds spatially, forming GR2989 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2989 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2989 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.
- [40031] GR2989 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2117 precursor RNA and GAM2118 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [40032] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2117 RNA and GAM2118 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively,

each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40033] GAM2117 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2117 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2117 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2117 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40034] GAM2118 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2118 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2118 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2118 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40035] It is appreciated that specific functions, and accordingly utilities, of GR2989 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2989 gene: GAM2117 target protein and GAM2118 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to

- [40036] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2990 (GR2990) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [40037] GR2990 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2990 gene was detected is described hereinabove with reference to Figs. 6-15.
- [40038] GR2990 gene encodes GR2990 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [40039] GR2990 precursor RNA folds spatially, forming GR2990 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2990 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2990 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.



- [40040] GR2990 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2119 precursor RNA and GAM2120 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [40041] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2119 RNA and GAM2120 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.
- [40042] GAM2119 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2119 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2119 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2119 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.
- [40043] GAM2120 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2120 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2120 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2120 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40044] It is appreciated that specific functions, and accordingly utilities, of GR2990 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2990 gene: GAM2119 target protein and GAM2120 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2119 and GAM2120

[40045] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2991 (GR2991) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[40046] GR2991 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2991 gene was detected is described hereinabove with reference to Figs. 6-15.

[40047] GR2991 gene encodes GR2991 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides

long.

[40048] GR2991 precursor RNA folds spatially, forming GR2991 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2991 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2991 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40049] GR2991 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2126 precursor RNA and GAM2127 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[40050] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2126 RNA and GAM2127 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40051] GAM2126 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of

GAM2126 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2126 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2126 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40052] GAM2127 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2127 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2127 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2127 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40053] It is appreciated that specific functions, and accordingly utilities, of GR2991 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2991 gene: GAM2126 target protein and GAM2127 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2126 and GAM2127

[40054] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record

2992(GR2992) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[40055] GR2992 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2992 gene was detected is described hereinabove with reference to Figs. 6-15.

[40056] GR2992 gene encodes GR2992 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40057] GR2992 precursor RNA folds spatially, forming GR2992 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2992 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2992 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40058] GR2992 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2129 precursor RNA and GAM2130 precursor RNA, herein schematically represented by GAM1

PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[40059] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2129 RNA and GAM2130 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40060] GAM2129 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2129 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2129 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2129 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40061] GAM2130 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2130 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2130 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2130 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40062] It is appreciated that specific functions, and accordingly utilities, of GR2992 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2992 gene: GAM2129 target protein and GAM2130 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2129 and GAM2130

[40063] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2993 (GR2993) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[40064] GR2993 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2993 gene was detected is described hereinabove with reference to Figs. 6-15.

[40065] GR2993 gene encodes GR2993 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40066] GR2993 precursor RNA folds spatially, forming GR2993 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2993 folded precursor RNA, herein designated GR FOLDED

PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2993 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40067] GR2993 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2131 precursor RNA and GAM2132 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[40068] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2131 RNA and GAM2132 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40069] GAM2131 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2131 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2131 target RNA, herein schematically



represented by GAM1 TARGET RNA into GAM2131 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40070] GAM2132 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2132 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2132 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2132 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40071] It is appreciated that specific functions, and accordingly utilities, of GR2993 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2993 gene: GAM2131 target protein and GAM2132 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2131 and GAM2132

[40072] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2994 (GR2994) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

- [40073] GR2994 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2994 gene was detected is described hereinabove with reference to Figs. 6-15.
- [40074] GR2994 gene encodes GR2994 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [40075] GR2994 precursor RNA folds spatially, forming GR2994 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2994 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2994 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.
- [40076] GR2994 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2138 precursor RNA and GAM2139 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [40077] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX

of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2138 RNA and GAM2139 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40078] GAM2138 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2138 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2138 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2138 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40079] GAM2139 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2139 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2139 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2139 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40080] It is appreciated that specific functions, and accordingly utilities, of GR2994 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2994 gene: GAM2138 target

protein and GAM2139 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2138 and GAM2139

[40081] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2995 (GR2995) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[40082] GR2995 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2995 gene was detected is described hereinabove with reference to Figs. 6-15.

[40083] GR2995 gene encodes GR2995 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40084] GR2995 precursor RNA folds spatially, forming GR2995 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2995 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2995 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40085] GR2995 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2140 precursor RNA, GAM2141 precursor RNA and GAM2142 precursor RNA, herein schematically represented by GAM1 PRECURSOR, GAM2 PRECURSOR and GAM3 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[40086] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2140 RNA, GAM2141 RNA and GAM2142 RNA respectively, herein schematically represented by GAM1 RNA, GAM2 RNA and GAM3 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40087] GAM2140 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2140 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2140 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2140 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40088] GAM2141 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2141 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2141 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2141 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40089] GAM2142 RNA, herein schematically represented by GAM3 binds complementarily to a target binding site located in an untranslated region of GAM2142 target RNA, herein schematically represented by GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2142 target RNA, herein schematically represented by GAM3 TARGET RNA into GAM2142 target protein, herein schematically represented by GAM3 TARGET PROTEIN, both of Fig. 8.

[40090] It is appreciated that specific functions, and accordingly utilities, of GR2995 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2995 gene: GAM2140 target protein, GAM2141 target protein and GAM2142 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2140, GAM2141 and GAM2142

- [40091] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2996 (GR2996) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [40092] GR2996 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2996 gene was detected is described hereinabove with reference to Figs. 6-15.
- [40093] GR2996 gene encodes GR2996 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [40094] GR2996 precursor RNA folds spatially, forming GR2996 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2996 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2996 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.
- [40095] GR2996 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into

at least 2 separate GAM precursor RNAs, GAM2146 precursor RNA and GAM2147 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[40096] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2146 RNA and GAM2147 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40097] GAM2146 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2146 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2146 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2146 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40098] GAM2147 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2147 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2147 target RNA, herein schematically



represented by GAM2 TARGET RNA into GAM2147 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40099] It is appreciated that specific functions, and accordingly utilities, of GR2996 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2996 gene: GAM2146 target protein and GAM2147 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2146 and GAM2147

[40100] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2997 (GR2997) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[40101] GR2997 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2997 gene was detected is described hereinabove with reference to Figs. 6-15.

[40102] GR2997 gene encodes GR2997 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40103] GR2997 precursor RNA folds spatially, forming GR2997 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2997 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2997 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40104] GR2997 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2148 precursor RNA and GAM2149 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[40105] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2148 RNA and GAM2149 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40106] GAM2148 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2148 target RNA, herein schematically represented by GAM1 TARGET

RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2148 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2148 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40107] GAM2149 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2149 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2149 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2149 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40108] It is appreciated that specific functions, and accordingly utilities, of GR2997 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2997 gene: GAM2148 target protein and GAM2149 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2148 and GAM2149

[40109] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2998(GR2998) gene, which encodes an operon-like cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[40110] GR2998 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2998 gene was detected is described hereinabove with reference to Figs. 6-15.

[40111] GR2998 gene encodes GR2998 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40112] GR2998 precursor RNA folds spatially, forming GR2998 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2998 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2998 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40113] GR2998 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2155 precursor RNA and GAM2156 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM

precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[40114] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2155 RNA and GAM2156 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40115] GAM2155 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2155 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2155 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2155 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40116] GAM2156 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2156 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2156 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2156 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40117] It is appreciated that specific functions, and accordingly utilities, of GR2998

gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2998 gene: GAM2155 target protein and GAM2156 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2155 and GAM2156

[40118] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 2999 (GR2999) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[40119] GR2999 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR2999 gene was detected is described hereinabove with reference to Figs. 6-15.

[40120] GR2999 gene encodes GR2999 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40121] GR2999 precursor RNA folds spatially, forming GR2999 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR2999 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as

hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR2999 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40122] GR2999 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2158 precursor RNA and GAM2159 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[40123] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2158 RNA and GAM2159 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40124] GAM2158 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2158 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2158 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2158 target protein, herein

schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40125] GAM2159 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2159 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2159 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2159 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40126] It is appreciated that specific functions, and accordingly utilities, of GR2999 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR2999 gene: GAM2158 target protein and GAM2159 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2158 and GAM2159

[40127] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 3000 (GR3000) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[40128] GR3000 gene, herein designated GR GENE, is a novel bioinformatically



detected regulatory, non protein coding, RNA gene. The method by which GR3000 gene was detected is described hereinabove with reference to Figs. 6-15.

[40129] GR3000 gene encodes GR3000 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40130] GR3000 precursor RNA folds spatially, forming GR3000 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3000 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR3000 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40131] GR3000 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2169 precursor RNA and GAM2170 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[40132] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in

length, GAM2169 RNA and GAM2170 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40133] GAM2169 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2169 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2169 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2169 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40134] GAM2170 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2170 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2170 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2170 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40135] It is appreciated that specific functions, and accordingly utilities, of GR3000 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3000 gene: GAM2169 target protein and GAM2170 target protein, herein schematically represented by

GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2169 and GAM2170

- [40136] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 3001 (GR3001) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [40137] GR3001 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR3001 gene was detected is described hereinabove with reference to Figs. 6-15.
- [40138] GR3001 gene encodes GR3001 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [40139] GR3001 precursor RNA folds spatially, forming GR3001 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3001 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR3001 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

- [40140] GR3001 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2186 precursor RNA and GAM2187 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [40141] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2186 RNA and GAM2187 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.
- [40142] GAM2186 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2186 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2186 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2186 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.
- [40143] GAM2187 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2187 target RNA, herein schematically represented by GAM2 TARGET

RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2187 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2187 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40144] It is appreciated that specific functions, and accordingly utilities, of GR3001 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3001 gene: GAM2186 target protein and GAM2187 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2186 and GAM2187

[40145] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 3002 (GR3002) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[40146] GR3002 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR3002 gene was detected is described hereinabove with reference to Figs. 6-15.

[40147] GR3002 gene encodes GR3002 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40148] GR3002 precursor RNA folds spatially, forming GR3002 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3002 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR3002 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40149] GR3002 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2193 precursor RNA and GAM2194 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[40150] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2193 RNA and GAM2194 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40151] GAM2193 RNA, herein schematically represented by GAM1 binds

complimentarily to a target binding site located in an untranslated region of GAM2193 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2193 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2193 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40152] GAM2194 RNA, herein schematically represented by GAM2 binds complimentarily to a target binding site located in an untranslated region of GAM2194 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2194 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2194 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40153] It is appreciated that specific functions, and accordingly utilities, of GR3002 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3002 gene: GAM2193 target protein and GAM2194 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2193 and GAM2194

[40154] Fig. 16 further provides a conceptual description of novel bioinformatically

detected regulatory gene, referred to here as Genomic Record

3003(GR3003) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[40155] GR3003 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR3003 gene was detected is described hereinabove with reference to Figs. 6-15.

[40156] GR3003 gene encodes GR3003 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40157] GR3003 precursor RNA folds spatially, forming GR3003 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3003 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR3003 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40158] GR3003 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2195 precursor RNA and



GAM2196 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[40159] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2195 RNA and GAM2196 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40160] GAM2195 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2195 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2195 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2195 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40161] GAM2196 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2196 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2196 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2196 target protein, herein

schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40162] It is appreciated that specific functions, and accordingly utilities, of GR3003 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3003 gene: GAM2195 target protein and GAM2196 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2195 and GAM2196

[40163] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 3004 (GR3004) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[40164] GR3004 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR3004 gene was detected is described hereinabove with reference to Figs. 6-15.

[40165] GR3004 gene encodes GR3004 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40166] GR3004 precursor RNA folds spatially, forming GR3004 folded precursor

RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3004 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR3004 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40167] GR3004 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2203 precursor RNA and GAM2204 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[40168] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2203 RNA and GAM2204 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40169] GAM2203 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2203 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2203 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2203 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40170] GAM2204 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2204 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2204 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2204 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40171] It is appreciated that specific functions, and accordingly utilities, of GR3004 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3004 gene: GAM2203 target protein and GAM2204 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2203 and GAM2204

[40172] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 3005 (GR3005) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

[40173] GR3005 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR3005 gene was detected is described hereinabove with reference to Figs. 6-15.

[40174] GR3005 gene encodes GR3005 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40175] GR3005 precursor RNA folds spatially, forming GR3005 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3005 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR3005 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40176] GR3005 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2213 precursor RNA and GAM2214 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to

## GAM PRECURSOR RNA of Fig. 8.

[40177] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2213 RNA and GAM2214 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40178] GAM2213 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2213 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2213 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2213 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40179] GAM2214 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2214 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2214 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2214 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40180] It is appreciated that specific functions, and accordingly utilities, of GR3005 gene, herein designated GR GENE, correlate with, and may be deduced

from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3005 gene: GAM2213 target protein and GAM2214 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2213 and GAM2214

[40181] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 3006 (GR3006) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[40182] GR3006 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR3006 gene was detected is described hereinabove with reference to Figs. 6-15.

[40183] GR3006 gene encodes GR3006 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40184] GR3006 precursor RNA folds spatially, forming GR3006 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3006 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the

nucleotide sequence of GR3006 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40185] GR3006 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2228 precursor RNA and GAM2229 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[40186] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2228 RNA and GAM2229 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40187] GAM2228 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2228 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2228 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2228 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.



[40188] GAM2229 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2229 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2229 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2229 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40189] It is appreciated that specific functions, and accordingly utilities, of GR3006 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3006 gene: GAM2228 target protein and GAM2229 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2228 and GAM2229

[40190] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 3007 (GR3007) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[40191] GR3007 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which

GR3007 gene was detected is described hereinabove with reference to Figs. 6-15.

[40192] GR3007 gene encodes GR3007 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40193] GR3007 precursor RNA folds spatially, forming GR3007 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3007 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR3007 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40194] GR3007 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2238 precursor RNA and GAM2239 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[40195] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2238 RNA and GAM2239 RNA respectively, herein

schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40196] GAM2238 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2238 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2238 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2238 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40197] GAM2239 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2239 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2239 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2239 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40198] It is appreciated that specific functions, and accordingly utilities, of GR3007 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3007 gene: GAM2238 target protein and GAM2239 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The

function of these target genes is elaborated hereinabove with reference to GAM2238 and GAM2239

- [40199] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 3008(GR3008) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [40200] GR3008 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR3008 gene was detected is described hereinabove with reference to Figs. 6-15.
- [40201] GR3008 gene encodes GR3008 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [40202] GR3008 precursor RNA folds spatially, forming GR3008 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3008 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR3008 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40203] GR3008 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2253 precursor RNA, GAM2254 precursor RNA and GAM2255 precursor RNA, herein schematically represented by GAM1 PRECURSOR, GAM2 PRECURSOR and GAM3 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[40204] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2253 RNA, GAM2254 RNA and GAM2255 RNA respectively, herein schematically represented by GAM1 RNA, GAM2 RNA and GAM3 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40205] GAM2253 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2253 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2253 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2253 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40206] GAM2254 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of

GAM2254 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2254 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2254 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40207] GAM2255 RNA, herein schematically represented by GAM3 binds complementarily to a target binding site located in an untranslated region of GAM2255 target RNA, herein schematically represented by GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2255 target RNA, herein schematically represented by GAM3 TARGET RNA into GAM2255 target protein, herein schematically represented by GAM3 TARGET PROTEIN, both of Fig. 8.

[40208] It is appreciated that specific functions, and accordingly utilities, of GR3008 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3008 gene: GAM2253 target protein, GAM2254 target protein and GAM2255 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2253, GAM2254 and GAM2255

[40209] Fig. 16 further provides a conceptual description of novel bioinformatically

detected regulatory gene, referred to here as Genomic Record 3009(GR3009) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[40210] GR3009 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR3009 gene was detected is described hereinabove with reference to Figs. 6-15.

[40211] GR3009 gene encodes GR3009 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40212] GR3009 precursor RNA folds spatially, forming GR3009 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3009 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR3009 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40213] GR3009 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2259 precursor RNA and

GAM2260 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[40214] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2259 RNA and GAM2260 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40215] GAM2259 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2259 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2259 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2259 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40216] GAM2260 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2260 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2260 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2260 target protein, herein



schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40217] It is appreciated that specific functions, and accordingly utilities, of GR3009 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3009 gene: GAM2259 target protein and GAM2260 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2259 and GAM2260

[40218] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 3010 (GR3010) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[40219] GR3010 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR3010 gene was detected is described hereinabove with reference to Figs. 6-15.

[40220] GR3010 gene encodes GR3010 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40221] GR3010 precursor RNA folds spatially, forming GR3010 folded precursor

RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3010 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR3010 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40222] GR3010 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2263 precursor RNA, GAM2264 precursor RNA and GAM2265 precursor RNA, herein schematically represented by GAM1 PRECURSOR, GAM2 PRECURSOR and GAM3 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[40223] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2263 RNA, GAM2264 RNA and GAM2265 RNA respectively, herein schematically represented by GAM1 RNA, GAM2 RNA and GAM3 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40224] GAM2263 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of

GAM2263 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2263 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2263 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40225] GAM2264 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2264 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2264 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2264 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40226] GAM2265 RNA, herein schematically represented by GAM3 binds complementarily to a target binding site located in an untranslated region of GAM2265 target RNA, herein schematically represented by GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2265 target RNA, herein schematically represented by GAM3 TARGET RNA into GAM2265 target protein, herein schematically represented by GAM3 TARGET PROTEIN, both of Fig. 8.

[40227] It is appreciated that specific functions, and accordingly utilities, of GR3010 gene, herein designated GR GENE, correlate with, and may be deduced

from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3010 gene: GAM2263 target protein, GAM2264 target protein and GAM2265 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2263, GAM2264 and GAM2265

[40228] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 3011(GR3011) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[40229] GR3011 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR3011 gene was detected is described hereinabove with reference to Figs. 6-15.

[40230] GR3011 gene encodes GR3011 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40231] GR3011 precursor RNA folds spatially, forming GR3011 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3011 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as

hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR3011 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40232] GR3011 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2267 precursor RNA and GAM2268 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[40233] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2267 RNA and GAM2268 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40234] GAM2267 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2267 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2267 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2267 target protein, herein

schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40235] GAM2268 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2268 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2268 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2268 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40236] It is appreciated that specific functions, and accordingly utilities, of GR3011 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3011 gene: GAM2267 target protein and GAM2268 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2267 and GAM2268

[40237] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 3012 (GR3012) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[40238] GR3012 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR3012 gene was detected is described hereinabove with reference to Figs. 6-15.

[40239] GR3012 gene encodes GR3012 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40240] GR3012 precursor RNA folds spatially, forming GR3012 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3012 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR3012 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40241] GR3012 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2271 precursor RNA and GAM2272 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[40242] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in

length, GAM2271 RNA and GAM2272 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40243] GAM2271 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2271 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2271 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2271 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40244] GAM2272 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2272 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2272 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2272 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40245] It is appreciated that specific functions, and accordingly utilities, of GR3012 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3012 gene: GAM2271 target protein and GAM2272 target protein, herein schematically represented by



GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2271 and GAM2272

[40246] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 3013 (GR3013) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[40247] GR3013 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR3013 gene was detected is described hereinabove with reference to Figs. 6-15.

[40248] GR3013 gene encodes GR3013 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40249] GR3013 precursor RNA folds spatially, forming GR3013 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3013 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR3013 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

- [40250] GR3013 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2276 precursor RNA and GAM2277 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [40251] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2276 RNA and GAM2277 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.
- [40252] GAM2276 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2276 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2276 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2276 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.
- [40253] GAM2277 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2277 target RNA, herein schematically represented by GAM2 TARGET

RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2277 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2277 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40254] It is appreciated that specific functions, and accordingly utilities, of GR3013 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3013 gene: GAM2276 target protein and GAM2277 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2276 and GAM2277

[40255] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 3014 (GR3014) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[40256] GR3014 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR3014 gene was detected is described hereinabove with reference to Figs. 6-15.

[40257] GR3014 gene encodes GR3014 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40258] GR3014 precursor RNA folds spatially, forming GR3014 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3014 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR3014 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40259] GR3014 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2278 precursor RNA and GAM2279 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[40260] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2278 RNA and GAM2279 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40261] GAM2278 RNA, herein schematically represented by GAM1 binds

complimentarily to a target binding site located in an untranslated region of GAM2278 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2278 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2278 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40262] GAM2279 RNA, herein schematically represented by GAM2 binds complimentarily to a target binding site located in an untranslated region of GAM2279 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2279 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2279 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40263] It is appreciated that specific functions, and accordingly utilities, of GR3014 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3014 gene: GAM2278 target protein and GAM2279 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2278 and GAM2279

[40264] Fig. 16 further provides a conceptual description of novel bioinformatically

detected regulatory gene, referred to here as Genomic Record

3015(GR3015) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[40265] GR3015 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR3015 gene was detected is described hereinabove with reference to Figs. 6-15.

[40266] GR3015 gene encodes GR3015 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40267] GR3015 precursor RNA folds spatially, forming GR3015 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3015 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR3015 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40268] GR3015 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2301 precursor RNA,

GAM2302 precursor RNA and GAM2303 precursor RNA, herein schematically represented by GAM1 PRECURSOR, GAM2 PRECURSOR and GAM3 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[40269] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2301 RNA, GAM2302 RNA and GAM2303 RNA respectively, herein schematically represented by GAM1 RNA, GAM2 RNA and GAM3 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40270] GAM2301 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2301 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2301 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2301 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40271] GAM2302 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2302 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby

inhibiting translation of GAM2302 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2302 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40272] GAM2303 RNA, herein schematically represented by GAM3 binds complementarily to a target binding site located in an untranslated region of GAM2303 target RNA, herein schematically represented by GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2303 target RNA, herein schematically represented by GAM3 TARGET RNA into GAM2303 target protein, herein schematically represented by GAM3 TARGET PROTEIN, both of Fig. 8.

[40273] It is appreciated that specific functions, and accordingly utilities, of GR3015 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3015 gene: GAM2301 target protein, GAM2302 target protein and GAM2303 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2301, GAM2302 and GAM2303

[40274] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 3016(GR3016) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one



target gene, the function and utility of which at least one target gene is known in the art.

[40275] GR3016 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR3016 gene was detected is described hereinabove with reference to Figs. 6-15.

[40276] GR3016 gene encodes GR3016 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40277] GR3016 precursor RNA folds spatially, forming GR3016 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3016 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR3016 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40278] GR3016 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2310 precursor RNA and GAM2311 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to

## GAM PRECURSOR RNA of Fig. 8.

[40279] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2310 RNA and GAM2311 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40280] GAM2310 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2310 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2310 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2310 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40281] GAM2311 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2311 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2311 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2311 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40282] It is appreciated that specific functions, and accordingly utilities, of GR3016 gene, herein designated GR GENE, correlate with, and may be deduced

from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3016 gene: GAM2310 target protein and GAM2311 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2310 and GAM2311

[40283] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 3017(GR3017) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[40284] GR3017 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR3017 gene was detected is described hereinabove with reference to Figs. 6-15.

[40285] GR3017 gene encodes GR3017 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40286] GR3017 precursor RNA folds spatially, forming GR3017 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3017 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the

nucleotide sequence of GR3017 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40287] GR3017 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM2314 precursor RNA, GAM2315 precursor RNA, GAM2316 precursor RNA and GAM2317 precursor RNA, herein schematically represented by GAM1 PRECURSOR, GAM2 PRECURSOR, GAM3 PRECURSOR and GAM4 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[40288] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2314 RNA, GAM2315 RNA, GAM2316 RNA and GAM2317 RNA respectively, herein schematically represented by GAM1 RNA, GAM2 RNA, GAM3 RNA and GAM4 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40289] GAM2314 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2314 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2314 target RNA, herein schematically

represented by GAM1 TARGET RNA into GAM2314 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40290] GAM2315 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2315 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2315 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2315 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40291] GAM2316 RNA, herein schematically represented by GAM3 binds complementarily to a target binding site located in an untranslated region of GAM2316 target RNA, herein schematically represented by GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2316 target RNA, herein schematically represented by GAM3 TARGET RNA into GAM2316 target protein, herein schematically represented by GAM3 TARGET PROTEIN, both of Fig. 8.

[40292] GAM2317 RNA, herein schematically represented by GAM4 binds complementarily to a target binding site located in an untranslated region of GAM2317 target RNA, herein schematically represented by GAM4 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2317 target RNA, herein schematically

represented by GAM4 TARGET RNA into GAM2317 target protein, herein schematically represented by GAM4 TARGET PROTEIN, both of Fig. 8.

[40293] It is appreciated that specific functions, and accordingly utilities, of GR3017 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3017 gene: GAM2314 target protein, GAM2315 target protein, GAM2316 target protein and GAM2317 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2314, GAM2315, GAM2316 and GAM2317

[40294] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 3018(GR3018) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[40295] GR3018 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR3018 gene was detected is described hereinabove with reference to Figs. 6-15.

[40296] GR3018 gene encodes GR3018 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40297] GR3018 precursor RNA folds spatially, forming GR3018 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3018 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR3018 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40298] GR3018 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2318 precursor RNA and GAM2319 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[40299] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2318 RNA and GAM2319 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40300] GAM2318 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2318 target RNA, herein schematically represented by GAM1 TARGET

RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2318 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2318 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40301] GAM2319 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2319 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2319 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2319 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40302] It is appreciated that specific functions, and accordingly utilities, of GR3018 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3018 gene: GAM2318 target protein and GAM2319 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2318 and GAM2319

[40303] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 3019 (GR3019) gene, which encodes an operon-like cluster of novel micro



RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[40304] GR3019 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR3019 gene was detected is described hereinabove with reference to Figs. 6-15.

[40305] GR3019 gene encodes GR3019 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40306] GR3019 precursor RNA folds spatially, forming GR3019 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3019 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR3019 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40307] GR3019 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2327 precursor RNA and GAM2328 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM

precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[40308] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2327 RNA and GAM2328 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40309] GAM2327 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2327 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2327 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2327 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40310] GAM2328 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2328 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2328 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2328 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40311] It is appreciated that specific functions, and accordingly utilities, of GR3019

gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3019 gene: GAM2327 target protein and GAM2328 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2327 and GAM2328

[40312] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 3020(GR3020) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[40313] GR3020 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR3020 gene was detected is described hereinabove with reference to Figs. 6-15.

[40314] GR3020 gene encodes GR3020 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40315] GR3020 precursor RNA folds spatially, forming GR3020 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3020 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as

hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR3020 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40316] GR3020 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2335 precursor RNA and GAM2336 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[40317] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2335 RNA and GAM2336 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40318] GAM2335 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2335 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2335 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2335 target protein, herein

schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40319] GAM2336 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2336 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2336 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2336 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40320] It is appreciated that specific functions, and accordingly utilities, of GR3020 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3020 gene: GAM2335 target protein and GAM2336 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2335 and GAM2336

[40321] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 3021 (GR3021) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[40322] GR3021 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR3021 gene was detected is described hereinabove with reference to Figs. 6-15.

[40323] GR3021 gene encodes GR3021 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40324] GR3021 precursor RNA folds spatially, forming GR3021 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3021 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR3021 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40325] GR3021 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2351 precursor RNA and GAM2352 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[40326] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in

length, GAM2351 RNA and GAM2352 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40327] GAM2351 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2351 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2351 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2351 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40328] GAM2352 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2352 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2352 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2352 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40329] It is appreciated that specific functions, and accordingly utilities, of GR3021 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3021 gene: GAM2351 target protein and GAM2352 target protein, herein schematically represented by

GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2351 and GAM2352

[40330] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 3022(GR3022) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[40331] GR3022 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR3022 gene was detected is described hereinabove with reference to Figs. 6-15.

[40332] GR3022 gene encodes GR3022 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40333] GR3022 precursor RNA folds spatially, forming GR3022 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3022 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR3022 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half



thereof, as is well known in the art.

- [40334] GR3022 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2362 precursor RNA and GAM2363 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [40335] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2362 RNA and GAM2363 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.
- [40336] GAM2362 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2362 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2362 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2362 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.
- [40337] GAM2363 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2363 target RNA, herein schematically represented by GAM2 TARGET

RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2363 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2363 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40338] It is appreciated that specific functions, and accordingly utilities, of GR3022 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3022 gene: GAM2362 target protein and GAM2363 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2362 and GAM2363

[40339] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 3023 (GR3023) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[40340] GR3023 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR3023 gene was detected is described hereinabove with reference to Figs. 6-15.

[40341] GR3023 gene encodes GR3023 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40342] GR3023 precursor RNA folds spatially, forming GR3023 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3023 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR3023 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40343] GR3023 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2371 precursor RNA and GAM2372 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[40344] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2371 RNA and GAM2372 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40345] GAM2371 RNA, herein schematically represented by GAM1 binds

complimentarily to a target binding site located in an untranslated region of GAM2371 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2371 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2371 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40346] GAM2372 RNA, herein schematically represented by GAM2 binds complimentarily to a target binding site located in an untranslated region of GAM2372 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2372 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2372 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40347] It is appreciated that specific functions, and accordingly utilities, of GR3023 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3023 gene: GAM2371 target protein and GAM2372 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2371 and GAM2372

[40348] Fig. 16 further provides a conceptual description of novel bioinformatically

detected regulatory gene, referred to here as Genomic Record 3024(GR3024) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[40349] GR3024 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR3024 gene was detected is described hereinabove with reference to Figs. 6-15.

[40350] GR3024 gene encodes GR3024 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40351] GR3024 precursor RNA folds spatially, forming GR3024 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3024 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR3024 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40352] GR3024 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2385 precursor RNA and

GAM2386 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[40353] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2385 RNA and GAM2386 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40354] GAM2385 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2385 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2385 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2385 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40355] GAM2386 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2386 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2386 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2386 target protein, herein

schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40356] It is appreciated that specific functions, and accordingly utilities, of GR3024 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3024 gene: GAM2385 target protein and GAM2386 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2385 and GAM2386

[40357] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 3025 (GR3025) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[40358] GR3025 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR3025 gene was detected is described hereinabove with reference to Figs. 6-15.

[40359] GR3025 gene encodes GR3025 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40360] GR3025 precursor RNA folds spatially, forming GR3025 folded precursor

RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3025 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR3025 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40361] GR3025 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2393 precursor RNA and GAM2394 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[40362] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2393 RNA and GAM2394 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40363] GAM2393 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2393 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as



BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2393 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2393 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40364] GAM2394 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2394 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2394 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2394 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40365] It is appreciated that specific functions, and accordingly utilities, of GR3025 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3025 gene: GAM2393 target protein and GAM2394 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2393 and GAM2394

[40366] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 3026 (GR3026) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

[40367] GR3026 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR3026 gene was detected is described hereinabove with reference to Figs. 6-15.

[40368] GR3026 gene encodes GR3026 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40369] GR3026 precursor RNA folds spatially, forming GR3026 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3026 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR3026 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40370] GR3026 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2413 precursor RNA and GAM2414 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to

## GAM PRECURSOR RNA of Fig. 8.

[40371] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2413 RNA and GAM2414 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40372] GAM2413 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2413 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2413 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2413 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40373] GAM2414 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2414 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2414 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2414 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40374] It is appreciated that specific functions, and accordingly utilities, of GR3026 gene, herein designated GR GENE, correlate with, and may be deduced

from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3026 gene: GAM2413 target protein and GAM2414 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2413 and GAM2414

[40375] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 3027(GR3027) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[40376] GR3027 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR3027 gene was detected is described hereinabove with reference to Figs. 6-15.

[40377] GR3027 gene encodes GR3027 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40378] GR3027 precursor RNA folds spatially, forming GR3027 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3027 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the

nucleotide sequence of GR3027 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40379] GR3027 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2415 precursor RNA and GAM2416 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[40380] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2415 RNA and GAM2416 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40381] GAM2415 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2415 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2415 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2415 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40382] GAM2416 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2416 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2416 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2416 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40383] It is appreciated that specific functions, and accordingly utilities, of GR3027 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3027 gene: GAM2415 target protein and GAM2416 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2415 and GAM2416

[40384] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 3028 (GR3028) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[40385] GR3028 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which

GR3028 gene was detected is described hereinabove with reference to Figs. 6-15.

[40386] GR3028 gene encodes GR3028 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40387] GR3028 precursor RNA folds spatially, forming GR3028 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3028 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR3028 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40388] GR3028 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2422 precursor RNA and GAM2423 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[40389] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2422 RNA and GAM2423 RNA respectively, herein

schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40390] GAM2422 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2422 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2422 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2422 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40391] GAM2423 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2423 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2423 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2423 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40392] It is appreciated that specific functions, and accordingly utilities, of GR3028 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3028 gene: GAM2422 target protein and GAM2423 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The



function of these target genes is elaborated hereinabove with reference to GAM2422 and GAM2423

[40393] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 3029(GR3029) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[40394] GR3029 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR3029 gene was detected is described hereinabove with reference to Figs. 6-15.

[40395] GR3029 gene encodes GR3029 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40396] GR3029 precursor RNA folds spatially, forming GR3029 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3029 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR3029 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

- [40397] GR3029 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2424 precursor RNA and GAM2425 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [40398] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2424 RNA and GAM2425 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.
- [40399] GAM2424 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2424 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2424 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2424 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.
- [40400] GAM2425 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2425 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2425 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2425 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40401] It is appreciated that specific functions, and accordingly utilities, of GR3029 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3029 gene: GAM2424 target protein and GAM2425 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2424 and GAM2425

[40402] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 3030 (GR3030) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[40403] GR3030 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR3030 gene was detected is described hereinabove with reference to Figs. 6-15.

[40404] GR3030 gene encodes GR3030 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides

long.

[40405] GR3030 precursor RNA folds spatially, forming GR3030 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3030 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR3030 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40406] GR3030 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2426 precursor RNA and GAM2427 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[40407] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2426 RNA and GAM2427 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40408] GAM2426 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of

GAM2426 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2426 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2426 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40409] GAM2427 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2427 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2427 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2427 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40410] It is appreciated that specific functions, and accordingly utilities, of GR3030 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3030 gene: GAM2426 target protein and GAM2427 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2426 and GAM2427

[40411] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record

3031(GR3031) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[40412] GR3031 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR3031 gene was detected is described hereinabove with reference to Figs. 6-15.

[40413] GR3031 gene encodes GR3031 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40414] GR3031 precursor RNA folds spatially, forming GR3031 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3031 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR3031 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40415] GR3031 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2445 precursor RNA and GAM2446 precursor RNA, herein schematically represented by GAM1

PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[40416] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2445 RNA and GAM2446 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40417] GAM2445 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2445 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2445 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2445 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40418] GAM2446 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2446 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2446 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2446 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40419] It is appreciated that specific functions, and accordingly utilities, of GR3031 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3031 gene: GAM2445 target protein and GAM2446 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2445 and GAM2446

[40420] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 3032 (GR3032) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[40421] GR3032 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR3032 gene was detected is described hereinabove with reference to Figs. 6-15.

[40422] GR3032 gene encodes GR3032 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40423] GR3032 precursor RNA folds spatially, forming GR3032 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3032 folded precursor RNA, herein designated GR FOLDED



PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR3032 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40424] GR3032 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2452 precursor RNA and GAM2453 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[40425] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2452 RNA and GAM2453 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40426] GAM2452 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2452 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2452 target RNA, herein schematically

represented by GAM1 TARGET RNA into GAM2452 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40427] GAM2453 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2453 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2453 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2453 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40428] It is appreciated that specific functions, and accordingly utilities, of GR3032 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3032 gene: GAM2452 target protein and GAM2453 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2452 and GAM2453

[40429] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 3033 (GR3033) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[40430] GR3033 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR3033 gene was detected is described hereinabove with reference to Figs. 6-15.

[40431] GR3033 gene encodes GR3033 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40432] GR3033 precursor RNA folds spatially, forming GR3033 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3033 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR3033 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40433] GR3033 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2455 precursor RNA and GAM2456 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[40434] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX

of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2455 RNA and GAM2456 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40435] GAM2455 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2455 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2455 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2455 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40436] GAM2456 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2456 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2456 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2456 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40437] It is appreciated that specific functions, and accordingly utilities, of GR3033 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3033 gene: GAM2455 target

protein and GAM2456 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2455 and GAM2456

[40438] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 3034(GR3034) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[40439] GR3034 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR3034 gene was detected is described hereinabove with reference to Figs. 6-15.

[40440] GR3034 gene encodes GR3034 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40441] GR3034 precursor RNA folds spatially, forming GR3034 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3034 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR3034 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40442] GR3034 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2462 precursor RNA and GAM2463 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[40443] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2462 RNA and GAM2463 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40444] GAM2462 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2462 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2462 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2462 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40445] GAM2463 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of

GAM2463 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2463 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2463 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40446] It is appreciated that specific functions, and accordingly utilities, of GR3034 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3034 gene: GAM2462 target protein and GAM2463 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2462 and GAM2463

[40447] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 3035 (GR3035) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[40448] GR3035 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR3035 gene was detected is described hereinabove with reference to Figs. 6-15.

[40449] GR3035 gene encodes GR3035 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40450] GR3035 precursor RNA folds spatially, forming GR3035 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3035 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR3035 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40451] GR3035 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2466 precursor RNA and GAM2467 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[40452] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2466 RNA and GAM2467 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.



[40453] GAM2466 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2466 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2466 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2466 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40454] GAM2467 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2467 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2467 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2467 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40455] It is appreciated that specific functions, and accordingly utilities, of GR3035 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3035 gene: GAM2466 target protein and GAM2467 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2466 and GAM2467

- [40456] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 3036(GR3036) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [40457] GR3036 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR3036 gene was detected is described hereinabove with reference to Figs. 6-15.
- [40458] GR3036 gene encodes GR3036 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [40459] GR3036 precursor RNA folds spatially, forming GR3036 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3036 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR3036 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.
- [40460] GR3036 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into

at least 2 separate GAM precursor RNAs, GAM2473 precursor RNA and GAM2474 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[40461] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2473 RNA and GAM2474 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40462] GAM2473 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2473 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2473 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2473 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40463] GAM2474 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2474 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2474 target RNA, herein schematically

represented by GAM2 TARGET RNA into GAM2474 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40464] It is appreciated that specific functions, and accordingly utilities, of GR3036 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3036 gene: GAM2473 target protein and GAM2474 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2473 and GAM2474

[40465] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 3037 (GR3037) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[40466] GR3037 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR3037 gene was detected is described hereinabove with reference to Figs. 6-15.

[40467] GR3037 gene encodes GR3037 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40468] GR3037 precursor RNA folds spatially, forming GR3037 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3037 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR3037 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40469] GR3037 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2478 precursor RNA and GAM2479 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[40470] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2478 RNA and GAM2479 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40471] GAM2478 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2478 target RNA, herein schematically represented by GAM1 TARGET

RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2478 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2478 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40472] GAM2479 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2479 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2479 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2479 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40473] It is appreciated that specific functions, and accordingly utilities, of GR3037 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3037 gene: GAM2478 target protein and GAM2479 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2478 and GAM2479

[40474] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 3038(GR3038) gene, which encodes an operon-like cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[40475] GR3038 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR3038 gene was detected is described hereinabove with reference to Figs. 6-15.

[40476] GR3038 gene encodes GR3038 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40477] GR3038 precursor RNA folds spatially, forming GR3038 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3038 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR3038 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40478] GR3038 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2480 precursor RNA and GAM2481 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM

precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[40479] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2480 RNA and GAM2481 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40480] GAM2480 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2480 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2480 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2480 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40481] GAM2481 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2481 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2481 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2481 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40482] It is appreciated that specific functions, and accordingly utilities, of GR3038



gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3038 gene: GAM2480 target protein and GAM2481 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2480 and GAM2481

[40483] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 3039(GR3039) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[40484] GR3039 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR3039 gene was detected is described hereinabove with reference to Figs. 6-15.

[40485] GR3039 gene encodes GR3039 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40486] GR3039 precursor RNA folds spatially, forming GR3039 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3039 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as

hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR3039 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40487] GR3039 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2484 precursor RNA and GAM2485 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[40488] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2484 RNA and GAM2485 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40489] GAM2484 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2484 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2484 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2484 target protein, herein

schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40490] GAM2485 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2485 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2485 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2485 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40491] It is appreciated that specific functions, and accordingly utilities, of GR3039 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3039 gene: GAM2484 target protein and GAM2485 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2484 and GAM2485

[40492] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 3040 (GR3040) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[40493] GR3040 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR3040 gene was detected is described hereinabove with reference to Figs. 6-15.

[40494] GR3040 gene encodes GR3040 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40495] GR3040 precursor RNA folds spatially, forming GR3040 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3040 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR3040 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40496] GR3040 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2487 precursor RNA and GAM2488 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[40497] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in

length, GAM2487 RNA and GAM2488 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40498] GAM2487 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2487 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2487 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2487 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40499] GAM2488 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2488 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2488 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2488 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40500] It is appreciated that specific functions, and accordingly utilities, of GR3040 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3040 gene: GAM2487 target protein and GAM2488 target protein, herein schematically represented by

GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2487 and GAM2488

[40501] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 3041 (GR3041) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[40502] GR3041 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR3041 gene was detected is described hereinabove with reference to Figs. 6-15.

[40503] GR3041 gene encodes GR3041 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40504] GR3041 precursor RNA folds spatially, forming GR3041 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3041 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR3041 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

- [40505] GR3041 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2493 precursor RNA and GAM2494 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [40506] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2493 RNA and GAM2494 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.
- [40507] GAM2493 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2493 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2493 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2493 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.
- [40508] GAM2494 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2494 target RNA, herein schematically represented by GAM2 TARGET

RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2494 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2494 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40509] It is appreciated that specific functions, and accordingly utilities, of GR3041 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3041 gene: GAM2493 target protein and GAM2494 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2493 and GAM2494

[40510] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 3042 (GR3042) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[40511] GR3042 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR3042 gene was detected is described hereinabove with reference to Figs. 6-15.

[40512] GR3042 gene encodes GR3042 precursor RNA, herein designated GR



PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40513] GR3042 precursor RNA folds spatially, forming GR3042 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3042 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR3042 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40514] GR3042 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2513 precursor RNA and GAM2514 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[40515] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2513 RNA and GAM2514 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40516] GAM2513 RNA, herein schematically represented by GAM1 binds

complimentarily to a target binding site located in an untranslated region of GAM2513 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2513 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2513 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40517] GAM2514 RNA, herein schematically represented by GAM2 binds complimentarily to a target binding site located in an untranslated region of GAM2514 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2514 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2514 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40518] It is appreciated that specific functions, and accordingly utilities, of GR3042 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3042 gene: GAM2513 target protein and GAM2514 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2513 and GAM2514

[40519] Fig. 16 further provides a conceptual description of novel bioinformatically

detected regulatory gene, referred to here as Genomic Record

3043(GR3043) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[40520] GR3043 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR3043 gene was detected is described hereinabove with reference to Figs. 6-15.

[40521] GR3043 gene encodes GR3043 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40522] GR3043 precursor RNA folds spatially, forming GR3043 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3043 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR3043 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40523] GR3043 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2523 precursor RNA and

GAM2524 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[40524] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2523 RNA and GAM2524 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40525] GAM2523 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2523 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2523 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2523 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40526] GAM2524 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2524 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2524 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2524 target protein, herein

schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40527] It is appreciated that specific functions, and accordingly utilities, of GR3043 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3043 gene: GAM2523 target protein and GAM2524 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2523 and GAM2524

[40528] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 3044 (GR3044) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[40529] GR3044 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR3044 gene was detected is described hereinabove with reference to Figs. 6-15.

[40530] GR3044 gene encodes GR3044 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40531] GR3044 precursor RNA folds spatially, forming GR3044 folded precursor

RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3044 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR3044 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40532] GR3044 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2532 precursor RNA and GAM2533 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[40533] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2532 RNA and GAM2533 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40534] GAM2532 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2532 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2532 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2532 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40535] GAM2533 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2533 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2533 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2533 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40536] It is appreciated that specific functions, and accordingly utilities, of GR3044 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3044 gene: GAM2532 target protein and GAM2533 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2532 and GAM2533

[40537] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 3045 (GR3045) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

[40538] GR3045 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR3045 gene was detected is described hereinabove with reference to Figs. 6-15.

[40539] GR3045 gene encodes GR3045 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40540] GR3045 precursor RNA folds spatially, forming GR3045 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3045 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR3045 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40541] GR3045 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2535 precursor RNA and GAM2536 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to



## GAM PRECURSOR RNA of Fig. 8.

[40542] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2535 RNA and GAM2536 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40543] GAM2535 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2535 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2535 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2535 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40544] GAM2536 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2536 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2536 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2536 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40545] It is appreciated that specific functions, and accordingly utilities, of GR3045 gene, herein designated GR GENE, correlate with, and may be deduced

from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3045 gene: GAM2535 target protein and GAM2536 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2535 and GAM2536

[40546] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 3046(GR3046) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[40547] GR3046 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR3046 gene was detected is described hereinabove with reference to Figs. 6-15.

[40548] GR3046 gene encodes GR3046 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40549] GR3046 precursor RNA folds spatially, forming GR3046 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3046 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the

nucleotide sequence of GR3046 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40550] GR3046 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2541 precursor RNA and GAM2542 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[40551] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2541 RNA and GAM2542 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40552] GAM2541 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2541 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2541 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2541 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40553] GAM2542 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2542 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2542 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2542 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40554] It is appreciated that specific functions, and accordingly utilities, of GR3046 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3046 gene: GAM2541 target protein and GAM2542 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2541 and GAM2542

[40555] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 3047 (GR3047) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[40556] GR3047 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which

GR3047 gene was detected is described hereinabove with reference to Figs. 6-15.

[40557] GR3047 gene encodes GR3047 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40558] GR3047 precursor RNA folds spatially, forming GR3047 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3047 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR3047 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40559] GR3047 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2543 precursor RNA, GAM2544 precursor RNA and GAM2545 precursor RNA, herein schematically represented by GAM1 PRECURSOR, GAM2 PRECURSOR and GAM3 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[40560] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in

length, GAM2543 RNA, GAM2544 RNA and GAM2545 RNA respectively, herein schematically represented by GAM1 RNA, GAM2 RNA and GAM3 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40561] GAM2543 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2543 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2543 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2543 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40562] GAM2544 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2544 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2544 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2544 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40563] GAM2545 RNA, herein schematically represented by GAM3 binds complementarily to a target binding site located in an untranslated region of GAM2545 target RNA, herein schematically represented by GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2545 target RNA, herein schematically represented by GAM3 TARGET RNA into GAM2545 target protein, herein schematically represented by GAM3 TARGET PROTEIN, both of Fig. 8.

[40564] It is appreciated that specific functions, and accordingly utilities, of GR3047 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3047 gene: GAM2543 target protein, GAM2544 target protein and GAM2545 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2543, GAM2544 and GAM2545

[40565] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 3048(GR3048) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[40566] GR3048 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR3048 gene was detected is described hereinabove with reference to Figs. 6-15.

[40567] GR3048 gene encodes GR3048 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40568] GR3048 precursor RNA folds spatially, forming GR3048 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3048 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR3048 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40569] GR3048 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2550 precursor RNA and GAM2551 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[40570] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2550 RNA and GAM2551 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40571] GAM2550 RNA, herein schematically represented by GAM1 binds



complimentarily to a target binding site located in an untranslated region of GAM2550 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2550 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2550 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40572] GAM2551 RNA, herein schematically represented by GAM2 binds complimentarily to a target binding site located in an untranslated region of GAM2551 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2551 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2551 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40573] It is appreciated that specific functions, and accordingly utilities, of GR3048 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3048 gene: GAM2550 target protein and GAM2551 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2550 and GAM2551

[40574] Fig. 16 further provides a conceptual description of novel bioinformatically

detected regulatory gene, referred to here as Genomic Record 3049(GR3049) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[40575] GR3049 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR3049 gene was detected is described hereinabove with reference to Figs. 6-15.

[40576] GR3049 gene encodes GR3049 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40577] GR3049 precursor RNA folds spatially, forming GR3049 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3049 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR3049 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40578] GR3049 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2555 precursor RNA and

GAM2556 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[40579] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2555 RNA and GAM2556 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40580] GAM2555 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2555 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2555 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2555 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40581] GAM2556 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2556 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2556 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2556 target protein, herein

schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40582] It is appreciated that specific functions, and accordingly utilities, of GR3049 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3049 gene: GAM2555 target protein and GAM2556 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2555 and GAM2556

[40583] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 3050 (GR3050) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[40584] GR3050 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR3050 gene was detected is described hereinabove with reference to Figs. 6-15.

[40585] GR3050 gene encodes GR3050 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40586] GR3050 precursor RNA folds spatially, forming GR3050 folded precursor

RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3050 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR3050 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40587] GR3050 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2562 precursor RNA and GAM2563 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[40588] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2562 RNA and GAM2563 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40589] GAM2562 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2562 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2562 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2562 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40590] GAM2563 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2563 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2563 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2563 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40591] It is appreciated that specific functions, and accordingly utilities, of GR3050 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3050 gene: GAM2562 target protein and GAM2563 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2562 and GAM2563

[40592] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 3051 (GR3051) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

[40593] GR3051 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR3051 gene was detected is described hereinabove with reference to Figs. 6-15.

[40594] GR3051 gene encodes GR3051 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40595] GR3051 precursor RNA folds spatially, forming GR3051 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3051 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR3051 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40596] GR3051 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2575 precursor RNA and GAM2576 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to

GAM PRECURSOR RNA of Fig. 8.

[40597] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2575 RNA and GAM2576 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40598] GAM2575 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2575 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2575 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2575 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40599] GAM2576 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2576 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2576 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2576 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40600] It is appreciated that specific functions, and accordingly utilities, of GR3051 gene, herein designated GR GENE, correlate with, and may be deduced



from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3051 gene: GAM2575 target protein and GAM2576 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2575 and GAM2576

[40601] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 3052(GR3052) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[40602] GR3052 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR3052 gene was detected is described hereinabove with reference to Figs. 6-15.

[40603] GR3052 gene encodes GR3052 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40604] GR3052 precursor RNA folds spatially, forming GR3052 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3052 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the

nucleotide sequence of GR3052 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

- [40605] GR3052 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2582 precursor RNA and GAM2583 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [40606] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2582 RNA and GAM2583 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.
- [40607] GAM2582 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2582 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2582 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2582 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40608] GAM2583 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2583 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2583 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2583 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40609] It is appreciated that specific functions, and accordingly utilities, of GR3052 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3052 gene: GAM2582 target protein and GAM2583 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2582 and GAM2583

[40610] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 3053 (GR3053) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[40611] GR3053 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which

GR3053 gene was detected is described hereinabove with reference to Figs. 6-15.

[40612] GR3053 gene encodes GR3053 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40613] GR3053 precursor RNA folds spatially, forming GR3053 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3053 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR3053 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40614] GR3053 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2584 precursor RNA and GAM2585 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[40615] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2584 RNA and GAM2585 RNA respectively, herein

schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40616] GAM2584 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2584 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2584 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2584 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40617] GAM2585 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2585 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2585 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2585 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40618] It is appreciated that specific functions, and accordingly utilities, of GR3053 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3053 gene: GAM2584 target protein and GAM2585 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The

function of these target genes is elaborated hereinabove with reference to GAM2584 and GAM2585

- [40619] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 3054(GR3054) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [40620] GR3054 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR3054 gene was detected is described hereinabove with reference to Figs. 6-15.
- [40621] GR3054 gene encodes GR3054 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [40622] GR3054 precursor RNA folds spatially, forming GR3054 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3054 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR3054 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

- [40623] GR3054 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2586 precursor RNA, GAM2587 precursor RNA and GAM2588 precursor RNA, herein schematically represented by GAM1 PRECURSOR, GAM2 PRECURSOR and GAM3 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [40624] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2586 RNA, GAM2587 RNA and GAM2588 RNA respectively, herein schematically represented by GAM1 RNA, GAM2 RNA and GAM3 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.
- [40625] GAM2586 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2586 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2586 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2586 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.
- [40626] GAM2587 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of

GAM2587 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2587 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2587 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40627] GAM2588 RNA, herein schematically represented by GAM3 binds complementarily to a target binding site located in an untranslated region of GAM2588 target RNA, herein schematically represented by GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2588 target RNA, herein schematically represented by GAM3 TARGET RNA into GAM2588 target protein, herein schematically represented by GAM3 TARGET PROTEIN, both of Fig. 8.

[40628] It is appreciated that specific functions, and accordingly utilities, of GR3054 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3054 gene: GAM2586 target protein, GAM2587 target protein and GAM2588 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2586, GAM2587 and GAM2588

[40629] Fig. 16 further provides a conceptual description of novel bioinformatically



detected regulatory gene, referred to here as Genomic Record 3055(GR3055) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[40630] GR3055 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR3055 gene was detected is described hereinabove with reference to Figs. 6-15.

[40631] GR3055 gene encodes GR3055 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40632] GR3055 precursor RNA folds spatially, forming GR3055 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3055 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR3055 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40633] GR3055 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2591 precursor RNA and

GAM2592 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[40634] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2591 RNA and GAM2592 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40635] GAM2591 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2591 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2591 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2591 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40636] GAM2592 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2592 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2592 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2592 target protein, herein

schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40637] It is appreciated that specific functions, and accordingly utilities, of GR3055 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3055 gene: GAM2591 target protein and GAM2592 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2591 and GAM2592

[40638] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 3056 (GR3056) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[40639] GR3056 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR3056 gene was detected is described hereinabove with reference to Figs. 6-15.

[40640] GR3056 gene encodes GR3056 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40641] GR3056 precursor RNA folds spatially, forming GR3056 folded precursor

RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3056 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR3056 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40642] GR3056 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2606 precursor RNA and GAM2607 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[40643] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2606 RNA and GAM2607 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40644] GAM2606 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2606 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2606 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2606 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40645] GAM2607 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2607 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2607 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2607 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40646] It is appreciated that specific functions, and accordingly utilities, of GR3056 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3056 gene: GAM2606 target protein and GAM2607 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2606 and GAM2607

[40647] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 3057 (GR3057) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

[40648] GR3057 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR3057 gene was detected is described hereinabove with reference to Figs. 6-15.

[40649] GR3057 gene encodes GR3057 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40650] GR3057 precursor RNA folds spatially, forming GR3057 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3057 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR3057 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40651] GR3057 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2608 precursor RNA and GAM2609 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to

GAM PRECURSOR RNA of Fig. 8.

[40652] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2608 RNA and GAM2609 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40653] GAM2608 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2608 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2608 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2608 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40654] GAM2609 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2609 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2609 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2609 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40655] It is appreciated that specific functions, and accordingly utilities, of GR3057 gene, herein designated GR GENE, correlate with, and may be deduced

from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3057 gene: GAM2608 target protein and GAM2609 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2608 and GAM2609

[40656] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 3058 (GR3058) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[40657] GR3058 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR3058 gene was detected is described hereinabove with reference to Figs. 6-15.

[40658] GR3058 gene encodes GR3058 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40659] GR3058 precursor RNA folds spatially, forming GR3058 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3058 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the



nucleotide sequence of GR3058 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

- [40660] GR3058 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2618 precursor RNA and GAM2619 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [40661] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2618 RNA and GAM2619 RNA respectively, herein schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.
- [40662] GAM2618 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2618 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2618 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2618 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40663] GAM2619 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2619 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2619 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2619 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40664] It is appreciated that specific functions, and accordingly utilities, of GR3058 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3058 gene: GAM2618 target protein and GAM2619 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2618 and GAM2619

[40665] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 3059 (GR3059) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

[40666] GR3059 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which

GR3059 gene was detected is described hereinabove with reference to Figs. 6-15.

[40667] GR3059 gene encodes GR3059 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.

[40668] GR3059 precursor RNA folds spatially, forming GR3059 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3059 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR3059 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

[40669] GR3059 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2623 precursor RNA and GAM2624 precursor RNA, herein schematically represented by GAM1 PRECURSOR and GAM2 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.

[40670] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2623 RNA and GAM2624 RNA respectively, herein

schematically represented by GAM1 RNA and GAM2 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

[40671] GAM2623 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2623 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2623 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2623 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.

[40672] GAM2624 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of GAM2624 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2624 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2624 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40673] It is appreciated that specific functions, and accordingly utilities, of GR3059 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3059 gene: GAM2623 target protein and GAM2624 target protein, herein schematically represented by GAM1 TARGET PROTEIN and GAM TARGET PROTEIN respectively. The

function of these target genes is elaborated hereinabove with reference to GAM2623 and GAM2624

- [40674] Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 3060(GR3060) gene, which encodes an operon-like cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.
- [40675] GR3060 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR3060 gene was detected is described hereinabove with reference to Figs. 6-15.
- [40676] GR3060 gene encodes GR3060 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long.
- [40677] GR3060 precursor RNA folds spatially, forming GR3060 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR3060 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, comprises a plurality of what is known in the art as hairpin structures. These hairpin structures are due to the fact that the nucleotide sequence of GR3060 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

- [40678] GR3060 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM2633 precursor RNA, GAM2634 precursor RNA, GAM2635 precursor RNA and GAM2636 precursor RNA, herein schematically represented by GAM1 PRECURSOR, GAM2 PRECURSOR, GAM3 PRECURSOR and GAM4 PRECURSOR respectively, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM PRECURSOR RNA of Fig. 8.
- [40679] The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2633 RNA, GAM2634 RNA, GAM2635 RNA and GAM2636 RNA respectively, herein schematically represented by GAM1 RNA, GAM2 RNA, GAM3 RNA and GAM4 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.
- [40680] GAM2633 RNA, herein schematically represented by GAM1 binds complementarily to a target binding site located in an untranslated region of GAM2633 target RNA, herein schematically represented by GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2633 target RNA, herein schematically represented by GAM1 TARGET RNA into GAM2633 target protein, herein schematically represented by GAM1 TARGET PROTEIN, both of Fig. 8.
- [40681] GAM2634 RNA, herein schematically represented by GAM2 binds complementarily to a target binding site located in an untranslated region of

GAM2634 target RNA, herein schematically represented by GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2634 target RNA, herein schematically represented by GAM2 TARGET RNA into GAM2634 target protein, herein schematically represented by GAM2 TARGET PROTEIN, both of Fig. 8.

[40682] GAM2635 RNA, herein schematically represented by GAM3 binds complementarily to a target binding site located in an untranslated region of GAM2635 target RNA, herein schematically represented by GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2635 target RNA, herein schematically represented by GAM3 TARGET RNA into GAM2635 target protein, herein schematically represented by GAM3 TARGET PROTEIN, both of Fig. 8.

[40683] GAM2636 RNA, herein schematically represented by GAM4 binds complementarily to a target binding site located in an untranslated region of GAM2636 target RNA, herein schematically represented by GAM4 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2636 target RNA, herein schematically represented by GAM4 TARGET RNA into GAM2636 target protein, herein schematically represented by GAM4 TARGET PROTEIN, both of Fig. 8.

[40684] It is appreciated that specific functions, and accordingly utilities, of GR3060 gene, herein designated GR GENE, correlate with, and may be deduced

from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the operon-like cluster of GR3060 gene: GAM2633 target protein, GAM2634 target protein, GAM2635 target protein and GAM2636 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM TARGET PROTEIN respectively. The function of these target genes is elaborated hereinabove with reference to GAM2633, GAM2634, GAM2635 and GAM2636.

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[40686] It is appreciated by persons skilled in the art that the present invention is not limited by what has been particularly shown and described hereinabove.

Rather the scope of the present invention includes both combinations and subcombinations of the various features described hereinabove as well as variations and modifications which would occur to persons skilled in the art upon reading the specifications and which are not in the prior art.

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